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197199

From: Whiteman, Brian
Sent: Tuesday, August 01, 2006 9:55 AM
To: STIC-Biotech/ChemLib
Subject: seq search

09966724

SEQ ID NO: 2

- 1) commercial databases
- 2) issued us patents and published us patent applications

oligo search SEQ ID NO: 2

- 1) commercial databases
 - 2) issued us patents and published us patent applications
- limit length to oligos with 5-500 nucleotides of SEQ ID NO: 2
please print first 45 hits

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Brian Whiteman
Remsen, 2D14
mail box 2C18
Patent Examiner- Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

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78544

2-491 AA
NA

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

✓ Other CGP

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 12:43:11 ; Search time 615 Seconds
(without alignments)
7216.659 Million cell updates/sec

Title: US-09-966-724B-2

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2372	100.0	2372	US-07-903-103-1	Sequence 1, Appl1
2	2372	100.0	2372	US-08-044-619A-1	Sequence 1, Appl1
3	2372	100.0	2372	US-08-283-911-1	Sequence 1, Appl1
4	2372	100.0	2372	US-08-245-500A-2	Sequence 2, Appl1
5	2372	100.0	2372	US-08-390-546-2	Sequence 2, Appl1
6	2372	100.0	2372	US-08-390-479A-2	Sequence 2, Appl1
7	2372	100.0	2372	US-08-557-393-2	Sequence 2, Appl1
8	2372	100.0	2372	US-08-390-516C-2	Sequence 2, Appl1
9	2372	100.0	2372	US-08-390-517A-2	Sequence 2, Appl1
10	2372	100.0	2372	US-08-390-515A-2	Sequence 2, Appl1
11	2372	100.0	2372	US-08-801-718-2	Sequence 2, Appl1
12	2372	100.0	2372	US-09-073-567-1	Sequence 1, Appl1
13	2372	100.0	2372	US-09-280-805-1	Sequence 1, Appl1
14	2372	100.0	2372	US-09-048-810-1	Sequence 1, Appl1
15	2372	100.0	2372	US-09-170-159A-2	Sequence 2, Appl1
16	2372	100.0	2372	US-09-480-718-43	Sequence 43, Appl1
17	2372	100.0	2372	US-09-541-848-1	Sequence 1, Appl1
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ALIGNMENTS

RESULT 1
US-07-903-103-1
; Sequence 1, Application US/07903103
; Patent No. 5411860
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,103
; FILING DATE: 19920623
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107,40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-07-903-103-1

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-08-044-619A-1

Sequence 1, Application US/08044619A

Patent No. 5420263

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY

APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MD2 GENE IN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G ST., N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/044,619A

FILING DATE: 07-APR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/903,103

FILING DATE: 23-JUN-1992

APPLICATION NUMBER: US 07/867,840

FILING DATE: 07-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107, 40148

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

TELEX: 197430 BMB UT

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-044-619A-1

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1501 CATCAACTTCTAATGATGATTTATTTATGACAGCAAGAAAGATGTAAGAGTTGAAA 1560
QY 1561 AAGAAACCCAGAGCAAAAGAGAGTGTGAAATCTAGTTGGCCCTTATATGCTTGAAC 1620
DB 1561 AAGAAACCCAGAGCAAAAGAGAGTGTGAAATCTAGTTGGCCCTTATATGCTTGAAC 1620
QY 1621 CTGTGTATTTGTCAGAGTGCACCTAAAAATGTTGCAATGTCATGAGCAAGAGAC 1680
DB 1621 CTGTGTATTTGTCAGAGTGCACCTAAAAATGTTGCAATGTCATGAGCAAGAGAC 1680
QY 1681 ATCTTATGCTGCTTATACATGTCGAAAGAGCTTAAAGAAAGATTAAGCCCTGCCAG 1740
DB 1681 ATCTTATGCTGCTTATACATGTCGAAAGAGCTTAAAGAAAGATTAAGCCCTGCCAG 1740
QY 1741 TATGTAGCAACCAATTCAGAAATGATGTCGTAATTTCCCTAGTGTGACCTGTCAT 1800
DB 1741 TATGTAGCAACCAATTCAGAAATGATGTCGTAATTTCCCTAGTGTGACCTGTCAT 1800
QY 1801 AAGAGATTAATATTTCTAATCTATATACTCTAGAAATTTGAGACAACCTGAATTTAT 1860
DB 1801 AAGAGATTAATATTTCTAATCTATATACTCTAGAAATTTGAGACAACCTGAATTTAT 1860
QY 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920
DB 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920

QY 1921 TGACCTACTTGTGTAGTGAATAGTGAATCTTACTATTAATTTGACTGTGATATGACT 1980
DB 1921 TGACCTACTTGTGTAGTGAATAGTGAATCTTACTATTAATTTGACTGTGATATGACT 1980
QY 1981 CATCTTTACCAACCACTCTTAATTTTAATTAATTAATTTTACTGCTGTCTTAATGAGA 2040
DB 1981 CATCTTTACCAACCACTCTTAATTTTAATTAATTTTACTGCTGTCTTAATGAGA 2040
QY 2041 TTTGTTTTTTTTTTCTTAATTAATGATATAGATTAATTAATTTTATTTTATTTT 2100
DB 2041 TTTGTTTTTTTTTTCTTAATTAATGATATAGATTAATTAATTTTATTTTATTTT 2100
QY 2101 AGACGAGTCTGTCTGTATACCAAGCTGAGAGTGCAGTGGGATCTTGCTCAGCA 2160
DB 2101 AGACGAGTCTGTCTGTATACCAAGCTGAGAGTGCAGTGGGATCTTGCTCAGCA 2160
QY 2161 AGCTGCTCCCTCCCGGGTTCGACCAATTCCTGCTCAGCTCCCAATTAAGCTTGGCC 2220
DB 2161 AGCTGCTCCCTCCCGGGTTCGACCAATTCCTGCTCAGCTCCCAATTAAGCTTGGCC 2220
QY 2221 TACAGTATCTGCCACACACACCTGGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
DB 2221 TACAGTATCTGCCACACACACCTGGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
QY 2281 ACCGTGTTAGCAGAGATGATCTGATCTCTGACCTGTGATCCGCCACCTCGGCTCC 2340
DB 2281 ACCGTGTTAGCAGAGATGATGATCTCTGACCTGTGATCCGCCACCTCGGCTCC 2340
QY 2341 CAAGTGTGGGATTTACAGCATGAGCCACCG 2372
DB 2341 CAAGTGTGGGATTTACAGCATGAGCCACCG 2372

RESULT 3
US-08-283-911-1
; Sequence 1, Application US/08283911
; Patent No. 5519118
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDX2 GENE IN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,911
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107,40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBWB DT
; INFORMATION FOR SEQ ID NO: 1:
;

SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-283-911-1

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTCTTCTGGGCGCTGTGTGGCCCTGTGTGTGCGAAAGATGGA 60
DB 1 GCACCGCGGAGCTTGGCTCTTCTGGGCGCTGTGTGGCCCTGTGTGTGCGAAAGATGGA 60
QY 61 GCAGAGAGCGGAGCCCGAGGGGCGCCGGAACCTCTGACCGAGATCCTGCTGCTTTGG 120
DB 61 GCAGAGAGCGGAGCCCGAGGGGCGCCGGAACCTCTGACCGAGATCCTGCTGCTTTGG 120
QY 121 CAGCCGAGAGACCGTCCCTCCCGGATTAGTCGACGAGCGCCAGTGCCTGGCCCG 180
DB 121 CAGCCGAGAGACCGTCCCTCCCGGATTAGTCGACGAGCGCCAGTGCCTGGCCCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCCAGGGGCTGTGCTTCCGAGTATGATGCCCGTG 240
DB 181 GAGAGTGAATGATCCCGAGGCGCCAGGGGCTGTGCTTCCGAGTATGATGCCCGTG 240
QY 241 AAGGAAACTGGGGAGTCTTGAGGGACCCCGACTCCAAGCGGAAAAACCCGGATGTGA 300
DB 241 AAGGAAACTGGGGAGTCTTGAGGGACCCCGACTCCAAGCGGAAAAACCCGGATGTGA 300
QY 301 GGAGGAGCGCAATGTGCAATACCAATGTCTGTACTGTATGATGTGTGTGAACCACT 360
DB 301 GGAGGAGCGCAATGTGCAATACCAATGTCTGTACTGTATGATGTGTGTGAACCACT 360
QY 361 CACAGATTCAGCTTGGAGAACAGAGACCCTGGTTAGACCAAGGCCATTGCTTTGAAGT 420
DB 361 CACAGATTCAGCTTGGAGAACAGAGACCCTGGTTAGACCAAGGCCATTGCTTTGAAGT 420
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DB 421 TATTTAAAGTCTGTGTGTGCAAAAAAGACATTATATCTATGAAGAAGTTCTTTTATC 480
QY 481 TTGGCCAGATATATATGATCTTAAACGATTTATATGATGAAGAACAAATATTTATAT 540
DB 481 TTGGCCAGATATATATGATCTTAAACGATTTATATGATGAAGAACAAATATTTATAT 540
QY 541 GTTCAATGATCTTCTAGAGAGATTTGTGGCGTGCAGACTTCTGTGAAAGAGACACA 600
DB 541 GTTCAATGATCTTCTAGAGAGATTTGTGGCGTGCAGACTTCTGTGAAAGAGACACA 600
QY 601 GGAATATATATACCATGATCTTACAGGAACCTGTAGTATCAATCAGCAGATCATCGG 660
DB 601 GGAATATATATACCATGATCTTACAGGAACCTGTAGTATCAATCAGCAGATCATCGG 660
QY 661 ACTCAGGTATCATCTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGATGATCAAAAG 720
DB 661 ACTCAGGTATCATCTGTGAGTGAAGAACAGGTGTCACTTGAAGTGGAGATGATCAAAAG 720
QY 721 ACCCTGTACAGAGCTTCAAGAAAGAAACCTTCACTTCACTTTGGTTTCTAGACAT 780
DB 721 ACCCTGTACAGAGCTTCAAGAAAGAAACCTTCACTTCACTTTGGTTTCTAGACAT 780

QY 781 CTACCTCATCTGAAGAGAGCAATTAGTGAACAGAGAAATTCAGATGATATCTG 840
DB 781 CTACCTCATCTGAAGAGAGCAATTAGTGAACAGAGAAATTCAGATGATATCTG 840
QY 841 GTGAACGACAAAGAAACCCCAAAATCTGATAGTATTTCCCTTCCCTTGTGATAAGCC 900
DB 841 GTGAACGACAAAGAAACCCCAAAATCTGATAGTATTTCCCTTCCCTTGTGATAAGCC 900
QY 901 TGGCTGTGTGTATATAGGAGATATGTTGTGAAGAAAGCACTAGCAAGTAACTACAG 960
DB 901 TGGCTGTGTGTATATAGGAGATATGTTGTGAAGAAAGCACTAGCAAGTAACTACAG 960
QY 961 GGAACGCATCGAATCCGGAATCTTGATGCTGTGTATGTAACAATTGAGGATTTGGTGG 1020
DB 961 GGAACGCATCGAATCCGGAATCTTGATGCTGTGTATGTAACAATTGAGGATTTGGTGG 1020
QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTATGATAGTAAATTTGAAGTTGAATCTTCGACTCAG 1080
DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTATGATAGTAAATTTGAAGTTGAATCTTCGACTCAG 1080
QY 1081 AAGATTATAGCTTTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGATATATC 1140
DB 1081 AAGATTATAGCTTTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGATATATC 1140
QY 1141 AAGTTATCTGTATCAGGAGGAGAGATGATACAGATTCATTGGAAGAACTCTGAAA 1200
DB 1141 AAGTTATCTGTATCAGGAGGAGAGATGATACAGATTCATTGGAAGAACTCTGAAA 1200
QY 1201 TTTCTTACTGACTATTTGGAATGCACTTCATGCAATGAATGAATCCCTCCCTCCAT 1260
DB 1201 TTTCTTACTGACTATTTGGAATGCACTTCATGCAATGAATGAATCCCTCCCTCCAT 1260
QY 1261 CACATTGCAACAGATGTGTGGCCCTTCTGTAGAAATTTGGCTTCCGTAAGATAAAGGAAAG 1320
DB 1261 CACATTGCAACAGATGTGTGGCCCTTCTGTAGAAATTTGGCTTCCGTAAGATAAAGGAAAG 1320
QY 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGCTGAAGAGGCT 1380
DB 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGCTGAAGAGGCT 1380
QY 1381 TTGATGTCCTGATTTGTAATAAAGCTATGTGAATGATCCAGAGGTCATGTGTGAGG 1440
DB 1381 TTGATGTCCTGATTTGTAATAAAGCTATGTGAATGATCCAGAGGTCATGTGTGAGG 1440
QY 1441 AAAATGATGATTAATTAACAAGCTTCACAATCAACAAGAAAGTGAAGCTATTTCTCAGC 1500
DB 1441 AAAATGATGATTAATTAACAAGCTTCACAATCAACAAGAAAGTGAAGCTATTTCTCAGC 1500
QY 1501 CATCAACTTCTAGTACATTTATTTATAGCAGCCAAAGAAATGTGAAGAAGTTGAAAGG 1560
DB 1501 CATCAACTTCTAGTACATTTATTTATAGCAGCCAAAGAAATGTGAAGAAGTTGAAAGG 1560
QY 1561 AAGAAACCCAAAGCAAGAGAGATGTGGAATTAAGTTGGCCCTTAATGCAATTGAAC 1620
DB 1561 AAGAAACCCAAAGCAAGAGAGATGTGGAATTAAGTTGGCCCTTAATGCAATTGAAC 1620
QY 1621 CTTGTGTGATTTGTCAAGGTGCAGCTTAAATAATGTTGCAATGTCACAAACAGAC 1680
DB 1621 CTTGTGTGATTTGTCAAGGTGCAGCTTAAATAATGTTGCAATGTCACAAACAGAC 1680
QY 1681 ATCTTATGCGCTGCTTTTACATGTGCAAGAGACTAAAGAAAGAAATTAAGCCCTGCGCAG 1740
DB 1681 ATCTTATGCGCTGCTTTTACATGTGCAAGAGACTAAAGAAAGAAATTAAGCCCTGCGCAG 1740
QY 1741 TATGTAGCAACCAATTCAAATGATGTGCTAATTTATTTCCCTTATGATGACCTGTAT 1800
DB 1741 TATGTAGCAACCAATTCAAATGATGTGCTAATTTATTTCCCTTATGATGACCTGTAT 1800
QY 1801 AAGAGAAATTAATTTCTAATATTAACCTTAAGAAATTTGAGACAACTGAAATTTAT 1860
DB 1801 AAGAGAAATTAATTTCTAATATTAACCTTAAGAAATTTGAGACAACTGAAATTTAT 1860

QY 1861 CACATATATCAAGTGAAGAAAAATGCTCAATTCACATAGATTTCTCTTAGTATAT 1920
DB 1861 CACATATATCAAGTGAAGAAAAATGCTCAATTCACATAGATTTCTCTTAGTATAT 1920
QY 1921 TGACCTACTTTGGTAGTGAATAGTAACTACTATTAATTTGCTGAATATAGTACT 1980
DB 1921 TGACCTACTTTGGTAGTGAATAGTAACTACTATTAATTTGCTGAATATAGTACT 1980
QY 1981 CATCTTTACACCAACTCTTAATTTTAATTAATTTCTACTCTGTAAATGAGAATAC 2040
DB 1981 CATCTTTACACCAACTCTTAATTTTAATTAATTTCTACTCTGTAAATGAGAATAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAATATATATATATGACATTTAAATGATATATTTTGTG 2100
DB 2041 TTGGTTTTTTTTTTCTTAATATATATATATGACATTTAAATGATATATTTTGTG 2100
QY 2101 AGACCGAGTCTTGTCTGTATACCCAGGCTGAGTGAAGTGGTATCTTGGCTACTGCA 2160
DB 2101 AGACCGAGTCTTGTCTGTATACCCAGGCTGAGTGAAGTGGTATCTTGGCTACTGCA 2160
QY 2161 AGCTGCGCCCTCCCGGGTTCGACCAATTCCTGCTCAGCCTCCCAATTAGCTGGCC 2220
DB 2161 AGCTGCGCCCTCCCGGGTTCGACCAATTCCTGCTCAGCCTCCCAATTAGCTGGCC 2220
QY 2221 TACAGTCACTGCGACACACCTGGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
DB 2221 TACAGTCACTGCGACACACCTGGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
QY 2281 ACCGTGTAGCCAGATGTCTGATCTCTGACCTCGTATCCGCCACTCGGCTTC 2340
DB 2281 ACCGTGTAGCCAGATGTCTGATCTCTGACCTCGTATCCGCCACTCGGCTTC 2340
QY 2341 CAAAGTGTGGGATTACAGGCGATGAGCCACCG 2372
DB 2341 CAAAGTGTGGGATTACAGGCGATGAGCCACCG 2372

RESULT 4
US-08-245-500A-2

/ Sequence 2, Application US/08245500A
/ Patent No. 5550023
/ GENERAL INFORMATION:
/ APPLICANT: BURRELL, MARILEE
/ APPLICANT: HILL, DAVID E.
/ APPLICANT: KINZLER, KENNETH W.
/ APPLICANT: VOGELSTEIN, BERT
/ TITLE OF INVENTION: AMPLIFICATION OF HUMAN MD2 GENE IN
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: BANNER, BIRCH, MCKIE AND BECKETT
/ STREET: 1001 G STREET, N.W.
/ CITY: WASHINGTON
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20001
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/245,500A
/ FILING DATE: 07-APR-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KAGAN, SARAH A.
/ REGISTRATION NUMBER: 32,141
/ REFERENCE/DOCKET NUMBER: 01107.42798
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-508-9100
/ TELEFAX: 202-508-9299
/ TELEX: 197430 BBMB UT

/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2372 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ CELL LINE: Caco-2
/ POSITION IN GENOME:
/ MAP POSITION: 12q12-14
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 312..1784
/ US-08-245-500A-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGCAGCTTGGCTCTTCTGGGCGCTGTGTGCGCTGTGTGTGCGAAAGATGA 60
DB 1 GCACCGCGCAGCTTGGCTCTTCTGGGCGCTGTGTGCGCTGTGTGTGCGAAAGATGA 60
QY 61 GCAGAAACCGAGCCCGAGGGGCGCGGACCCCTGACCGAGATCTGCTGCTTCG 120
DB 61 GCAGAAACCGAGCCCGAGGGGCGCGGACCCCTGACCGAGATCTGCTGCTTCG 120
QY 61 GCAGAAACCGAGCCCGAGGGGCGCGGACCCCTGACCGAGATCTGCTGCTTCG 120
DB 61 GCAGAAACCGAGCCCGAGGGGCGCGGACCCCTGACCGAGATCTGCTGCTTCG 120
QY 121 CAGCCAGAGACGCTCCCTCCCGGATTAAGTGTGCTAGAGCGCCCAAGTGCCTGGCCG 180
DB 121 CAGCCAGAGACGCTCCCTCCCGGATTAAGTGTGCTAGAGCGCCCAAGTGCCTGGCCG 180
QY 121 CAGCCAGAGACGCTCCCTCCCGGATTAAGTGTGCTAGAGCGCCCAAGTGCCTGGCCG 180
DB 121 CAGCCAGAGACGCTCCCTCCCGGATTAAGTGTGCTAGAGCGCCCAAGTGCCTGGCCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCGGCGCTGCTTCCGCACTAGTCCCGCGT 240
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QY 181 GAGAGTGAATGATCCCGAGGCGCGGCGCTGCTTCCGCACTAGTCCCGCGT 240
DB 181 GAGAGTGAATGATCCCGAGGCGCGGCGCTGCTTCCGCACTAGTCCCGCGT 240
QY 241 AAGGAACTGGGAGTCTTGAAGGACCCCGACTCCAGCGGAAACCCCGAGATGTA 300
DB 241 AAGGAACTGGGAGTCTTGAAGGACCCCGACTCCAGCGGAAACCCCGAGATGTA 300
QY 241 AAGGAACTGGGAGTCTTGAAGGACCCCGACTCCAGCGGAAACCCCGAGATGTA 300
DB 241 AAGGAACTGGGAGTCTTGAAGGACCCCGACTCCAGCGGAAACCCCGAGATGTA 300
QY 301 GGAGCAGGCAATGCAATACCAATGCTGTACTAGATGATGCTGTAAACACT 360
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DB 361 CACAGATTCAGCTTCGGAACAAGACCTGCTTGAACCAAGCCATTGCTTTGAAGT 420
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DB 421 TATTAAAGCTGTGTGCAAAAAGACCTTACTATGAAAGAGTTCTTTTATC 480
QY 481 TTGGCCAGTATATATGACTAAACGATTATATGATGAGAGCAACAATATGTATAT 540
DB 481 TTGGCCAGTATATATGACTAAACGATTATATGATGAGAGCAACAATATGTATAT 540
QY 541 GTTCAATGATCTTGAAGATTTGTTGGCGTCCAACTTCTGTGAAAGAGCACA 600
DB 541 GTTCAATGATCTTGAAGATTTGTTGGCGTCCAACTTCTGTGAAAGAGCACA 600
QY 601 GGAATAATATATCAATGATCTACAGAACTTGTGTGTGCAATGACGAGATCATCG 660
DB 601 GGAATAATATATCAATGATCTACAGAACTTGTGTGTGCAATGACGAGATCATCG 660
QY 661 ACTCAGTACATCTGTGAGTGAAGACAGGTCACTTGAAGTGGAGTGAATCAAAAG 720
DB 661 ACTCAGTACATCTGTGAGTGAAGACAGGTCACTTGAAGTGGAGTGAATCAAAAG 720
QY 721 ACCTTGACAGAGCTTCAAGAGAAACCTTCACTTCACTTGTGTTTCAAGCAT 780
DB 721 ACCTTGACAGAGCTTCAAGAGAAACCTTCACTTCACTTGTGTTTCAAGCAT 780

Db 721 ACCCTGTACAGAGCTTCAGGAAAGAAACCTTCATCTTCACATTTGGTTCTACAGCAT 780
Qy 781 CTACCTCATCTAGAGAGAGCAATTAGTGA CAGAAGAAATTCAGATGAATTAATCTG 840
Db 781 CTACCTCATCTAGAGAGAGCAATTAGTGA CAGAAGAAATTCAGATGAATTAATCTG 840
Qy 841 GTGAACGACAAAGAAACCGCCCAAAATCTGATAGTATTTCCCTTCCCTTGTATGAAAGCC 900
Db 841 GTGAACGACAAAGAAACCGCCCAAAATCTGATAGTATTTCCCTTCCCTTGTATGAAAGCC 900
Qy 901 TGGCTCTGTGTATTAATAGGAGATATGTTGTGAAGAACAGTACGATGAATCTACAG 960
Db 901 TGGCTCTGTGTATTAATAGGAGATATGTTGTGAAGAACAGTACGATGAATCTACAG 960
Qy 961 GGAGCGCATCGAATCCGGATCTTGATGCTGTGTATGTAACATTCAGGGATGATGATG 1020
Db 961 GGAGCGCATCGAATCCGGATCTTGATGCTGTGTATGTAACATTCAGGGATGATGATG 1020
Qy 1021 ATCAGATTCAGTTTCAGATCAGTTTATGTTAGTAATTTGAAATCTCTGCACTCAG 1080
Db 1021 ATCAGATTCAGTTTCAGATCAGTTTATGTTAGTAATTTGAAATCTCTGCACTCAG 1080
Qy 1081 AAGATTATAGCTTATGTAAGAGACAAAGAACTCTCAGATGAAGATGATGATATATC 1140
Db 1081 AAGATTATAGCTTATGTAAGAGACAAAGAACTCTCAGATGAAGATGATGATATATC 1140
Qy 1141 AAGTTACTGTATACGAGGAGGAGATGATACAGATTCATTTGAAAGATCTGAAA 1200
Db 1141 AAGTTACTGTATACGAGGAGGAGATGATACAGATTCATTTGAAAGATCTGAAA 1200
Qy 1201 TTTCCCTTACGTCATTTGGAATTCGACTTCATGCAATGAATGAATCCCTCCCTCCAT 1260
Db 1201 TTTCCCTTACGTCATTTGGAATTCGACTTCATGCAATGAATGAATCCCTCCCTCCAT 1260
Qy 1261 CACATTCGACAGATGTTGGGCTTCGTGAGAAATTTGGCTCTGAAATTAAGGAAAG 1320
Db 1261 CACATTCGACAGATGTTGGGCTTCGTGAGAAATTTGGCTCTGAAATTAAGGAAAG 1320
Qy 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAAATCTGAAATCTCACAAGCTGAAAGAGGCT 1380
Db 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAAATCTGAAATCTCACAAGCTGAAAGAGGCT 1380
Qy 1381 TTGATGTCCTGATTTGTAATAAACTATGTGAATGATTCGAGAGTCAATGTTGAGG 1440
Db 1381 TTGATGTCCTGATTTGTAATAAACTATGTGAATGATTCGAGAGTCAATGTTGAGG 1440
Qy 1441 AAAATGATATAAATTTACAGAGCTTCAATCACAAGAAAGTGAAGCTATTTCTCAGC 1500
Db 1441 AAAATGATATAAATTTACAGAGCTTCAATCACAAGAAAGTGAAGCTATTTCTCAGC 1500
Qy 1501 CATCAACTCTGATGATTTATTTATAGCAGCCAGAAGATGTAAGAGTTGAAAGG 1560
Db 1501 CATCAACTCTGATGATTTATTTATAGCAGCCAGAAGATGTAAGAGTTGAAAGG 1560
Qy 1561 AAGAAACCCAGAGAAAGAGAGTGTGAATCTGTTGCCCTTAATGCAATGAAC 1620
Db 1561 AAGAAACCCAGAGAAAGAGAGTGTGAATCTGTTGCCCTTAATGCAATGAAC 1620
Qy 1621 CTGTGTGATTTGTCAAGGTGCACTAAATATGTTGCAATGTCATGCAAAACAGAGC 1680
Db 1621 CTGTGTGATTTGTCAAGGTGCACTAAATATGTTGCAATGTCATGCAAAACAGAGC 1680
Qy 1681 ATCTTAATGCTGCTTTACATGTCAGAGAGTAAAGAAAGAAAGTAAAGCCCTGCCAG 1740
Db 1681 ATCTTAATGCTGCTTTACATGTCAGAGAGTAAAGAAAGAAAGTAAAGCCCTGCCAG 1740
Qy 1741 TATGTAGACAACTATTAATGATGCTAACTAATTTCCCTGATGCACTGCTAT 1800
Db 1741 TATGTAGACAACTATTAATGATGCTAACTAATTTCCCTGATGCACTGCTAT 1800
Qy 1801 AAGAGATTAATTAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
Db 1801 AAGAGATTAATTAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860

Qy 1861 CACATATATCAAGTGAAGAAATGCTCAATTGATGATTTCTTCTTTAGTATTAAT 1920
Db 1861 CACATATATCAAGTGAAGAAATGCTCAATTGATGATTTCTTCTTTAGTATTAAT 1920
Qy 1921 TGAATCTATTTGTATGTAAGTATGTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Db 1921 TGAATCTATTTGTATGTAAGTATGTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Qy 1981 CATCTTTACACCACTCTTAATTTAAATTAATTTACTCTGTCTTAATGAAGATAC 2040
Db 1981 CATCTTTACACCACTCTTAATTTAAATTAATTTACTCTGTCTTAATGAAGATAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2100
Db 2041 TTGGTTTTTTTTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2100
Qy 2101 AGACGAGTCTGCTCTGTATACCAAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 2160
Db 2101 AGACGAGTCTGCTCTGTATACCAAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 2160
Qy 2161 AGCTTGCCCTCCCGGTTTCGACCAATTCCTGCTCAGCCTCCCAATTAAGCTTGCC 2220
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Qy 2221 TACAGTATCTGACACACACCTGCTAATTTTGTACTTTTATGAGACAGGGTTTC 2280
Db 2221 TACAGTATCTGACACACACCTGCTAATTTTGTACTTTTATGAGACAGGGTTTC 2280
Qy 2281 ACCGTTTACGAGATGCTGTGATCTGTAACCTCGATCCCGGCTCCGCTCC 2340
Db 2281 ACCGTTTACGAGATGCTGTGATCTGTAACCTCGATCCCGGCTCCGCTCC 2340
Qy 2341 CAAAGTCTGGATTTACAGGCAATGAGCCACCG 2372
Db 2341 CAAAGTCTGGATTTACAGGCAATGAGCCACCG 2372
RESULT 5
US-08-390-546-2
Sequence 2, Application US/08390546
Patent No. 5606044
GENERAL INFORMATION:
APPLICANT: BURRILL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,546
CLASSIFICATION: 536
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107, 42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299

TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-546-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCCGAGCTTGGCTCTTCTGGGGCTGTGTGCTGTGTGCGAAAGATGA 60
DB 1 GCACCGCCGAGCTTGGCTCTTCTGGGGCTGTGTGCTGTGTGCGAAAGATGA 60
QY 61 GCANAAGCCGAGCCGAGGGGGGGCCGAGCCCTGAGCCGAGATCCGTGCTTCG 120
DB 61 GCANAAGCCGAGCCGAGGGGGGGCCGAGCCCTGAGCCGAGATCCGTGCTTCG 120
QY 121 CAGCCAGAGACGCTCCCTCCCGGATTAGTGCTAGAGGCCCAAGTCCCTGGCCG 180
DB 121 CAGCCAGAGACGCTCCCTCCCGGATTAGTGCTAGAGGCCCAAGTCCCTGGCCG 180
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DB 181 GAGAGTGAATGATCCCCGAGGCCGAGGCGTGTGCTTCGCGAGTAGTCCCTGG 240
QY 181 GAGAGTGAATGATCCCCGAGGCCGAGGCGTGTGCTTCGCGAGTAGTCCCTGG 240
DB 181 GAGAGTGAATGATCCCCGAGGCCGAGGCGTGTGCTTCGCGAGTAGTCCCTGG 240
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DB 241 AAGGAACTGGGGAGTCTTGAAGGACCCCGGACTCCAGCCGAGAAACCCCGAGTGTGA 300
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DB 721 ACCCTGTACAGAGCTTCAGAAAGAAACCTTCATCTTCACATTTGTTCTAGACAT 780
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DB 781 CTACCTCATCTAGAAAGAGACCAATTAAGTGAAGAGAAATTCAGATGAATATCTG 840
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QY 1261 CACATTGCAAGATGTTGGGCCCTTGTGAGAAATTTGGCTTCTGAATATTAAGGAAAG 1320
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Db 1801 AAGAGATATATATTTCTAATAATTAACCTAGGAATTAGACAAGTAATTTATT 1860
Qy 1861 CACATATATCAAGTAGAAGAAATAGCCTCAATTCACATAGATTTCTTCTTATTAAT 1920
Db 1861 CACATATATCAAGTAGAAGAAATAGCCTCAATTCACATAGATTTCTTCTTATTAAT 1920
Qy 1921 TGACCTACTTTGGTAGTGAATAGTAATCTTACTAATAATTTAGCTTGAATAGAGT 1980
Db 1921 TGACCTACTTTGGTAGTGAATAGTAATCTTACTAATAATTTAGCTTGAATAGAGT 1980
Qy 1981 CATCTCTTACCAACTCTTAATTTAATAATTTCTCTCTTAAATGAAAGTAC 2040
Db 1981 CATCTCTTACCAACTCTTAATTTAATAATTTCTCTCTTAAATGAAAGTAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGG 2100
Db 2041 TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGG 2100
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Db 2101 AAGACGAGTCTGCTCTGTTACCCAGCTGAGTGAAGTGAATCTTGCTCACTGCA 2160
Qy 2161 AGCTCTGCTCTCCCGGGTTCGACCAATCTCTGCTCAAGCTCCCAATTAAGTGGCC 2220
Db 2161 AGCTCTGCTCTCCCGGGTTCGACCAATCTCTGCTCAAGCTCCCAATTAAGTGGCC 2220
Qy 2221 TACAGTATCTGCAACACACCTGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
Db 2221 TACAGTATCTGCAACACACCTGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
Qy 2281 ACCGTTTAGCAGATGATGATCTCTGATCTGATCCGCCACTCGGCTCC 2340
Db 2281 ACCGTTTAGCAGATGATGATCTCTGATCTGATCCGCCACTCGGCTCC 2340
Qy 2341 CAAAGTCTGGGATTTACAGGATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTTACAGGATGAGCCACCG 2372

RESULT 6
US-08-390-479A-2
Sequence 2, Application US/08390479A
Patent No. 5618921
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF, LTD.
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,479A
FILING DATE: 02-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107, 48992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME: 12q12-14
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-479A-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAACGCGGAGACTTGGCTGCTTCTGGGGGCTGTGGCCCTGTGTGTGGAAAGATGGA 60
Db 1 GCAACGCGGAGACTTGGCTGCTTCTGGGGGCTGTGTGTGGAAAGATGGA 60
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Db 61 GCAAGAGCGGAGCCGAGGAGGCGCGGACCCCTCTGACCGAGATCCGCTGCTTGG 120
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Db 421 TATTAAGTCTGTGTGTGCAAAAAGACCTTAATATGATGATGATGATGATGATGAT 480
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QY 721 ACCTGTACAGAGCTTCAGGAGAGAGAAACCTTCATCTTCAATTTGGTTTCTAGACCAT 780
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Db 781 CTACCTCATCTAGAGAGAGAGCAATTAGTGAACAAGAAATTCAGATGATTAATCTTG 840
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Db 1021 ATCCAGATTCAGTTTCAATCAGATCAGTTAGTGAATTTGAAGTTGAATCTCCGACTGAG 1080
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QY 1141 AAGTTATCTGTGTATAGAGAGAGAGAGATGATTAAGATTCATTTGAAGAAATCTGAAA 1200
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Db 1261 CACATTGCAACAGATGTTGGGCTTCCTGTGAATTTGGCTCTGTAAGTAAAGGAGAAAG 1320
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Db 1381 TTGATGTTCTGATTTGTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 AAAATGATGATTAATTAACAAGAGTTCACATCAACAAGAAAGTGAAGCTATTTCTGAGC 1500
Db 1441 AAAATGATGATTAATTAACAAGAGTTCACATCAACAAGAAAGTGAAGCTATTTCTGAGC 1500
QY 1501 CATCAACTTCTAGTGAAGATTAATTAATAGCAGCAAGAGATGGAAGAGTTGAAAGAG 1560
Db 1501 CATCAACTTCTAGTGAAGATTAATTAATAGCAGCAAGAGATGGAAGAGTTGAAAGAG 1560
QY 1561 AAGAAACCCAG 1620
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QY 1621 CTGTGTGTATTTGTCAAGAGTTCAGCTTAAGAAATGTTGCAATTCATGCAAGAGAG 1680
Db 1621 CTGTGTGTATTTGTCAAGAGTTCAGCTTAAGAAATGTTGCAATTCATGCAAGAGAG 1680
QY 1681 ATCTTATGAGCTCTTATCATGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ATCTTATGAGCTCTTATCATGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 TATGTAGACAAACATTCGAATGATGCTAACTTAATTTCCCTTAAGTTGAGAGAGAG 1800
Db 1741 TATGTAGACAAACATTCGAATGATGCTAACTTAATTTCCCTTAAGTTGAGAGAGAG 1800
QY 1801 AAGAGATTTATATTTCTAATATTAACCTAGAGATTTAGACAACTGAATTTAT 1860

Db 1801 AAGAGATTTATATTTCTAATATTAACCTAGAGATTTAGACAACTGAATTTAT 1860
QY 1861 CACATATATCAAGTGAAGAAATGCTCAATTCATAGATTTCTTCTTATGATAT 1920
Db 1861 CACATATATCAAGTGAAGAAATGCTCAATTCATAGATTTCTTCTTATGATAT 1920
QY 1921 TGACCTACTTGTATAGTGAATAGTGAATATCTTAATTAATTTGAATATAGTACT 1980
Db 1921 TGACCTACTTGTATAGTGAATAGTGAATATCTTAATTAATTTGAATATAGTACT 1980
QY 1981 CATCTTTACACCACTCTTAATTTTAATTAATTTCTAATCTGCTTAAATGAGAGTAC 2040
Db 1981 CATCTTTACACCACTCTTAATTTTAATTAATTTCTAATCTGCTTAAATGAGAGTAC 2040
QY 2041 TTTGTTTTTTTTTTCTTAATTAATGATGATGATTAATTAATTAATTTATTTT 2100
Db 2041 TTTGTTTTTTTTTTCTTAATTAATGATGATGATTAATTAATTAATTTATTTT 2100
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QY 2161 AGCTTGCTCTTCCCGGCTTGCACACATTTCTGCTGCTGCTCCCAATTAAGTGGCC 2220
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QY 2341 CAAAGTCTGGAGATTAACAGGATGAGCCACCG 2372
Db 2341 CAAAGTCTGGAGATTAACAGGATGAGCCACCG 2372

RESULT 7
US-08-557-393-2
Sequence 2, Application US/08557393
Patent No. 5702903
GENERAL INFORMATION:
APPLICANT: BURELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MD2 GENE IN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,393
CLASSIFICATION: 435
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,500
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 HBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-557-393-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTGCTTCTGAGGCTGTGTGCGCTGTGTGTCGAAAGATGA 60
Db 1 GCACCGCGGAGCTTGGCTGCTTCTGAGGCTGTGTGCGCTGTGTGTCGAAAGATGA 60
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Db 661 ACTCAGGTACATCTGTAGTGAAGAACAGGTGTCACTTGAAGGTGGAGTGAACAAAG 720
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Db 721 ACCCTGTACAAGGCTTCAGAAAGAAACCTTCATCTTCAATTTGTTCTTACACAT 780
QY 781 CTACCTCATCTTGAAGAGAGCAATTAATGAGACAGAAAGAAATTAATGATTTCTG 840
Db 781 CTACCTCATCTTGAAGAGAGCAATTAATGAGACAGAAAGAAATTAATGATTTCTG 840
QY 841 GTGAACGACAAAGAAAGCCCAAACTGATGATTTCCCTTCCTTGTGAAGAGCC 900
Db 841 GTGAACGACAAAGAAAGCCCAAACTGATGATTTCCCTTCCTTGTGAAGAGCC 900
QY 901 TGGCTCTGTGTAAATGAAGAGATATGTGTGAAGAAAGACAGTACAGTGAATCTACAG 960
Db 901 TGGCTCTGTGTAAATGAAGAGATATGTGTGAAGAAAGACAGTACAGTGAATCTACAG 960
QY 961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTGAATGAACATTCAGGTGATGCTGG 1020
Db 961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTGAATGAACATTCAGGTGATGCTGG 1020
QY 1021 ATCAGGATTCAGTTTCAAGTCAAGTTAGTGAATTTGAAGTGAATCTTCGACTCAG 1080
Db 1021 ATCAGGATTCAGTTTCAAGTCAAGTTAGTGAATTTGAAGTGAATCTTCGACTCAG 1080
QY 1081 AAGATTATAGCTTGTAGTGAAGAGCAAGAACTCTCAGATGAAGTGAAGTATATC 1140
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QY 1141 AAGTTACTGTGTATCAGGAGGAGAGTGAATCAGATTCATTGGAAGAAATCTGAA 1200
Db 1141 AAGTTACTGTGTATCAGGAGGAGAGTGAATCAGATTCATTGGAAGAAATCTGAA 1200
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Db 1201 TTTCTTGTGCTGACTTATGGAATGCACTTCAATGCAATGAATGAAATCCCTTCAT 1260
QY 1261 CACATTGCAACAGATGTTGGGCTTCGTGAGAAATTTGCTTCGTAAGATTAAGGAAAG 1320
Db 1261 CACATTGCAACAGATGTTGGGCTTCGTGAGAAATTTGCTTCGTAAGATTAAGGAAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGAAATCTCAACAGCTGAAGAGGCT 1380
Db 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGAAATCTCAACAGCTGAAGAGGCT 1380
QY 1381 TTGATGTTCTGTATTTGTAAGAACTATATGATGATTCAGAGAGTCAATGTGTGAGG 1440
Db 1381 TTGATGTTCTGTATTTGTAAGAACTATATGATGATTCAGAGAGTCAATGTGTGAGG 1440
QY 1441 AAAATGATGATTAATTTCAAGAGCTTCAATCAAGAAAGTGAAGCTATTTCTCAG 1500
Db 1441 AAAATGATGATTAATTTCAAGAGCTTCAATCAAGAAAGTGAAGCTATTTCTCAG 1500
QY 1501 CATCACTTCTAGTGAATTAATTTATAGAGCCAAAGATGTGAAGATTTGAAGG 1560
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QY 1561 AAGAAACCCAGACAAAGAGAGTGTGAATCTAAGTTTGGCCCTTAATGCCATTGAAC 1620
Db 1561 AAGAAACCCAGACAAAGAGAGTGTGAATCTAAGTTTGGCCCTTAATGCCATTGAAC 1620
QY 1621 CTGTGTGATTTGTCAAGGTGCACTTAAGAAATGTTGCAATGTCAGAAACAGAGC 1680
Db 1621 CTGTGTGATTTGTCAAGGTGCACTTAAGAAATGTTGCAATGTCAGAAACAGAGC 1680
QY 1681 ATCTTATGAGCTGCTTTATCATGTGCAAGAAAGCTTAAGAAAGATTAAGCCCTCCAG 1740
Db 1681 ATCTTATGAGCTGCTTTATCATGTGCAAGAAAGCTTAAGAAAGATTAAGCCCTCCAG 1740
QY 1741 TATGTAGCAACCAATTCAAATGATTTGTGCTAATTTCCCTAGTGTGACTGTAT 1800

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Db 1741 TATGAGCAACCAATTCAAATGATGTGCTAACTTATTTCCCTAGTGAACCTGTAT 1800
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Db 2281 ACCGTGTAGCCAGGATGCTGATCTCTGACCTGATCGGCCACCTGAGCTTC 2340
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RESULT 8
US-08-390-516C-2
; Sequence 2, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRILL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDMA GENE IN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
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NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMBB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-516C-2

Query Match
Best Local Similarity 100.0%; Score 2372; DB 2; Length 2372;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCGCGCAGCTTGGCTTCTGGGGCTGTGTGGCCCTGTGTGTGGAAGATGA 60
Db 1 GCACCGCGCAGCTTGGCTTCTGGGGCTGTGTGGCCCTGTGTGTGGAAGATGA 60
Qy 61 GCAGAACCCGAGCCGAGGGGGCCGACCCCTCTGACCGAGATCTGCTGTTTC 120
Db 61 GCAGAACCCGAGCCGAGGGGGCCGACCCCTCTGACCGAGATCTGCTGTTTC 120
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Qy 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTGTGCTTCCGACAGTACAGTCCCGTG 240
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QY 721 ACCCTGTACAGAGCTTCAGAGAGAGAACTTCATCTTCACATTTGGTTTTCAGACAT 780
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DB 841 GTGAAGCAGAAAG 900
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DB 1381 TTGATGTTCTGTGATTTGTAAG 1440
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DB 1441 AAAATGATGATTAATTAACAAG 1500
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DB 1801 AAGAGATTAATTAATTTCTAATTAATTAATTCCTAGTGAAGTGAAGTGAAGTGAAGTGAAG 1860
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DB 1921 TGACCTACTTGTGTGATGAG 1980
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DB 2041 TTGTTTTTTTTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2100
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DB 2101 AGACGAGCTGCTCTGTATACAG 2160
QY 2161 AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
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DB 2161 AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
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DB 2341 CAAAGTGTGGGATTAACAG 2400
RESULT 9
US-08-390-517A-2
; Sequence 2, Application US/08390517A
; Patent No. 5736338
; GENERAL INFORMATION:
; APPLICANT: BURELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDX2 GENE IN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,517A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 HBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-517A-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGCGAGCTTGGCTGCTTGGGGCCCTGTGAGCCCTGTGTGCGAAAGATGA 60
DB 1 GCACCGCGCGAGCTTGGCTGCTTGGGGCCCTGTGTGCGAAAGATGA 60
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DB 721 ACCTTGTAACAAGACCTTCAGGAAGAAACCTTCATCTTCACATTTGGTTCTAGACCAT 780
QY 781 CTACCTCATCTGAAGAGAGCAATTTAGTGAACAGAAAGAAATTCAGATGAATATCTG 840
DB 781 CTACCTCATCTGAAGAGAGCAATTTAGTGAACAGAAAGAAATTCAGATGAATATCTG 840
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DB 841 GTGAACGCAAAAGAAAAGCCCAATCTGATATATTTCCCTTCTTGTGAAAGCC 900
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DB 901 TGCGTCTGTGTATATAAGGAGATATGTTGTGAAGAGCAGTAGCAGTAATCTACAG 960
QY 961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTAAGTGAACATTCAGGTATGTTGG 1020
DB 961 GGAAGCCATCGAATCCGATCTTGAATGCTGTGTAAGTGAACATTCAGGTATGTTGG 1020
QY 1021 ATCAGATTCAGTTTCAATGATCAGTTTGTAGTGAATTTGAAGTGAATCTCTGACCTGAG 1080
DB 1021 ATCAGATTCAGTTTCAATGATCAGTTTGTAGTGAATTTGAAGTGAATCTCTGACCTGAG 1080
QY 1081 AAGATTATAGCTTATAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGATATATC 1140
DB 1081 AAGATTATAGCTTATAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGATATATC 1140
QY 1141 AAGTTACTGTGTATCAGGACAGGAGAGTATACAGATTCATTTGAAGAAATCCTGAA 1200
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QY 1201 TTTCTTACGATGATTAAGAAATGACCTTCATGCAATGAATGAATCCCTCCAT 1260
DB 1201 TTTCTTACGATGATTAAGAAATGACCTTCATGCAATGAATGAATCCCTCCAT 1260
QY 1261 CACATTGCAAGATGTTGGCCCTTCGTGAGAAATTTGCTTCGTAAGATTAAGGGAAG 1320
DB 1261 CACATTGCAAGATGTTGGCCCTTCGTGAGAAATTTGCTTCGTAAGATTAAGGGAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACACACTGAAGGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACACACTGAAGGGCT 1380
QY 1381 TTGATGTTCTGATTTGTAATAAACTATAGTAATGATTCAGAGAGTCATGTGTAAG 1440
DB 1381 TTGATGTTCTGATTTGTAATAAACTATAGTAATGATTCAGAGAGTCATGTGTAAG 1440
QY 1441 AAAATGATGATTAATTAACAAGCTTCACATCAACAGAAAGTGAAGCTATTTCTACG 1500
DB 1441 AAAATGATGATTAATTAACAAGCTTCACATCAACAGAAAGTGAAGCTATTTCTACG 1500
QY 1501 CATCAACTTCTAGTGAATTAATTTATGACAGCAAGAAAGTGAAGGTTTGAAGGG 1560
DB 1501 CATCAACTTCTAGTGAATTAATTTATGACAGCAAGAAAGTGAAGGTTTGAAGGG 1560
QY 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTGGCCCTTAATGCAATTAAG 1620
DB 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTGGCCCTTAATGCAATTAAG 1620
QY 1621 CTTGTGTATTTGTCAAGGTGCACTTAATAATGTTGCAATGCAAGCAAGAGC 1680
DB 1621 CTTGTGTATTTGTCAAGGTGCACTTAATAATGTTGCAATGCAAGCAAGAGC 1680
QY 1681 ATCTTATGCGCTGCTTTACATGTCAGAAAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
DB 1681 ATCTTATGCGCTGCTTTACATGTCAGAAAGCTAAAGAAAGAAATAGCCCTGCCAG 1740

QY 1741 TATGTAGACAACTTCAATGATGCTAATCTTATTTCCCTAGTGTGCTAT 1800
DB 1741 TATGTAGACAACTTCAATGATGCTAATCTTATTTCCCTAGTGTGCTAT 1800
QY 1801 AAGAGATATATATTTCTAATATTAACCTAGGAATTTAGACAACTGAAATTTAT 1860
DB 1801 AAGAGATATATATTTCTAATATTAACCTAGGAATTTAGACAACTGAAATTTAT 1860
QY 1861 CACATATATCAAGGAGAAATGCTCAATTCACATATATTTCTTCTTATATAT 1920
DB 1861 CACATATATCAAGGAGAAATGCTCAATTCACATATATTTCTTCTTATATAT 1920
QY 1921 TGACCTACTTGTGTAGTGAATGTAATTAATTAATTTGACTTGAATATAGT 1980
DB 1921 TGACCTACTTGTGTAGTGAATGTAATTAATTAATTTGACTTGAATATAGT 1980
QY 1981 CATCTTTACCACTCTTAATTTTAATTAATTTCTGCTTAATGAGAATAC 2040
DB 1981 CATCTTTACCACTCTTAATTTTAATTAATTTCTGCTTAATGAGAATAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAATATGTAATGACATTTAAATGTAATTTATTTT 2100
DB 2041 TTGGTTTTTTTTTTCTTAATATGTAATGACATTTAAATGTAATTTATTTT 2100
QY 2101 AGACGAGCTGTCTGTATACCAAGGCTGAGTGAAGTGAATCTTGCTCACTGA 2160
DB 2101 AGACGAGCTGTCTGTATACCAAGGCTGAGTGAAGTGAATCTTGCTCACTGA 2160
QY 2161 AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
DB 2161 AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
QY 2221 TACAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
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QY 2281 ACCGCTTACGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
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QY 2341 CAAAGTGTGAGGATTAAGGATTAAGGATTAAGGATTAAGGATTAAGG 2372
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RESULT 10
US-08-390-515A-2
Sequence 2, Application US/08390515A
Parent No. 5756455
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDN2 GENE IN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,515A
FILING DATE: 07-APR-1993

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-515A-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTGCTTCTGCGGCGCTGTGTGCTGTGTGCGAAAGATGA 60
DB 1 GCACCGCGGAGCTTGGCTGCTTCTGCGGCGCTGTGTGCTGTGTGCGAAAGATGA 60
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DB 241 AAGGAACTGGGAGTCTTGAAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
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DB 361 CACAGATTCAGCTTCGGAACAAGAGACCTGCTGATGACCAAGGCAATGCTTGAAGT 420
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DB 421 TATTTAAGTCTGTTGTGCACAAAAAGACCTTATATCTATGAAAGGTTCTTTTATATC 480
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DB 541 GTTCAATGATCTTCTAGAGATTTGTTGGCGTGCAGGCTTCTGTGAAAGAGACA 600
QY 601 GGAAAAATATATCAATGATCTATGAGAGAACTTGTATGATGATGAGAGAAATATCGG 660

Db 601 GGAATAATATATACATGATCTACAGAACTTGATGATGATCATGACGAGAAATCATGG 660
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Db 1081 AAGATTAAGCTTATGAG 1140
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Db 1141 AAGTATCTGTATCAG 1200
Qy 1201 TTTCTTATCTGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1260
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Qy 1861 CACATATATCAAAAGTGAAGAAATGCTTCATTCATGATGATGATGATGATGATGAT 1920
Db 1861 CACATATATCAAAAGTGAAGAAATGCTTCATTCATGATGATGATGATGATGATGAT 1920
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Qy 1981 CATCTTATCAACCAACTCTATATTTAAATTAATTAATTAATTAATTAATTAATTAAT 2040
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Qy 2221 TACAGTATCTGCAACACACCTGCTAATTTTGTATCTTTATGATGATGATGATGATG 2280
Db 2221 TACAGTATCTGCAACACACCTGCTAATTTTGTATCTTTATGATGATGATGATGATG 2280
Qy 2281 ACCGTGATGAG 2340
Db 2281 ACCGTGATGAG 2340
Qy 2341 CAAAGTCTGGGATTTACAGCATGAGCCAGC 2372
Db 2341 CAAAGTCTGGGATTTACAGCATGAGCCAGC 2372
RESULT 11
US-08-801-718-2
; Sequence 2, Application US/08801718
; Patent No. 5858976
; GENERAL INFORMATION:
; APPLICANT: BURELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDN2 GENE IN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,718

FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,515
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-801-718-2

Query Match 100.0%; Score 2372; DB 2; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTGCTTGGGGCTGTGTGCGCCCTGTGTGCGAAAGATGGA 60
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DB 61 GCAAGAGCGAGCGCGAGGGGCGGCGGAGCCCTCTGAGCCGAGATCTCTGCTTTG 120
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DB 121 CAGCCAGAGGACCGTCTCTCCCGGATTAGTGCCTGAGAGCGCCAGTGCCTGCGCCG 180
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DB 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAATCTCAACACAGCTGAAGGGCT 1380
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QY 781 CTACCTCATTTAGAGAGAGAGCAATTAAGTGAAGAGAGAAATTCAGATGAATTAATCTG 840
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DB 1021 ATCAGAGATTCAGTTTCAAGTCAAGTTTGAAGTTGAATCTCTGACTCAG 1080
QY 1081 AAGATTATAGCCCTTAG 1140
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DB 1441 AAAATGATATTAATTAACAAG 1500
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QY 1681 ATCTATGAGCTGCTTATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 ATCTATGAGCTGCTTATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 TATGTAGACCAACATTCATTAATGATGCTTAATTTCCCTGAGTTGACCTGTCTAT 1800
DB 1741 TATGTAGACCAACATTCATTAATGATGCTTAATTTCCCTGAGTTGACCTGTCTAT 1800

QY 1801 AAGAGATTAATATATTTCTAATATTAACCTAGAGATTTAGACAACTGAATTAAT 1860
DB 1801 AAGAGATTAATATATTTCTAATATTAACCTAGAGATTTAGACAACTGAATTAAT 1860
QY 1861 CACATATATCAAGTGAAG 1920
DB 1861 CACATATATCAAGTGAAG 1920
QY 1921 TGACCTACTTTGGTATGAG 1980
DB 1921 TGACCTACTTTGGTATGAG 1980
QY 1981 CATCTTTACACCAACTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2040
DB 1981 CATCTTTACACCAACTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2040
QY 2041 TTTGTTTTTTTTTTCTTAAT 2100
DB 2041 TTTGTTTTTTTTTTCTTAAT 2100
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DB 2101 AAGCGAGCTTGTCTGTATACCGAGCTGAGAGTGAAGTGAATCTTGCTCACTGCA 2160
QY 2161 AGCTGCGCTCCCGGGTTGCGACCATCTCTGCTGAGCTCCCAATTAAGTTGGCC 2220
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DB 2221 TACAGTATCTGCAACACACACCTGCTAATTTTGTATCTTTAGAGAGAGAGAGAGAG 2280
QY 2281 ACCGTGTAGCCAGAGATGCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGAT 2340
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QY 2341 CAAAGTGTGAGATTAACAG 2372
DB 2341 CAAAGTGTGAGATTAACAG 2372

RESULT 13
US-09-280-805-1
Sequence 1, Application US/09280805
Patent No. 6184212
GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDN2
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: U.S.A.
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,805
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 09/048,810
FILING DATE: March 26, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
ANTI-SENSE: No
PUBLICATION INFORMATION:
AUTHORS: Oliner, J.D.
AUTHORS: Kinzler, K.W.
AUTHORS: Melzer, P.S.
AUTHORS: George, D.L.
AUTHORS: Vogelstein, B.
TITLE: Amplification of a gene encoding a
TITLE: p53-associated protein in human sarcomas
JOURNAL: Nature
VOLUME: 358
ISSUE: 6381
PAGES: 80-83
DATE: 02-JUL-1992
US-09-280-805-1

Query Match 100.0%; Score 2372; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2372; Conservative 0;

QY 1 GCACCGCGGAGCTTGGCTCTTCTGGGCGCTGTGTGCGCTGTGTGTGGAAGATGGA 60
DB 1 GCACCGCGGAGCTTGGCTCTTCTGGGCGCTGTGTGCGCTGTGTGTGGAAGATGGA 60
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DB 121 CAGCGAGAGGACCGGCTCCCGGATTAAGTCGTAAGAGGCGCAGTGGCCCTGGCCCG 180
QY 181 GAGAGTGTGATGATCCCGAGGCGCAGGCGCTGTGCTTCCGACAGTGTGATGATGATG 240
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QY 241 AAGGAACTGGGAGTCTTTGAGGGACCCCGACTCCAGCGGAAAAAAGGAGTGTGA 300
DB 241 AAGGAACTGGGAGTCTTTGAGGGACCCCGACTCCAGCGGAAAAAAGGAGTGTGA 300
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DB 301 GGAGAGGCAATGTGCAATACCAATGTCTGTACTGTACTGTGTGTGTGTGTGTGTGT 360
QY 361 CACAGATTCGACCTTCGAAACAAGAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 361 CACAGATTCGACCTTCGAAACAAGAGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 421 TATTAAGTCTGT 480
DB 421 TATTAAGTCTGT 480
QY 481 TTGGCCAGATTAATGT 540
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QY 541 GTTCAATGATCTTGT 600
DB 541 GTTCAATGATCTTGT 600
QY 601 GGAATAATATATACCATGATCTACAGGAACCTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB 601 GGAATAATATATACCATGATCTACAGGAACCTGTGTGTGTGTGTGTGTGTGTGTGT 660

QY 661 ACTCAGGATCATCTGT 720
DB 661 ACTCAGGATCATCTGT 720
QY 721 ACCTGT 780
DB 721 ACCTGT 780
QY 781 CTACCTCATCTGT 840
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QY 841 GTGAACGACAAAGAAAGCCCAAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 GTGAACGACAAAGAAAGCCCAAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 TGGCTGT 960
DB 901 TGGCTGT 960
QY 961 GGAGCCCATGTGAATCCGGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
DB 961 GGAGCCCATGTGAATCCGGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
QY 1021 ATCAGGATTCAGTTTGT 1080
DB 1021 ATCAGGATTCAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
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QY 1141 AAGTACTGT 1200
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QY 1201 TTTCTGT 1260
DB 1201 TTTCTGT 1260
QY 1261 CACATTGTGAACGATGT 1320
DB 1261 CACATTGTGAACGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
QY 1321 AATAAGGGGAAATCTGT 1380
DB 1321 AATAAGGGGAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
QY 1381 TTGATGTCTGT 1440
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QY 1441 AAAATGATGATTAATTAACAAGCTTCAATCAATCAATCAATCAATCAATCAATCA 1500
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QY 1501 CATCACTTGT 1560
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QY 1561 AAGAAACCAAGACAAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
DB 1561 AAGAAACCAAGACAAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
QY 1621 CTGT 1680
DB 1621 CTGT 1680
QY 1681 ATCTTATGCGCTGT 1740
DB 1681 ATCTTATGCGCTGT 1740

1741 TATGTAGACCAACCAATTCATATGATGCTAACTTATTCCTAGTACCTGCTAT 1800
1741 TATGTAGACCAACCAATTCATATGATGCTAACTTATTCCTAGTACCTGCTAT 1800
1801 AAGAGATTTATATTTCTACTATATATACCTTAGAATTTAGCAACCTGAATTTATT 1860
1801 AAGAGATTTATATTTCTACTATATATACCTTAGAATTTAGCAACCTGAATTTATT 1860
1861 CACATATATCAAGTGAAGAAATGCCCAATTCACATAGATTTCTTCTTTAGTAAAT 1920
1861 CACATATATCAAGTGAAGAAATGCCCAATTCACATAGATTTCTTCTTTAGTAAAT 1920
1921 TGACCTACTTGTGTAGTGAATAGTGAATCTTAACTTAACTTGAATTTAGT 1980
1921 TGACCTACTTGTGTAGTGAATAGTGAATCTTAACTTAACTTGAATTTAGT 1980
1981 CATCTTTACCAACCACTCTTAATTTTAAATTTTCTACTCTGTCTTAAATGAGAGTAC 2040
1981 CATCTTTACCAACCACTCTTAATTTTAAATTTTCTACTCTGTCTTAAATGAGAGTAC 2040
2041 TTGGTTTTTTTTTTCTTAAATATGATATATGACATTTTAAATGATATTTTCTTTT 2100
2041 TTGGTTTTTTTTTTCTTAAATATGATATATGACATTTTAAATGATATTTTCTTTT 2100
2101 AGACGAGTCTCTCTGTTACCAAGCTGAGTGAAGTGAATTTGCTCACTGCA 2160
2101 AGACGAGTCTCTCTGTTACCAAGCTGAGTGAAGTGAATTTGCTCACTGCA 2160
2161 AGCTGACCTCTCCCGGGTTCGACCAATTCCTGCTGACCTCCCAATTTAGCTGGCC 2220
2161 AGCTGACCTCTCCCGGGTTCGACCAATTCCTGCTGACCTCCCAATTTAGCTGGCC 2220
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2221 TACAGTATCTGACCAACCACTGCTAATTTTGTACTTTTATGATAGACAGGGTTTC 2280
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2341 CAAAGTCTGGGATTAACAGGATGAGCCACCG 2372
2341 CAAAGTCTGGGATTAACAGGATGAGCCACCG 2372
2341 CAAAGTCTGGGATTAACAGGATGAGCCACCG 2372

RESULT 14
US-09-048-810-1
Sequence 1, Application US/09048810
Patent No. 6238921
GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
TITLE OF INVENTION: MODULATION OF HUMAN MDM2 EXPRESSION
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marleton
STATE: NJ
COUNTRY: U.S.A.
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,810
FILING DATE: herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey

REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0302
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-779-2400
TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Oliner, J.D.
AUTHORS: Kintler, K.W.
AUTHORS: Meltzer, P.S.
AUTHORS: George, D. L.
AUTHORS: Vogelstein, B.
TITLE: Amplification of a gene encoding a
TITLE: p53-associated protein in human sarcomas
JOURNAL: Nature
VOLUME: 358
ISSUE: 6381
PAGES: 80-83
DATE: 02-JUL-1992
US-09-048-810-1

Query Match 100.0%; Score 2372; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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361 CACAGATTCACCTTGGAAACAAAGACCCCTGGTGAACCAAGCATTTGTAAGT 420
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541 GTTCAAAATGATCTTGAAGAGATTTGTTGGCGTCCAAAGCTTCTGTGAAGAGCACA 600
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Db	781	CTACCTCATTAAGAGAGCAATTAGTAGACAGAAAGAAATTCAGATGAATTAATCTG	840
Qy	841	GTGAACGACAAAGAAAAGCCCAAAATCTGATGTAATTTCCCTTCTTGATGAAGCC	900
Db	841	GTGAACGACAAAGAAAAGCCCAAAATCTGATGTAATTTCCCTTCTTGATGAAGCC	900
Qy	901	TGGCTCTGTGTGTAATTAAGGGAGATATGTGTGAAGAAAGAGTAGACGTAACTCAAG	960
Db	901	TGGCTCTGTGTGTAATTAAGGGAGATATGTGTGAAGAAAGAGTAGACGTAACTCAAG	960
Qy	961	GGACGCCATCCGATCCCGATCTTGAATGCTGTGTGAAGTGAACATTCAGGTATGGTTGG	1020
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Qy	1141	AAGTTACTGTGTATCAGCGACGGGGAGGTGATACAGATTCAATTGGAAGAAATCCTGAAA	1200
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Db	1201	TTTCTTATAGCTGATATTGGAATGCAATGCACCTTCATGCAATGAATGCAATCCCCCTTCAT	1260
Qy	1261	CACATTGCAACGATGTTGGGCCCTTCGTGAAGAAATTTGGCTTCGTGAAGTAAAGGGAAG	1320
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Qy	1321	ATTAAGGGGAAATCTCTGAGAAAGCCAAACCTGAAAACCTCAACAAGCTGAAGAGGCT	1380
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Db	1741	TATGTAGACAAACCAATTCGAATGATTTGTGCTAACTTATTTCCCTAATGACCGTCAT	1800
QY	1801	AAGGAATATATATTTCTTAACCTATATACCTTAGAATTTAGACAACCTGAATTTATT	1860
Db	1801	AAGGAATATATATTTCTTAACCTATATACCTTAGAATTTAGACAACCTGAATTTATT	1860
QY	1861	CACATATATCAAAGTGAGAAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT	1920
Db	1861	CACATATATCAAAGTGAGAAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT	1920
QY	1921	TGACCTACTTTGTAGTAGGAATAGTAATCTTAATTTGACTTGAATATAGTAC	1980
Db	1921	TGACCTACTTTGTAGTAGGAATAGTAATCTTAATTTGACTTGAATATAGTAC	1980
QY	1981	CATCCCTTACACCAACTCTTAATTTTAAATTAATTTCTACTCTGTCTTAAATGAGAAATAC	2040
Db	1981	CATCCCTTACACCAACTCTTAATTTTAAATTAATTTCTACTCTGTCTTAAATGAGAAATAC	2040
QY	2041	TTGGTTTTTTTTTCTTAATATGTATATGACATTTTAAATGTAACTTATATTTTTTTTG	2100
Db	2041	TTGGTTTTTTTTTCTTAATATGTATATGACATTTTAAATGTAACTTATATTTTTTTTG	2100
QY	2101	AGACCGAGCTTGTCTCTGTTTACCCAGGCTGGAGTGCAGTGGGTATCTTGGCTCACTGCA	2160
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US-09-170-159A-2			
; Sequence 2, Application US/09170159A			
; Patent No. 639755			
; GENERAL INFORMATION:			
; APPLICANT: BURELL, MARILEE			
; HILL, DAVID E.			
; KINZLER, KENNETH W.			
; VOGELSTEIN, BERT			
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN			
; HUMAN TUMORS			
NUMBER OF SEQUENCES: 5			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT			
STREET: 1001 G STREET, N.W.			
CITY: WASHINGTON			
STATE: D.C.			
COUNTRY: USA			
ZIP: 20001			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/170,159A			
FILING DATE: 13-Oct-1998			


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Qy 1861 CACATATATCAAAAGTAGAAAAATGCTCAATTCACATAGATTTCTTCTTTAGTAAAT 1920
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Qy 1921 TGACCTACTTTGGTAGTAGATAGTAACTACTATTAATTTGACTTGAATATGTAGCT 1980
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Qy 2161 AGCTCTGCGCCTCCCGGGTTCGACACATTTCTGCTCAGGCTCCCAATTAGTTGGCC 2220
Db 2161 AGCTCTGCGCCTCCCGGGTTCGACACATTTCTGCTCAGGCTCCCAATTAGTTGGCC 2220
Qy 2221 TACAGTCATCTGCCACCAACCTGGCTAATTTTGTACTTTTGTAGTAGAGACAGGTTTC 2280
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Qy 2281 ACCGTGTAGCCAGATGTCTCGATCTCTGACTCGTGAATCCGCCACTTGGCTTCC 2340
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Qy 2341 CAAAGTGCTGGGATTACAGGCATGAGCCACCG 2372
Db 2341 CAAAGTGCTGGGATTACAGGCATGAGCCACCG 2372
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Search completed: August 4, 2006, 19:57:17
Job time : 621 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 11:23:53 ; Search time 1486 Seconds
(without alignments)
11129.323 Million cell updates/sec

Title: US-09-966-724B-2

Perfect score: 2372

Sequence: 1 GCACCGCGCGAGACTTGCTGCTG.....ATTACAGGCGATGAGCACC 2372

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2372	100.0	2372	2	AAQ49891 Human MDM
2	2372	100.0	2372	2	AAQ94589 Human MDM
3	2372	100.0	2372	2	AAAT45151 Human MDM
4	2372	100.0	2372	2	AAAT66410 Human MDM
5	2372	100.0	2372	2	AAAT62065 Human MDM
6	2372	100.0	2372	2	AAAT20549 Human MDM
7	2372	100.0	2372	2	AAAT28876 Human MDM
8	2372	100.0	2372	2	AAAT4836 Human MDM
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12	2372	100.0	2372	2	AAAT35093 Human MDM
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16	2372	100.0	2372	2	AAAT29240 Human MDM
17	2372	100.0	2372	2	AAAT62113 Human MDM
18	2372	100.0	2372	2	AAAT42713 Human MDM

19	2372	100.0	2372	6	ABV94130
20	2372	100.0	2372	6	AAI43913
21	2372	100.0	2372	9	ADA02667
22	2372	100.0	2372	10	ADB72405
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39	1956.4	82.5	2174	10	ADQ95151
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ALIGNMENTS

RESULT 1	
ID	AAQ49891 standard; cDNA; 2372 BP.
XX	
AC	AAQ49891;
XX	
DT	25-MAR-2003 (revised)
DT	05-MAY-1994 (first entry)
XX	
DE	Human MDM2 gene.
XX	
KW	p53 gene; tumour suppressor gene; regulation; cellular proliferation; cellular transformation; carcinoma; human; tumour; MDM2; inhibition;
KW	gene amplification; ss.
OS	Homo sapiens.
XX	
PH	Key
FT	CDS
FT	Location/Qualifiers
FT	312..1787
FT	/*tag= a
FT	/product= "Human MDM2"
XX	
PN	W09320238-A2.
XX	
PD	14-OCT-1993.
XX	
PF	07-APR-1993; 93WO-US003199.
XX	
PR	07-APR-1992; 92US-00867840.
PR	23-JUN-1992; 92US-00903103.
XX	
PA	(UNYD) UNIV JOHNS HOPKINS.
XX	
PI	Burrell M, Hill DE, Kinzler KW, Vogelstein B;
XX	
DR	WPI: 1993-336944/42.
DR	P-PSDB; AAK42175.
XX	
PT	Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene expression, also new DNA, MDM2 protein, antibodies and treatment of sarcoma by inhibiting MDM2 expression.
PT	


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DB 1861 CACATATATCAAGTGAAGAAAATGCTCAATTCACATAGATTCTCTCTTAGATATAT 1920
QY 1921 TCACCTACTTGTGTAGTGAATATGTAAATATCTATATATTTGACTTGAATATGTAGCT 1980
DB 1921 TCACCTACTTGTGTAGTGAATATGTAAATATCTATATATTTGACTTGAATATGTAGCT 1980
QY 1981 CATCTCTTACACCAACTCTCTAATTTAATTAATTTCTACTGCTCTTAATGAGAGTAC 2040
DB 1981 CATCTCTTACACCAACTCTCTAATTTAATTAATTTCTACTGCTCTTAATGAGAGTAC 2040
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DB 2041 TTGGTTTTTTTTTCTTAATATGTATATGACATTTAAATGTAATATTTTGTG 2100
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DB 2101 AAGACGAGCTTGTCTGTATACCGAGCTGAGTGAAGTGTATCTTGCTCACTGCA 2160
QY 2161 AGCTGACCTCCCGGGTTCGACCATCTCTGCTGACCTCCCATTTAGCTTGGCC 2220
DB 2161 AGCTGACCTCCCGGGTTCGACCATCTCTGCTGACCTCCCATTTAGCTTGGCC 2220
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DB 2221 TACAGTCACTCTGCAACACACCTGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
QY 2281 ACCGTTTATGCCAGATGCTGATCTCTCTGACCTGATGATCCGCCACTTGCGCTTC 2340
DB 2281 ACCGTTTATGCCAGATGCTGATCTCTCTGACCTGATGATCCGCCACTTGCGCTTC 2340
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DB 2341 CAAAGTGTGGGATTTACAGGCAATGAGCCACCG 2372

RESULT 2
AA094589
ID AA094589 standard; cDNA; 2372 BP.
AC AA094589;
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AC 16-OCT-2003 (revised)
DT 01-NOV-1995 (first entry)
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DE Human MDM2 gene.
XX
KM MDM2; sarcoma; diagnostic; DNA probe; ds.
XX
OS Homo sapiens; (cell line CaCo-2).
XX
FH Key Location/Qualifiers
FT CDS 312..1784
FT /tag= a
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PN US5420263-A.
XX
PD 30-MAY-1995.
XX
PF 07-APR-1993; 93US-00044619.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-OUN-1992; 92US-00903103.
XX
PA (UUYO ) UNITV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW;
XX
DR WPI: 1995-206312/27.
XX
DR P-PSDB; AAF76696.
XX
PT New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
treatment of tumours.

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XX
PS Claim 1; Col 19-24; 34pp; English.
XX
CC The human MDM2 gene is genetically altered (i.e. amplified) in human
CC tumour cells. Detecting that the gene has become amplified or detecting
CC increased gene product expression (using probes, proteins, antibodies and
CC inhibitors) allow diagnosis and therapy of cancers such as colorectal
CC carcinoma, lung cancer and chronic myelogenous leukaemia. The human MDM2
CC protein binds to human p53 and allows the cell to escape from p53-
CC regulated growth. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 2372; BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCGCGGAGCTTGGCTGCTTCTTGAGGCGCTGTGTGCGCTGTGTGCGAAAGATGA 60
DB 1 GCACCGCGGAGCTTGGCTGCTTCTTGAGGCGCTGTGTGCGCTGTGTGCGAAAGATGA 60
QY 61 GCAAGAGCCGAGCCCGAGGCGCGCGGACCCCTTGACCGAATCCTGCTGCTTTCG 120
DB 61 GCAAGAGCCGAGCCCGAGGCGCGCGGACCCCTTGACCGAATCCTGCTGCTTTCG 120
QY 121 CAGCCAGAGACACCGTCCCTCCCGGATTAAGCGGTAGAGAGGCGCCAGTCCGCTG 180
DB 121 CAGCCAGAGACACCGTCCCTCCCGGATTAAGCGGTAGAGAGGCGCCAGTCCGCTG 180
QY 181 GAGAGTGAATATATCCCGAGGCGCGAGGCGTGTGCTTCCGAGTATGATGCCCCGTG 240
DB 181 GAGAGTGAATATATCCCGAGGCGCGAGGCGTGTGCTTCCGAGTATGATGCCCCGTG 240
QY 241 AAGAAATCTGGGAGTCTTTGAGGAGACCCCGACCTCCAGCGGAAACCCTGGATGTGA 300
DB 241 AAGAAATCTGGGAGTCTTTGAGGAGACCCCGACCTCCAGCGGAAACCCTGGATGTGA 300
QY 301 GAGGAGGCAATATGTGCAATACCAATCTGTCTGATCTATGATGCTGTATACCACT 360
DB 301 GAGGAGGCAATATGTGCAATACCAATCTGTCTGATCTATGATGCTGTATACCACT 360
QY 361 CACAGATTCAGCTTCGGAACAAGAGACCTGCTTGAAGCAAGCATTCGCTTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAAGAGACCTGCTTGAAGCAAGCATTCGCTTTGAAGT 420
QY 421 TATTAAGTCTGTGTGACAAAAAGACACTTATATCTATGAAAGGTTCTTTTATC 480
DB 421 TATTAAGTCTGTGTGACAAAAAGACACTTATATCTATGAAAGGTTCTTTTATC 480
QY 481 TTGGCCAGTATATTAAGTAAACGATTAATGATGAGAGCAACAATTTGATAT 540
DB 481 TTGGCCAGTATATTAAGTAAACGATTAATGATGAGAGCAACAATTTGATAT 540
QY 541 GTTCAAAATGATCTTGAAGAGATTTGTTGGGTGCCAAGCTTCTGTGAAGAAGCACA 600
DB 541 GTTCAAAATGATCTTGAAGAGATTTGTTGGGTGCCAAGCTTCTGTGAAGAAGCACA 600
QY 601 GGAATAATATATACATGATCTACAGGAACCTTGATAGTCAATGACAGATCATCGG 660
DB 601 GGAATAATATATACATGATCTACAGGAACCTTGATAGTCAATGACAGATCATCGG 660
QY 661 ACTCAGGTACATCTGTAGTGAAGAACAGGTGCACTTGAAAGTGTATCAAAAG 720
DB 661 ACTCAGGTACATCTGTAGTGAAGAACAGGTGCACTTGAAAGTGTATCAAAAG 720
QY 721 ACCTGTACAAGAGCTTCAAGAAAGAACTTCAATCTTCAATTTGGTTCTTGAAGCAT 780
DB 721 ACCTGTACAAGAGCTTCAAGAAAGAACTTCAATCTTCAATTTGGTTCTTGAAGCAT 780
QY 781 CTACCTCATTTGAAGAGAGCAATTAAGTGAAGAGAAATTCAGATGAATATCTG 840
DB 781 CTACCTCATTTGAAGAGAGCAATTAAGTGAAGAGAAATTCAGATGAATATCTG 840

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QY 841 GTGACGACAAAGAAAAGCCACAAATCTGATAGTATTCCTTCCTTTCCTTGTATGAAAGCC 900
Db 841 GTGACGACAAAGAAAAGCCACAAATCTGATAGTATTCCTTCCTTTCCTTGTATGAAAGCC 900
QY 901 TGGCTCTGTGTATTAATGAGAGATGTTGTGAAAAGACAGTAGCAATCTACAG 960
Db 901 TGGCTCTGTGTATTAATGAGAGATGTTGTGAAAAGACAGTAGCAATCTACAG 960
QY 961 GGAGGCGCATGGAATCCGATCTGATGCTGGGTATGAGAACATTCAGGTATGAGTGG 1020
Db 961 GGAGGCGCATGGAATCCGATCTGATGCTGGGTATGAGAACATTCAGGTATGAGTGG 1020
QY 1021 ATCAGATTCAGATTTCAGATCAGTTAGTATGATTTGAAGTTGAATCTCTCAGCTCAG 1080
Db 1021 ATCAGATTCAGATTTCAGATCAGTTAGTATGATTTGAAGTTGAATCTCTCAGCTCAG 1080
QY 1081 AAGATTATAGCCTTAGTAAAGAGACAAAGAACTCTCAGATGAGATGATGATATATC 1140
Db 1081 AAGATTATAGCCTTAGTAAAGAGACAAAGAACTCTCAGATGAGATGATGATATATC 1140
QY 1141 AAGTTACTGTGTATGAGGACGGGAGAGTATGATGATTCATTTGAAGAAATCTCGAAA 1200
Db 1141 AAGTTACTGTGTATGAGGACGGGAGAGTATGATGATTCATTTGAAGAAATCTCGAAA 1200
QY 1201 TTTCTTCTAGCTGACTATTTGAAAATGCACTTCATGCAATGAAATGAAATCCCTTCAT 1260
Db 1201 TTTCTTCTAGCTGACTATTTGAAAATGCACTTCATGCAATGAAATGAAATCCCTTCAT 1260
QY 1261 CACATTCGACAGATGTTGGGCTTCGTGAGAAATTTGCTTCGAAATGAAAGGAAAAG 1320
Db 1261 CACATTCGACAGATGTTGGGCTTCGTGAGAAATTTGCTTCGAAATGAAAGGAAAAG 1320
QY 1321 AATAAGGGGAAATCTCTGAGAAAGCCAAACCTGCAACAGCTGAGAGGGCT 1380
Db 1321 AATAAGGGGAAATCTCTGAGAAAGCCAAACCTGCAACAGCTGAGAGGGCT 1380
QY 1381 TTGATGTTCTGATGTTGTAATAAACTATATGATGATTCAGAGAGTCAATGTTGAGG 1440
Db 1381 TTGATGTTCTGATGTTGTAATAAACTATATGATGATTCAGAGAGTCAATGTTGAGG 1440
QY 1441 AAAATGATGATTAATAATTAACAAGCTTCACATCAACAAGAAAGTGAAGCTATTCAGC 1500
Db 1441 AAAATGATGATTAATAATTAACAAGCTTCACATCAACAAGAAAGTGAAGCTATTCAGC 1500
QY 1501 CATCACTCTCTAGTATGATATTTATATGAGGACCAAGAGATGTAAGGTTGAAAGGG 1560
Db 1501 CATCACTCTCTAGTATGATATTTATATGAGGACCAAGAGATGTAAGGTTGAAAGGG 1560
QY 1561 AAGAAACCAAGACAAAGAGAGTGTGATCTAGTTGCCCCCTTAATGCCATTGAAC 1620
Db 1561 AAGAAACCAAGACAAAGAGAGTGTGATCTAGTTGCCCCCTTAATGCCATTGAAC 1620
QY 1621 CTGTTGATGATTTGTCAAGGTTCAGCTAAAAATGTTGCAATTCATGCAAAACAGAC 1680
Db 1621 CTGTTGATGATTTGTCAAGGTTCAGCTAAAAATGTTGCAATTCATGCAAAACAGAC 1680
QY 1681 ATCTTATGCGCTGCTTTACATGTGCAAGAGACTTAAAGAAAGAAATAGCCCTGCCAG 1740
Db 1681 ATCTTATGCGCTGCTTTACATGTGCAAGAGACTTAAAGAAAGAAATAGCCCTGCCAG 1740
QY 1741 TATGTAGACCAACCAATTCAAATGATGCTACTAATTTCCCTAGTTGACCTGTCTAT 1800
Db 1741 TATGTAGACCAACCAATTCAAATGATGCTACTAATTTCCCTAGTTGACCTGTCTAT 1800
QY 1801 AAGAGATTATATATTTCTAATATATTAACCTAGGAATTTAGACAACCTGAATTTAT 1860
Db 1801 AAGAGATTATATATTTCTAATATATTAACCTAGGAATTTAGACAACCTGAATTTAT 1860
QY 1861 CACATATATCAAGTAGAAGAAATGCTCAATTCACATATATTTCTCTTATAGTATAT 1920
Db 1861 CACATATATCAAGTAGAAGAAATGCTCAATTCACATATATTTCTCTTATAGTATAT 1920
QY 1921 TGACCTACTTGTGTATGTAATGTAATACTATATATTTGACTGAAATATGATGCT 1980

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Db 1921 TGACCTACTTGTGTATGTAATGTAATACTATATATTTGACTGAAATATGATGCT 1980
QY 1981 CATCTTTACACCAACTCTTAATTTTAAATTAATTTTCACTGCTTAAATGAGAGTAC 2040
Db 1981 CATCTTTACACCAACTCTTAATTTTAAATTAATTTTCACTGCTTAAATGAGAGTAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAATATATATGATGATTTAAATGTAATTTATTTTGG 2100
Db 2041 TTGGTTTTTTTTTTCTTAATATATATGATGATTTAAATGTAATTTATTTTGG 2100
QY 2101 AGACGAGTCTTGTCTGTTAACCCAGGCTGAGTGCAGTGGTATCTTGCTCACTGCA 2160
Db 2101 AGACGAGTCTTGTCTGTTAACCCAGGCTGAGTGCAGTGGTATCTTGCTCACTGCA 2160
QY 2161 AGCTTGCTGCTCCCGGCTTGACACATTCCTCCGCTCAGCCCTCCAAATAGCTGGCC 2220
Db 2161 AGCTTGCTGCTCCCGGCTTGACACATTCCTCCGCTCAGCCCTCCAAATAGCTGGCC 2220
QY 2221 TACAGTCACTGACCAACCACTGAGCTAATTTTGTACTTTTATAGAGACAGGTTTC 2280
Db 2221 TACAGTCACTGACCAACCACTGAGCTAATTTTGTACTTTTATAGAGACAGGTTTC 2280
QY 2281 ACCGTTTACGACAGATGCTGATCTCTGACCTGATGATCCGCCACCTCGGCTTC 2340
Db 2281 ACCGTTTACGACAGATGCTGATCTCTGACCTGATGATGATCCGCCACCTCGGCTTC 2340
QY 2341 CAAAGTGTGGGATTTACAGGATGAGCCACCG 2372
Db 2341 CAAAGTGTGGGATTTACAGGATGAGCCACCG 2372

RESULT 3
AAT45151
ID AAT45151 standard; cDNA; 2372 BP.
XX
AC AAT45151;
XX
AC 25-MAR-2003 (revised)
XX
DT 28-JAN-1997 (first entry)
XX
DE Human MDM-2 gene cDNA clone, involved in tumour-development.
XX
KW p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
XX antibody fusion protein; therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 312..1787
FT /*tag= a
XX
XX US5550023-A.
XX PN
XX PD 27-AUG-1996.
XX
XX 18-MAY-1994; 94US-00245500.
XX
XX 07-APR-1992; 92US-00867840.
XX PR 23-JUN-1992; 92US-00903103.
XX PR 07-APR-1993; 93US-00044619.
XX
XX (UNGO ) UNIV JOHNS HOPKINS.
XX PA
XX PI Vogelstein B, Kinzler KW;
XX DR MPI; 1996-401591/40.
XX DR P-PSDB; AAM07887.
XX
XX PT Identification of cpds. interfering with human MDM2/p53 binding - useful
XX as therapeutic agents to treat human neoplastic cells.
XX
XX Example 1; Col 21-26; 36P; English.

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XX AAT45151 is a cDNA clone of the human MDM-2 gene derived from a human
CC colon carcinoma cell line CaCo-2. The MDM-2 protein produced by this
CC clone is used in a method for identifying compounds that interfere with
CC the binding of p53 and MDM-2. In binding the p53 protein, the MDM-2
CC protein releases a cell from p53-regulated growth, allowing cancers to
CC develop. Therefore compounds identified as interfering with the binding
CC of MDM-2 to p53 are potentially useful in the treatment of human
CC neoplastic cells. In the method pref. one or both of the proteins is a
CC fusion protein esp. with an antibody or antibody fragment which aids
CC separation and identification. (Updated on 25-MAR-2003 to correct PF
CC field.)

Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCTGTGTCGCTGTGTGCGAAAGATGGA 60
1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCTGTGTCGCTGTGTGCGAAAGATGGA 60
61 GCAGAGCCGAGGCCCGGAGGGGGCGCGGACCCCTCTGACCGAGATCCTGCTGTTG 120
61 GCAGAGCCGAGGCCCGGAGGGGGCGCGGACCCCTCTGACCGAGATCCTGCTGTTG 120
121 CAGCCAGAGGACCCGCTCCCGGATTAGTGCAGAGCGCCAGTCCCTGCGCCG 180
121 CAGCCAGAGGACCCGCTCCCGGATTAGTGCAGAGCGCCAGTCCCTGCGCCG 180
181 GAGAGTGAATATCCCGAGGGCCGAGGGCGTGTGCTTCCGAGTAGTCAATCCCCG 240
181 GAGAGTGAATATCCCGAGGGCCGAGGGCGTGTGCTTCCGAGTAGTCAATCCCCG 240
241 AAGGAACTGSGGAGTCTTGAAGGACCCCGGACTCCAGCGGAAACCCCGATGTA 300
241 AAGGAACTGSGGAGTCTTGAAGGACCCCGGACTCCAGCGGAAACCCCGATGTA 300
301 GGAGCAGGCAATGTGCAATACCAATGTGTGTACTGATGATGATGATGATGATG 360
301 GGAGCAGGCAATGTGCAATACCAATGTGTGTACTGATGATGATGATGATGATG 360
361 CACAGATTCAGCTTCGGAACAAGAGACCTGTGTAAGCAAAAGCATTTGTAAGT 420
361 CACAGATTCAGCTTCGGAACAAGAGACCTGTGTAAGCAAAAGCATTTGTAAGT 420
421 TATTAAGTCTGTGTCACAAAAGACATTTATCTATGAAAGGTTCTTTTATC 480
421 TATTAAGTCTGTGTCACAAAAGACATTTATCTATGAAAGGTTCTTTTATC 480
481 TTGGCAGTATATATGACTAAACATTTATGATGAGAGCAACAATATTTATAT 540
481 TTGGCAGTATATATGACTAAACATTTATGATGAGAGCAACAATATTTATAT 540
541 TTGGCAGTATATATGACTAAACATTTATGATGAGAGCAACAATATTTATAT 540
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541 GTTCAATGATTTTCTAAGAGTTTGTGGCTGCAAGCTTCTCTGTGAAGACACA 600
541 GTTCAATGATTTTCTAAGAGTTTGTGGCTGCAAGCTTCTCTGTGAAGACACA 600
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541 GTTCAATGATTTTCTAAGAGTTTGTGGCTGCAAGCTTCTCTGTGAAGACACA 600
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601 GGAATATATATACATGATCTACAGAACTTGTGTGATGATCAATACGAGATATG 660
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601 GGAATATATATACATGATCTACAGAACTTGTGTGATGATCAATACGAGATATG 660
661 ACTCAGGTATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGATGATCAAA 720
661 ACTCAGGTATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGATGATCAAA 720
721 ACCTGTCAAGAGCTTCAAGAGAAACCTTCACTTCAATTTGTTTCAAGCAT 780
721 ACCTGTCAAGAGCTTCAAGAGAAACCTTCACTTCAATTTGTTTCAAGCAT 780
721 ACCTGTCAAGAGCTTCAAGAGAAACCTTCACTTCAATTTGTTTCAAGCAT 780
721 ACCTGTCAAGAGCTTCAAGAGAAACCTTCACTTCAATTTGTTTCAAGCAT 780
781 CTACCTCATCTGAAGAGCAATTAAGTGAAGAGAAATTCAGATGATATATC 840
781 CTACCTCATCTGAAGAGCAATTAAGTGAAGAGAAATTCAGATGATATATC 840
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781 CTACCTCATCTGAAGAGCAATTAAGTGAAGAGAAATTCAGATGATATATC 840
841 GTGAAGCAAAAGAAACCCCAATCTGATATGATTTTCCCTTCTTGTGAAGCC 900
841 GTGAAGCAAAAGAAACCCCAATCTGATATGATTTTCCCTTCTTGTGAAGCC 900
841 GTGAAGCAAAAGAAACCCCAATCTGATATGATTTTCCCTTCTTGTGAAGCC 900
901 TGGCTGTGTGTAATTAAGAGATATGTTGAAAGAGAGTACAGATCTACAG 960
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901 TGGCTGTGTGTAATTAAGAGATATGTTGAAAGAGAGTACAGATCTACAG 960
901 TGGCTGTGTGTAATTAAGAGATATGTTGAAAGAGAGTACAGATCTACAG 960
961 GGAAGCATGATCCGATCTTGTGATGCTGTGTAAGTGAATTCAGATGATGAT 1020
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1081 AAGATTTATGCTTGTGTAAGAGCAAGAACTCTCAGATGAAGTGAAGTATATC 1140
1081 AAGATTTATGCTTGTGTAAGAGCAAGAACTCTCAGATGAAGTGAAGTATATC 1140
1081 AAGATTTATGCTTGTGTAAGAGCAAGAACTCTCAGATGAAGTGAAGTATATC 1140
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1321 ATTAAGGGGAAATCTCTGGAAGCAAACTGGAATCTCAACAAGCTGAAGAGGCT 1380
1321 ATTAAGGGGAAATCTCTGGAAGCAAACTGGAATCTCAACAAGCTGAAGAGGCT 1380
1321 ATTAAGGGGAAATCTCTGGAAGCAAACTGGAATCTCAACAAGCTGAAGAGGCT 1380
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1501 CATCACTTCTATGATGATTTATTTATGAGCAGCAAGAGATGTAAGGTTGAAAG 1560
1501 CATCACTTCTATGATGATTTATTTATGAGCAGCAAGAGATGTAAGGTTGAAAG 1560
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1561 AAGAAACCCAGCAAGAGAGAGTGTGATCTTATGTTGCTTATGATGATGATG 1620
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1621 CTGTGTGATTTTCAAGGTGACCTTAAATGTTGATGATGATGATGATGATG 1680
1621 CTGTGTGATTTTCAAGGTGACCTTAAATGTTGATGATGATGATGATGATG 1680
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1681 ATCTATGAGCTGCTTCAATGATGATGATGATGATGATGATGATGATGATG 1740
1741 TATGTAGCAACCAATCAATGATGATGATGATGATGATGATGATGATGATG 1800
1741 TATGTAGCAACCAATCAATGATGATGATGATGATGATGATGATGATGATG 1800
1741 TATGTAGCAACCAATCAATGATGATGATGATGATGATGATGATGATGATG 1800
1741 TATGTAGCAACCAATCAATGATGATGATGATGATGATGATGATGATGATG 1800
1801 AAGAAATTAATTAATTTTAACTATATTAACCTAGGAATTAAGAACTGAAAT 1860
1801 AAGAAATTAATTAATTTTAACTATATTAACCTAGGAATTAAGAACTGAAAT 1860
1801 AAGAAATTAATTAATTTTAACTATATTAACCTAGGAATTAAGAACTGAAAT 1860
1801 AAGAAATTAATTAATTTTAACTATATTAACCTAGGAATTAAGAACTGAAAT 1860
1861 CACATATATCAAGAGGAAAGTGCCTCAATCAATGATGATGATGATGATGAT 1920
1861 CACATATATCAAGAGGAAAGTGCCTCAATCAATGATGATGATGATGATGAT 1920
1861 CACATATATCAAGAGGAAAGTGCCTCAATCAATGATGATGATGATGATGAT 1920
1861 CACATATATCAAGAGGAAAGTGCCTCAATCAATGATGATGATGATGATGAT 1920
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QY	1921	TGACCTTATTTGGTAGTGGGAATAGTGAATACTTATACATATTAATTTGACTTGAATATGTAGCT	1980
Db	1921	TGACCTTACTTTGGTAGTGGGAATAGTGAATACTTACTTAAATTTGACTTGAATATGTAGCT	1980
QY	1981	CATCCTTTACACAACTCCATAATTTTAAATATTTTCACTCTGTCTTAAATAGAGAACTAC	2040
Db	1981	CATCCTTTACCAACACTCTATAATTTTAAATATATTTTCACTCTGTCTTAAATAGAGAACTAC	2040
QY	2041	TTGGTTTTTTTTTCTTAATATGTATATGACATTTAAATGTAACTTATATTTTTTTTG	2100
Db	2041	TTGGTTTTTTTTTCTTAAATATGTATATGTACATTTAAATGTAACTTATATTTTTTTTG	2100
QY	2101	AGACCGAGCTTGCTCTGTATCCAGAGCTGAGTGAAGTGGGTATCTTGGCTCACTGCA	2160
Db	2101	AGACCGAGCTTGCTCTGTATCCAGAGCTGAGTGAAGTGGGTATCTTGGCTCACTGCA	2160
QY	2161	AGCTCTGCCCTCCCGGGTTCGACACATTTCTCTGCCCTCAAGCTCCCAATTAGCTTGACC	2220
Db	2161	AGCTCTGCCCTCCCGGGTTCGACACATTTCTCTGCCCTCAAGCTCCCAATTAGCTTGACC	2220
QY	2221	TACAGTCACTTCGCCAACCACTCTGGCTAATTTTTTGTACTTTTATGTAGAACAAGGTTTC	2280
Db	2221	TACAGTCACTTCGCCAACCACTCTGGCTAATTTTTTGTACTTTTATGTAGAACAAGGTTTC	2280
QY	2281	ACCGTGTAGACAGAGATGCTTCGATCTCTGACCTCGTGAATCGGCCCACTCGGCTCC	2340
Db	2281	ACCGTGTAGACAGAGATGCTTCGATCTCTGACCTCGTGAATCGGCCCACTCGGCTCC	2340
QY	2341	CAAACTGCTGGGATTTACAGCGATGAGCCACCG	2372
Db	2341	CAAACTGCTGGGATTTACAGCGATGAGCCACCG	2372

Accession ID	Gene	Protein	Location/Qualifiers
AA166410	standard; cDNA, 2372 BP.		
AA166410;			
25-MAR-2003	(revised)		
14-SEP-2000	(revised)		
18-JUN-1997	(first entry)		
Human MDM2 coding sequence.			
Human; MDM2 protein; antibody; detection; cancer; diagnosis;			
p53-regulated growth; ds.			
Homo sapiens.			
Key	Location/Qualifiers		
CDS	312..1787		
FT	/*tag= a		
FT	/product= "MDM2"		
US5618921-A.			
08-APR-1997.			
17-FEB-1995;	95US-00390479.		
07-APR-1992;	92US-00867840.		
23-JUN-1992;	92US-00903103.		
07-APR-1993;	93US-00044619.		
UNIV JOHNS HOPKINS.			
Vogelstein B, Kinzler KW, Burrell M, Hill DE;			
WPI, 1997-225474/20.			
P-PSDB; AAM15463.			

PT	Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX	
PS	Claim 1; Col 19-24; 35pp; English.
XX	
CC	This sequence encodes the human MDM2 protein. Antibodies that
CC	specifically bind to human MDM2 protein may be used for detecting
CC	elevated expression of the MDM2 gene in a human tissue or body fluid
CC	sample, esp. for cancer diagnosis. The antibodies may be used to
CC	interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
CC	to sequester p53 and allow the cell to escape from p53-regulated growth.
CC	(N.B. Revised record issued to correct the sequence analysis field.)
CC	(Updated on 25-MAR-2003 to correct pr field.)
XX	
SQ	Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
	Query Match 100.0%; Score 2372; DB 2; Length 2372;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 GCACCGCCGAGCTTGCTGCTTCTGGGGCTGTGTGCGCCTGTGTGTGGAAGAATGGA 60
OY	1 GCACCGCCGAGCTTGCTGCTTCTGGGGCTGTGTGCGCCTGTGTGTGGAAGAATGGA 60
OY	61 GCAAGAACCCGAGCCCCAGGGGGCGGCCGCACCCTCTGACCGAATCCBCTGCTTTGC 120
Db	61 GCAAGAACCCGAGCCCCAGGGGGCGGCCGCACCCTCTGACCGAATCTCTGCTTTGC 120
OY	121 CAGCCAGGAGACCGCTCCCTCCCGGATTATGTCGTAGACGCGCCCATGTGCTTGCCC 180
Db	121 CAGCCAGGAGACCGCTCCCTCCCGGATTATGTCGTAGACGCGCCCATGTGCTTGCCC 180
OY	181 GAGAGTGAATGATCCCGGAGGCCCGGGCGTCTGTCTCCGAGTAGTCAGTCCCGTG 240
Db	181 GAGAGTGAATGATCCCGGAGGCCCGGGCGTCTGTCTCCGAGTAGTCAGTCCCGTG 240
OY	241 AAGGAACTGGGGAGTCTTTAGAGGACCCCCGACTCCAGCCCGGAAAACCCCGAGTGA 300
Db	241 AAGGAACTGGGGAGTCTTTAGAGGACCCCCGACTCCAGCCCGGAAAACCCCGAGTGA 300
OY	301 GGAGAGGCGAATGTGCAATACCAACATGTCTGTACTAGTAGTGCTGTAAACCACT 360
Db	301 GGAGAGGCGAATGTGCAATACCAACATGTCTGTACTAGTAGTGCTGTAAACCACT 360
OY	361 CACAGATTCAGGCTTCGGAACAAGAGCCCTGGTTAGCAAAGCCATTGCTTTGAAGT 420
Db	361 CACAGATTCAGGCTTCGGAACAAGAGCCCTGGTTAGCAAAGCCATTGCTTTGAAGT 420
OY	421 TATTAAAGTCTGTGGTGCAAAAAAGACCTTAATCTATGAAAAGGTTCTTTTTATC 480
Db	421 TATTAAAGTCTGTGGTGCAAAAAAGACCTTAATCTATGAAAAGGTTCTTTTTATC 480
OY	481 TTGGCCAGATATATATNGACTAAAGCATTAATATATGATGAGAGCAACAATATTATAT 540
Db	481 TTGGCCAGATATATATNGACTAAAGCATTAATATATGATGAGAGCAACAATATTATAT 540
OY	541 GTTCAATATGATCTTCTAGAGATTTGTTGGCGTCCAAGCTTCTCTGTGAAGACACA 600
Db	541 GTTCAATATGATCTTCTAGAGATTTGTTGGCGTCCAAGCTTCTCTGTGAAGACACA 600
OY	601 GGAATAATATATACATGATCTACAGGAACCTTGTAAGTCAATCAGCAGGATATCTCG 660
Db	601 GGAATAATATATACATGATCTACAGGAACCTTGTAAGTCAATCAGCAGGATATCTCG 660
OY	661 ACTCAGGTACATCTGTGAGTGGAACAGGTGTCACTTGGAAGTGGAGTATCAAAAG 720
Db	661 ACTCAGGTACATCTGTGAGTGGAACAGGTGTCACTTGGAAGTGGAGTATCAAAAG 720
OY	721 ACCTGTACAAAGGCTTCAGAAAGAAACCTTCAATCTTCACTTTGTTTGTAGCAAT 780
Db	721 ACCTGTACAAAGGCTTCAGAAAGAAACCTTCAATCTTCACTTTGTTTGTAGCAAT 780
OY	781 CTACCTCATCTAAGAGAGCAATTAAGTACAGAAAGAAATTCAGTGAATTAATCTTG 840
Db	781 CTACCTCATCTAAGAGAGCAATTAAGTACAGAAAGAAATTCAGTGAATTAATCTTG 840

Db 781 CTACCTCATCTAGAGAGAGCAATTAGTGAGACAGAGAGAAATTCAGATGAAATTAATCTG 840
Qy 841 GTGACGACAAAGAAAACGCCACAATTCGATAGTAATTCCTTCCTTCCTTGAGAAAGCC 900
Db 841 GTGACGACAAAGAAAACGCCACAATTCGATAGTAATTCCTTCCTTCCTTGAGAAAGCC 900
Qy 901 TGGCTCTGTGTATATAGGAGATATGTGTGAAAAGAGCAGTAGCAGTAATCTACAG 960
Db 901 TGGCTCTGTGTATATAGGAGATATGTGTGAAAAGAGCAGTAGCAGTAATCTACAG 960
Qy 961 GGAAGCCATCAGATCCGGATCTTGATGCTGTGTAAAGTAACATTCAGGTGATGGTGG 1020
Db 961 GGAAGCCATCAGATCCGGATCTTGATGCTGTGTAAAGTAACATTCAGGTGATGGTGG 1020
Qy 1021 ATGAGATTCAGTTTACAGATTCAGTATAGCTAGAAATTTGAAAGTTGAAATCTCTGACTCAG 1080
Db 1021 ATGAGATTCAGTTTACAGATTCAGTATAGCTAGAAATTTGAAAGTTGAAATCTCTGACTCAG 1080
Qy 1081 AAGATTATAGCCTTAGTGAAGAGACAAGAACTCTCAGATGAAGTGAATGAGGTATATC 1140
Db 1081 AAGATTATAGCCTTAGTGAAGAGACAAGAACTCTCAGATGAAGTGAATGAGGTATATC 1140
Qy 1141 AAGTACTGTGTATCAGGACAGGGAGAGTATACAGATTCATTGGAAGAGATCTGAAA 1200
Db 1141 AAGTACTGTGTATCAGGACAGGGAGAGTATACAGATTCATTGGAAGAGATCTGAAA 1200
Qy 1201 TTTCTTACCTGACTATTTGGAATGCACTTCATGCAATGAATGAATCCCTCCCTTCAT 1260
Db 1201 TTTCTTACCTGACTATTTGGAATGCACTTCATGCAATGAATGAATCCCTCCCTTCAT 1260
Qy 1261 CACATTGCAACAGATGTGGGCTTCGTGAGAAATGGCTCTCTGAAATGAAGAGGAAAG 1320
Db 1261 CACATTGCAACAGATGTGGGCTTCGTGAGAAATGGCTCTCTGAAATGAAGAGGAAAG 1320
Qy 1321 ATPAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGCTGAAGAGGCT 1380
Db 1321 ATPAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGCTGAAGAGGCT 1380
Qy 1381 TTGATGTCTGTATTTGAAAAAACTATGTGATGATTCAGAGAGTCAATGTTGAGG 1440
Db 1381 TTGATGTCTGTATTTGAAAAAACTATGTGATGATTCAGAGAGTCAATGTTGAGG 1440
Qy 1441 AAAATGATGATTAATTAACAAGCTTCAATCAACAAGAGTGAAGCTATTCACAC 1500
Db 1441 AAAATGATGATTAATTAACAAGCTTCAATCAACAAGAGTGAAGCTATTCACAC 1500
Qy 1501 CATCAACTTCTAGTAGCATTATTTATAGAGCCAAAGATGGAAGAGTTGAAAGG 1560
Db 1501 CATCAACTTCTAGTAGCATTATTTATAGAGCCAAAGATGGAAGAGTTGAAAGG 1560
Qy 1561 AAGAAACCCAGAACAAGAGAGTGTGAATCTAGTTGCCCTTAAATGCCATTGAAC 1620
Db 1561 AAGAAACCCAGAACAAGAGAGTGTGAATCTAGTTGCCCTTAAATGCCATTGAAC 1620
Qy 1621 CTTGTGTGTTTGTCAAGGTGCACTTAAATGTTGCAATGTCATGGCAAAACAGGAC 1680
Db 1621 CTTGTGTGTTTGTCAAGGTGCACTTAAATGTTGCAATGTCATGGCAAAACAGGAC 1680
Qy 1681 ATCTTATGAGCTGCTTATCATGTGCAAGAGCTAAAGAAAGAAATAGACCTGCCAG 1740
Db 1681 ATCTTATGAGCTGCTTATCATGTGCAAGAGCTAAAGAAAGAAATAGACCTGCCAG 1740
Qy 1741 TATGTAGACAACTTCAATGATGTGTCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
Db 1741 TATGTAGACAACTTCAATGATGTGTCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
Qy 1801 AAGAGATATATATTTCTAATATTAACCTTGAAGATTTGACAACTGAATTTAT 1860
Db 1801 AAGAGATATATATTTCTAATATTAACCTTGAAGATTTGACAACTGAATTTAT 1860
Qy 1861 CACATATATCAAGTGAAGAAATGCCCTCAATTCACATAGATTTCTCTCTTAGTAAAT 1920
Db 1861 CACATATATCAAGTGAAGAAATGCCCTCAATTCACATAGATTTCTCTCTTAGTAAAT 1920

Qy 1921 TGACCTACTTTGGTAGTGAATAGTGAATTAATTAATTTGACTGAATATAGCT 1980
Db 1921 TGACCTACTTTGGTAGTGAATAGTGAATTAATTAATTTGACTGAATATAGCT 1980
Qy 1981 CATCTTTACACCACTCCCTAAATTTAAATTAATTTCTACTGTCTTAAATGAGAGTAC 2040
Db 1981 CATCTTTACACCACTCCCTAAATTTAAATTAATTTCTACTGTCTTAAATGAGAGTAC 2040
Qy 2041 TTGTTTTTTTTTTCTTAAATATGTAATGACATTTAAATGTAATTAATTTTGTG 2100
Db 2041 TTGTTTTTTTTTTCTTAAATATGTAATGACATTTAAATGTAATTAATTTTGTG 2100
Qy 2101 AAGACGATCTGCTCTGTATCCAGAGCTGAGAGTGAAGAGGAGTCTGACTGCA 2160
Db 2101 AAGACGATCTGCTCTGTATCCAGAGCTGAGAGTGAAGAGGAGTCTGACTGCA 2160
Qy 2161 AGCTGACCTCCCGGGTTGCAACATTCCTGCTCAGCCTCCCAATTAAGCTTGACC 2220
Db 2161 AGCTGACCTCCCGGGTTGCAACATTCCTGCTCAGCCTCCCAATTAAGCTTGACC 2220
Qy 2221 TACAGTCAATCTGCCACACACACCTGGCTAATTTTGTACTTTAGTAGAGAGAGGTTTC 2280
Db 2221 TACAGTCAATCTGCCACACACACCTGGCTAATTTTGTACTTTAGTAGAGAGAGGTTTC 2280
Qy 2281 ACCGTGTAGCCAGATGATCTCTGATCTCTGACCTGATCCGCCACCTGGCTCC 2340
Db 2281 ACCGTGTAGCCAGATGATCTCTGATCTCTGACCTGATCCGCCACCTGGCTCC 2340
Qy 2341 CAAAGTCTGGGATTAACAGGCAATGAGCCAGC 2372
Db 2341 CAAAGTCTGGGATTAACAGGCAATGAGCCAGC 2372

RESULT 5
AAT62065
ID AAT62065 standard; cDNA; 2372 BP.
XX
AC AAT62065;
XX
DT 25-MAR-2003 (revised)
DT 05-JUN-1997 (first entry)
XX
XX
DE Human MDM2 cDNA.
XX
XX Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
KW elevation; expression; diagnosis; neoplasia; neoplastic transformation;
KW sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia; ds.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 312..1787
FT /*tag= a
FT /product= "MDM2"
XX
PN US5606044-A.
XX
PD 25-FEB-1997.
XX
PF 17-FEB-1995; 95US-00390546.
XX
XX 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
XX
PA (U930) UNIV JOHNS HOPKINS.
XX
XX Kinzler KW, Vogelstein B, Hill DE, Burrell M;
PI WPI; 1997-153623/14.
DR P-PSDB; AAW13380.
XX

PT Detection of amplification of human MDM2 gene - useful for diagnosis of
PT neoplasia or potential neoplastic transformation.

PS Claim 1; Col 21-24; 35pp; English.

XX The present sequence is the human MDM2 cDNA, which was isolated from a
CC human CaCo-2 colonic carcinoma cell cDNA library using a murine MDM2 cDNA
CC probe. The MDM2 cDNA can be used as a probe to detect the amplification
CC or elevated expression of a human MDM2 gene, which is diagnostic of
CC neoplasia or the potential for neoplastic transformation, useful for the
CC detection of, e.g. sarcomas, colorectal carcinoma, lung cancer and
CC chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to correct FP
CC field.)

CC Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCACCGCCGAGCTTGGCTTCTTGGGCGCTGTGCGCCCTGTGTGCGAAAGATGGA 60
DB 1 GCACCGCCGAGCTTGGCTTCTTGGGCGCTGTGTGCGCCCTGTGTGCGAAAGATGGA 60
QY 61 GCAGAGCCGAGCCGAGGCGGCGCGGACCCCTTGAACCGAGATCTGTGCTTTCG 120
DB 61 GCAGAGCCGAGCCGAGGCGGCGCGGACCCCTTGAACCGAGATCTGTGCTTTCG 120
QY 61 GCAGAGCCGAGCCGAGGCGGCGCGGACCCCTTGAACCGAGATCTGTGCTTTCG 120
DB 61 GCAGAGCCGAGCCGAGGCGGCGCGGACCCCTTGAACCGAGATCTGTGCTTTCG 120
QY 121 CAGCCAGAGACGCTGCTTCCCTCCGAGTTAGTCGACGAGCGCCAGTGCCTTGCCCG 180
DB 121 CAGCCAGAGACGCTGCTTCCCTCCGAGTTAGTCGACGAGCGCCAGTGCCTTGCCCG 180
QY 121 CAGCCAGAGACGCTGCTTCCCTCCGAGTTAGTCGACGAGCGCCAGTGCCTTGCCCG 180
DB 121 CAGCCAGAGACGCTGCTTCCCTCCGAGTTAGTCGACGAGCGCCAGTGCCTTGCCCG 180
QY 181 GAGAGTGAATATATCCCCGAGGCGCGGAGTGTGCTTCCGAGTGAATATATATATAT 240
DB 181 GAGAGTGAATATATCCCCGAGGCGCGGAGTGTGCTTCCGAGTGAATATATATATAT 240
QY 181 GAGAGTGAATATATCCCCGAGGCGCGGAGTGTGCTTCCGAGTGAATATATATATAT 240
DB 181 GAGAGTGAATATATCCCCGAGGCGCGGAGTGTGCTTCCGAGTGAATATATATATAT 240
QY 241 AAGGAACTGGGAGTCTTGAAGGACCCCGGACTCCAGCGGAGAAACCCCGAGTGTGA 300
DB 241 AAGGAACTGGGAGTCTTGAAGGACCCCGGACTCCAGCGGAGAAACCCCGAGTGTGA 300
QY 301 GAGAGCGCAATATGTCATATACCAATATCTGTATCTATGATGTGCTGTACCACT 360
DB 301 GAGAGCGCAATATGTCATATACCAATATCTGTATCTATGATGTGCTGTACCACT 360
QY 301 GAGAGCGCAATATGTCATATACCAATATCTGTATCTATGATGTGCTGTACCACT 360
DB 301 GAGAGCGCAATATGTCATATACCAATATCTGTATCTATGATGTGCTGTACCACT 360
QY 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGTTAGACCAAGCATTTGTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGTTAGACCAAGCATTTGTTGAAGT 420
QY 421 TATTAAGTCTGTGCTGTGCAAAAAAGACATTAATCTATGAAGAAGTCTTTTATATC 480
DB 421 TATTAAGTCTGTGCTGTGCAAAAAAGACATTAATCTATGAAGAAGTCTTTTATATC 480
QY 481 TTGGCCAGTATTTATGACTAAACGATTAATGATGAAGAACCAACATTTGATATAT 540
DB 481 TTGGCCAGTATTTATGACTAAACGATTAATGATGAAGAACCAACATTTGATATAT 540
QY 541 TTGGCCAGTATTTATGACTAAACGATTAATGATGAAGAACCAACATTTGATATAT 540
DB 541 TTGGCCAGTATTTATGACTAAACGATTAATGATGAAGAACCAACATTTGATATAT 540
QY 541 GTTCAATGATCTTCTAGAGAGATTTGTTGGCGTGCAGCTTCTCTGTGAAGAAGACA 600
DB 541 GTTCAATGATCTTCTAGAGAGATTTGTTGGCGTGCAGCTTCTCTGTGAAGAAGACA 600
QY 601 GGAATAATATATACATGATCTACAGGACCTTGTATGATCAATCAAGAGATCTCGG 660
DB 601 GGAATAATATATACATGATCTACAGGACCTTGTATGATCAATCAAGAGATCTCGG 660
QY 661 ACTCAGTATCATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTGAATCAAG 720
DB 661 ACTCAGTATCATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTGAATCAAG 720
QY 721 ACTCAGTATCATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTGAATCAAG 780
DB 721 ACTCAGTATCATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTGAATCAAG 780
QY 781 CTAACCTCATCTAGAGAGAGCAATTAGTGAACAGAGAAATTCAGATGAATATCTG 840
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DB 781 CTAACCTCATCTAGAGAGAGCAATTAGTGAACAGAGAAATTCAGATGAATATCTG 840
QY 841 GTGAACGACAAAGAAAACGACAAATCTGATGATATTTCCCTTTGATGAAGCC 900
DB 841 GTGAACGACAAAGAAAACGACAAATCTGATGATATTTCCCTTTGATGAAGCC 900
QY 901 TGGCTGTGTGTATTAAGGAGATATGTTGTGAAGAAGAGTGAAGTGAATCTACAG 960
DB 901 TGGCTGTGTGTATTAAGGAGATATGTTGTGAAGAAGAGTGAAGTGAATCTACAG 960
QY 901 TGGCTGTGTGTATTAAGGAGATATGTTGTGAAGAAGAGTGAAGTGAATCTACAG 960
DB 901 TGGCTGTGTGTATTAAGGAGATATGTTGTGAAGAAGAGTGAAGTGAATCTACAG 960
QY 961 GAGAGCCATCGAATCCGATTTTGATGCTGTGTGAAGTGAATCTACAGTGAATGTTGG 1020
DB 961 GAGAGCCATCGAATCCGATTTTGATGCTGTGTGAAGTGAATCTACAGTGAATGTTGG 1020
QY 1021 ATCAGATTCAGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 ATCAGATTCAGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 AAGATTATAGCTTATGTAAGAAGACAAAGACTCTCAGATGAAGATGATGATGATATTC 1140
DB 1081 AAGATTATAGCTTATGTAAGAAGACAAAGACTCTCAGATGAAGATGATGATGATATTC 1140
QY 1141 AAGTTACTGTATTCAGGAGGAGAGTGAATCAAGATTCATTTGAAGAAGATCTGAAA 1200
DB 1141 AAGTTACTGTATTCAGGAGGAGAGTGAATCAAGATTCATTTGAAGAAGATCTGAAA 1200
QY 1201 TTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
DB 1201 TTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 CACATTCGACAGATGTTGGGCTTCTGTGAAGATTTGGCTTCTGTGAAGATTAAGGAAAG 1320
DB 1261 CACATTCGACAGATGTTGGGCTTCTGTGAAGATTTGGCTTCTGTGAAGATTAAGGAAAG 1320
QY 1321 AATAAGGAGAAATCTCTGAAGAAAGCCAAATCTGAAGAAATCTGAAGAAAGGAGCT 1380
DB 1321 AATAAGGAGAAATCTCTGAAGAAAGCCAAATCTGAAGAAATCTGAAGAAAGGAGCT 1380
QY 1381 TTGATGCTCTGATGTAAGAAACCTATGATGATGATGATGATGATGATGATGATGATG 1440
DB 1381 TTGATGCTCTGATGTAAGAAACCTATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1441 AAAATGATGATTAATTAACAAGGTTCAATCAATCAAGAAAGTGAAGATTAATTCAGC 1500
DB 1441 AAAATGATGATTAATTAACAAGGTTCAATCAATCAAGAAAGTGAAGATTAATTCAGC 1500
QY 1501 CATCAACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
DB 1501 CATCAACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
QY 1561 AAGAAACCCAGACAAAGAGAGTGAATCTGATGATGATGATGATGATGATGATGATGATG 1620
DB 1561 AAGAAACCCAGACAAAGAGAGTGAATCTGATGATGATGATGATGATGATGATGATGATG 1620
QY 1621 CTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
DB 1621 CTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 ATCTATGAGCTGCTTATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
DB 1681 ATCTATGAGCTGCTTATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
QY 1741 TATGTAGCAACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
DB 1741 TATGTAGCAACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
QY 1801 AAGAGATTAATTAATTTCTAATATATACCTTGAAGATTTGAACCACTGAATTTAT 1860
DB 1801 AAGAGATTAATTAATTTCTAATATATACCTTGAAGATTTGAACCACTGAATTTAT 1860
QY 1861 CACATTAATCAAGTGAAGAAATGCTCAATTCATGATGATTTCTTCTTTATGATAT 1920
DB 1861 CACATTAATCAAGTGAAGAAATGCTCAATTCATGATGATTTCTTCTTTATGATAT 1920
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Db 1861 CACATATATCAAGTGAAGAAATGCTCATATTCATAGATTTCTTCTTAGTATTAAT 1920
QY 1921 TGACCTACTTTGGTAGGAAATAGTAATCTACTATATATTGACTTGAATAGTACCT 1980
Db 1921 TGACCTACTTTGGTAGGAAATAGTAATCTACTATATATTGACTTGAATAGTACCT 1980
QY 1981 CATCTTTTACACCAACTCTCTAATTTTAAATATTTTCTACTCTGCTTAAATGAGATAC 2040
Db 1981 CATCTTTTACACCAACTCTCTAATTTTAAATATTTTCTACTCTGCTTAAATGAGATAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAATATTAATTTATTTTGG 2100
Db 2041 TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAATATTAATTTATTTTGG 2100
QY 2101 AGACGAGTCTGCTCTGTTTACCCAGCTGGAGTGAAGTGGTGTGCTTGGCTCATGCA 2160
Db 2101 AGACGAGTCTGCTCTGTTTACCCAGCTGGAGTGAAGTGGTGTGCTTGGCTCATGCA 2160
QY 2161 AGCTTGACCTCTCCCGGGTTGCGACCAATCTCTGCTCAGCTCCCAATTAAGCTTGGCC 2220
Db 2161 AGCTTGACCTCTCCCGGGTTGCGACCAATCTCTGCTCAGCTCCCAATTAAGCTTGGCC 2220
QY 2221 TACAGTCACTCTGCGACCACTGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
Db 2221 TACAGTCACTCTGCGACCACTGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
QY 2281 ACCGTGTAGCCAGGATGCTGCTGATCTCTGACCTGCTGATCCGCCACCTTGGCTTC 2340
Db 2281 ACCGTGTAGCCAGGATGCTGCTGATCTCTGACCTGCTGATCCGCCACCTTGGCTTC 2340
QY 2341 CAAAGTGTGGGATTACAGGATGAGCCACCG 2372
Db 2341 CAAAGTGTGGGATTACAGGATGAGCCACCG 2372

RESULT 6
AAV20549
ID AAV20549 standard; cDNA; 2372 BP.
XX
AC AAV20549;
XX
DT 18-JUN-1998 (first entry)
XX
DE Human MDM2 encoding cDNA.
XX
KW Human; MDM2; tumour; cancer; diagnosis; neoplastic disease;
KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 312..1787
FT /tag= a
FT /product= "MDM2"
XX
PN US5736338-A.
XX
PD 07-APR-1998.
XX
PF 17-FEB-1995; 95US-00390517.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UYGO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;
DR WPI; 1998-239206/21.
DR P-PSDB; AAV48241.
XX
PT Cancer diagnosis - by determination of MDM2 protein.

XX
PS Claim 1; Col 21-24; 35pp; English.
XX
CC The present sequence encodes human MDM2 (hMDM2) which is used in the
CC method of the present invention. The present invention describes a method
CC for diagnosing a neoplastic disease caused by overexpression of MDM2
CC protein. The method comprises detecting an elevated cellular amount of
CC this protein. The method is useful for the diagnosis of sarcoma,
CC especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma
XX
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCGCGGAGCTTGGCTGCTTCTGCGGCGCTGTGTGCGCTGTGTGCGAAAGATGA 60
Db 1 GCACCGCGGAGCTTGGCTGCTTCTGCGGCGCTGTGTGCGCTGTGTGCGAAAGATGA 60
QY 61 GCAGAGCCCGAGCCGAGGGGCGCGCGACCCCTCTGACCGAGATCTGCTGCTTTCG 120
Db 61 GCAGAGCCCGAGCCGAGGGGCGCGCGACCCCTCTGACCGAGATCTGCTGCTTTCG 120
QY 121 CAGCCAGAGACCGGCTCCCGGATTAGGCGTACAGAGCGCCAGTGCCTGGCCCG 180
Db 121 CAGCCAGAGACCGGCTCCCGGATTAGGCGTACAGAGCGCCAGTGCCTGGCCCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCGGCGTGTGCTTCCGAGTATGATGATCCCGG 240
Db 181 GAGAGTGAATGATCCCGAGGCGCGGCGTGTGCTTCCGAGTATGATGATCCCGG 240
QY 241 AAGGAAATCTGGGAGTCTTGAAGGACCCCGACTCCAGCCGAGAAACCCCGAGTGA 300
Db 241 AAGGAAATCTGGGAGTCTTGAAGGACCCCGACTCCAGCCGAGAAACCCCGAGTGA 300
QY 301 GGAGCAGGCAATNGCAATATACCAATGCTGATCTGATGCTGATGCTGATACCACT 360
Db 301 GGAGCAGGCAATNGCAATATACCAATGCTGATCTGATGCTGATGCTGATACCACT 360
QY 361 CACAGATTCACCTTCGAAACAAGAGACCTGCTTGAACCAAGCATTGCTTGAAGT 420
Db 361 CACAGATTCACCTTCGAAACAAGAGACCTGCTTGAACCAAGCATTGCTTGAAGT 420
QY 421 TATTAAGTCTGTGGTGCACAAAAGACCTTAATATATGAAGGTTCTTTTATC 480
Db 421 TATTAAGTCTGTGGTGCACAAAAGACCTTAATATATGAAGGTTCTTTTATC 480
QY 481 TTGGCCAGTATATATGACTTAACGATTAATGATGAGAGCAACAATTTGATAT 540
Db 481 TTGGCCAGTATATATGACTTAACGATTAATGATGAGAGCAACAATTTGATAT 540
QY 541 GTTCAATGATCTTTCAGAGATTGTTGGGCTGCAAGCTTCTGTGAAGAGACACA 600
Db 541 GTTCAATGATCTTTCAGAGATTGTTGGGCTGCAAGCTTCTGTGAAGAGACACA 600
QY 601 GGAAATATATATCAATGATCTACAGGAACTTGATGATGATGATGATGATGAT 660
Db 601 GGAAATATATATCAATGATCTACAGGAACTTGATGATGATGATGATGATGAT 660
QY 661 ACTCAGTATCATCTGTGATGAGAAACAGGTGTCACTTGAAGTGGAGTGAATCA 720
Db 661 ACTCAGTATCATCTGTGATGAGAAACAGGTGTCACTTGAAGTGGAGTGAATCA 720
QY 721 ACCTGTACAAAGCTTCAGAAAGAAACCTTCACTTCACTTCACTTCACTTCA 780
Db 721 ACCTGTACAAAGCTTCAGAAAGAAACCTTCACTTCACTTCACTTCACTTCA 780
QY 781 CTACCTCATCTTGAAGAGAGCAATTAAGTGAACAGAAATTCAGATGATATCTG 840
Db 781 CTACCTCATCTTGAAGAGAGCAATTAAGTGAACAGAAATTCAGATGATATCTG 840
QY 841 GTGAACGACAAAGAAACCCCAAAATCTGATGATGATTTCCCTTCTTGTGATGAAGCC 900

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Db      ||| 841 GTGAACGCAAAAGAAAAGCCCAAAATCGATAGATTCCCTTCTTTGATGAAAGCC 900
Qy      ||| 901 TGGCTCTGTGTGTAATAAGGAGATATGTGTGAAAGAGATGACGTGAATCTTAAG 960
Db      ||| 901 TGGCTCTGTGTGTAATAAGGAGATATGTGTGAAAGAGATGACGTGAATCTTAAG 960
Qy      ||| 961 GGAGGCCATCGAATCCGATCTTGATGTGTGTAAGTGAACAATTCAGGTGTTGGTGG 1020
Db      ||| 961 GGAGGCCATCGAATCCGATCTTGATGTGTGTAAGTGAACAATTCAGGTGTTGGTGG 1020
Qy      ||| 1021 ATCAGAGTTCAAGTTCAATCAATGTTAGTGAATTTGAAGTGAATCTCTCGACTGAG 1080
Db      ||| 1021 ATCAGAGTTCAAGTTCAATCAATGTTAGTGAATTTGAAGTGAATCTCTCGACTGAG 1080
Qy      ||| 1081 AAGATTATAGCTTATAGTGAAGAGCAAGAACTCTCAGATGAAATATATAGATATTC 1140
Db      ||| 1081 AAGATTATAGCTTATAGTGAAGAGCAAGAACTCTCAGATGAAATATATAGATATTC 1140
Qy      ||| 1141 AAGTTACTGTGTATCAGGCAAGGAGATGATACAGATTCAATTTGAAGAGATCTTGAAA 1200
Db      ||| 1141 AAGTTACTGTGTATAGGCAAGGAGAGATGATACAGATTCAATTTGAAGAGATCTTGAAA 1200
Qy      ||| 1201 TTTCTTAGCTGACTATTTGGAATGCACTTCATGCAATGAAATGAAATCCCTTCAT 1260
Db      ||| 1201 TTTCTTAGCTGACTATTTGGAATGCACTTCATGCAATGAAATGAAATCCCTTCAT 1260
Qy      ||| 1261 CACATTTGACACAGATGTTGGGCTTCGTGAGAAATTTGGCTTCCCTTAAGTAAAGGAAAG 1320
Db      ||| 1261 CACATTTGACACAGATGTTGGGCTTCGTGAGAAATTTGGCTTCCCTTAAGTAAAGGAAAG 1320
Qy      ||| 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACAGCTGAAAGAGGCT 1380
Db      ||| 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACAGCTGAAAGAGGCT 1380
Qy      ||| 1381 TTGATGTTCTGATTTGTAATAAACTATATGTAATGATTTCCAGAGATCATGTGTTGAGG 1440
Db      ||| 1381 TTGATGTTCTGATTTGTAATAAACTATATGTAATGATTTCCAGAGATCATGTGTTGAGG 1440
Qy      ||| 1441 AAAATGATGATTAATAATTACACAGCTTCACATCAACAGAAAGTGAAGCTATTTCTGAC 1500
Db      ||| 1441 AAAATGATGATTAATAATTACACAGCTTCACATCAACAGAAAGTGAAGCTATTTCTGAC 1500
Qy      ||| 1501 CATCAACTCTCTAGTGAATTTATTTATAGAGCCCAAGAGATGTAAGAGTTTGAAGAGG 1560
Db      ||| 1501 CATCAACTCTCTAGTGAATTTATTTATAGAGCCCAAGAGATGTAAGAGTTTGAAGAGG 1560
Qy      ||| 1561 AAGAAACCCCAAGACAAAGAGAGTGTGAATCTAGTTGCCCCCTTAATGCCATTGAAC 1620
Db      ||| 1561 AAGAAACCCCAAGACAAAGAGAGTGTGAATCTAGTTGCCCCCTTAATGCCATTGAAC 1620
Qy      ||| 1621 CTTGTGTGATTTGTCAAGGTGCACTTAAATAATGCTTGTGCTTCCATGCAAAACAGAGC 1680
Db      ||| 1621 CTTGTGTGATTTGTCAAGGTGCACTTAAATAATGCTTGTGCTTCCATGCAAAACAGAGC 1680
Qy      ||| 1681 ATCTTATGAGCCCTGCTTTTACATGTGCAAGAGCTAAGAGAAAGAAAGAAAGTAAAGCCCTGCGCAG 1740
Db      ||| 1681 ATCTTATGAGCCCTGCTTTTACATGTGCAAGAGCTAAGAGAAAGAAAGTAAAGCCCTGCGCAG 1740
Qy      ||| 1741 TATGTAGACAAACCAATTCATATGATTTGCTTATTTCCCTTATGAGCTGTCTAT 1800
Db      ||| 1741 TATGTAGACAAACCAATTCATATGATTTGCTTATTTCCCTTATGAGCTGTCTAT 1800
Qy      ||| 1801 AAGAGAAATTAATATTTCTTACTATATACCTTAGAATTTTGAACAACCTGAAATTTAT 1860
Db      ||| 1801 AAGAGAAATTAATATTTCTTACTATATACCTTAGAATTTTGAACAACCTGAAATTTAT 1860
Qy      ||| 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTCTTAGTATAT 1920
Db      ||| 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTCTTAGTATAT 1920
Qy      ||| 1921 TGACCTACTTTGTGTAGTGAATAGTGAATTAATTAATTTGACTGAATATGTAGCT 1980

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Db      ||| 1921 TGACCTACTTTGTGTAGTGAATAGTGAATTAATTAATTTGACTGAATATGTAGCT 1980
Qy      ||| 1981 CATCTTTTACACCAACTCTTAATTTTAAATATTTCTACTGTCTTAAATGAGAAATGAC 2040
Db      ||| 1981 CATCTTTTACACCAACTCTTAATTTTAAATATTTCTACTGTCTTAAATGAGAAATGAC 2040
Qy      ||| 2041 TTGGTTTTTTTTTTCTTAATATATATGATGACATTTAAATGTAATTTATTTTGTG 2100
Db      ||| 2041 TTGGTTTTTTTTTTCTTAATATATATGATGACATTTAAATGTAATTTATTTTGTG 2100
Qy      ||| 2101 AGACCGAGTCTTGTCTGTTTACCAAGGCTGAGAGGAGTGGGTATCTTGCTCACTGCA 2160
Db      ||| 2101 AGACCGAGTCTTGTCTGTTTACCAAGGCTGAGAGGAGTGGGTATCTTGCTCACTGCA 2160
Qy      ||| 2161 AGCTTGCCCTCCCGGGGTTGCAACATTTCTCTGCTCAAGCTCCCAATTAAGTTGGCC 2220
Db      ||| 2161 AGCTTGCCCTCCCGGGGTTGCAACATTTCTCTGCTCAAGCTCCCAATTAAGTTGGCC 2220
Qy      ||| 2221 TACAGTCACTGCAACCAACACTGAGCTAATTTTGTATCTTTTATAGTGAAGACAGGTTTC 2280
Db      ||| 2221 TACAGTCACTGCAACCAACACTGAGCTAATTTTGTATCTTTTATAGTGAAGACAGGTTTC 2280
Qy      ||| 2281 ACCGTGTTAGCCAGATAGTCTCGATCTCTGACTCGTGAATCGGCCCACTCGGCTCC 2340
Db      ||| 2281 ACCGTGTTAGCCAGATAGTCTCGATCTCTGACTCGTGAATCGGCCCACTCGGCTCC 2340
Qy      ||| 2341 CAAAGTGTGGGATTTACAGCATGAGCCACG 2372
Db      ||| 2341 CAAAGTGTGGGATTTACAGCATGAGCCACG 2372

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RESULT 7
AAV28876
ID AAV28876 standard; cdNA; 2372 BP.
XX
XX AAV28876;
XX
XX 10-AUG-1998 (first entry)
XX
XX DE Human MDM2 gene.
XX
XX KW Human; p53; MDM2; tumour; growth inhibition; amplification;
XX malignant fibrous histiocytoma; liposarcoma; db.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 312..1787
XX FT /*tag= a
XX FT /product= "MDM2 protein"
XX
XX PN US5756455-A.
XX
XX PD 26-MAY-1998.
XX
XX PF 17-FEB-1995; 95US-00390515.
XX
XX PR 07-APR-1992; 92US-00867840.
XX PR 23-JUN-1992; 92US-00903103.
XX PR 07-APR-1993; 93US-00044619.
XX
XX PA (U90 ) UNIV JOHNS HOPKINS.
XX
XX PI Vogelstein B, Kinzler KW;
XX
XX DR WPI; 1998-321574/28.
XX DR P-PSDB; AAW57241.
XX
XX PT Inhibiting growth of tumour cells having MDM2 gene amplification - with
XX p53 protein fragment.
XX
XX Example 1; Col 19-24; 40bp; English.
XX

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CC A method has been developed for inhibiting the growth of tumour cells
CC containing a human MDM2 gene amplification. The method comprises creating
CC the tumour cells with a DNA molecule that expresses a polypeptide capable
CC of binding to human MDM2 protein. The present sequence represents the
CC human MDM2 gene. The present invention describes three preferred
CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino
CC acids 1-50 of p53 (see AAM57240); (2) the polypeptide comprises amino
CC acids 13-41 of p53 (see AAM57240) and at least one additional p53
CC residues on the N- or C-terminal side, provided that the polypeptide
CC lacks the homoligomerisation domain of p53; (3) the polypeptide
CC comprises amino acids 13-41 of p53 (see AAM57241) and at least nine
CC additional p53 residues on the N- or C-terminal side, provided that the
CC polypeptide lacks amino acids 138-193 of p53. Some malignant fibrous
CC histiocytomas and liposarcomas have an MDM2 gene amplification, so
CC detection of increased expression of MDM2 gene products indicates
CC tumourigenesis

XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACCGCGAGCTTGGCTCTTCTGCGGCTGTGTGCGCTGTGTGCGAAAGATGA 60
DB 1 GCAACCGCGAGCTTGGCTCTTCTGCGGCTGTGTGCGCTGTGTGCGAAAGATGA 60
QY 61 GCAGAGCCGAGCCGAGGCGCGCGCGAGCCCTCTGACCGAGATCTCTGCTCTTTCG 120
DB 61 GCAGAGCCGAGCCGAGGCGCGCGCGAGCCCTCTGACCGAGATCTCTGCTCTTTCG 120
QY 61 GCAGAGCCGAGCCGAGGCGCGCGCGAGCCCTCTGACCGAGATCTCTGCTCTTTCG 120
DB 61 GCAGAGCCGAGCCGAGGCGCGCGCGAGCCCTCTGACCGAGATCTCTGCTCTTTCG 120
QY 121 CAGCCAGAGACCGCTCCCTCCCGATTAGTGCCTGACGAGCGCCGAGGCTTGGCCCG 180
DB 121 CAGCCAGAGACCGCTCCCTCCCGATTAGTGCCTGACGAGCGCCGAGGCTTGGCCCG 180
QY 121 CAGCCAGAGACCGCTCCCTCCCGATTAGTGCCTGACGAGCGCCGAGGCTTGGCCCG 180
DB 121 CAGCCAGAGACCGCTCCCTCCCGATTAGTGCCTGACGAGCGCCGAGGCTTGGCCCG 180
QY 181 GAGAGTGATGATCCCGAGGCGCGCGCGCTGCTCCGAGATGACGATCCCGCTG 240
DB 181 GAGAGTGATGATCCCGAGGCGCGCGCGCTGCTCCGAGATGACGATCCCGCTG 240
QY 181 GAGAGTGATGATCCCGAGGCGCGCGCGCTGCTCCGAGATGACGATCCCGCTG 240
DB 181 GAGAGTGATGATCCCGAGGCGCGCGCGCTGCTCCGAGATGACGATCCCGCTG 240
QY 241 AAGGAACTGGGAGGCTTGAAGGACCCCGACTCCAGCGCGAAACCCCGAGTGTGA 300
DB 241 AAGGAACTGGGAGGCTTGAAGGACCCCGACTCCAGCGCGAAACCCCGAGTGTGA 300
QY 301 GAGAGCGGCAATGTGCAATACCAATGTCTGTACTGTAGTGTGCTGTACCACT 360
DB 301 GAGAGCGGCAATGTGCAATACCAATGTCTGTACTGTAGTGTGCTGTACCACT 360
QY 301 GAGAGCGGCAATGTGCAATACCAATGTCTGTACTGTAGTGTGCTGTACCACT 360
DB 301 GAGAGCGGCAATGTGCAATACCAATGTCTGTACTGTAGTGTGCTGTACCACT 360
QY 361 CACAGATTCAGCTTGGGAAACAAGAGCCCTGTGACCAAAAGCCATTGCTTGAAGT 420
DB 361 CACAGATTCAGCTTGGGAAACAAGAGCCCTGTGACCAAAAGCCATTGCTTGAAGT 420
QY 421 TATTAAGTCTGTGTGACCAAAAAGACATTAATCTAATGAAGAGTCTTTTATTC 480
DB 421 TATTAAGTCTGTGTGACCAAAAAGACATTAATCTAATGAAGAGTCTTTTATTC 480
QY 421 TATTAAGTCTGTGTGACCAAAAAGACATTAATCTAATGAAGAGTCTTTTATTC 480
DB 421 TATTAAGTCTGTGTGACCAAAAAGACATTAATCTAATGAAGAGTCTTTTATTC 480
QY 481 TTGGCCAGTATATATGACTAAACGATTAATGATGAGAAACAACATTTGATAT 540
DB 481 TTGGCCAGTATATATGACTAAACGATTAATGATGAGAAACAACATTTGATAT 540
QY 541 GTTCAAATGATCTTGAAGAGATTTGTTGGGCTGCAAGCTTCTCTGGAAGAGACA 600
DB 541 GTTCAAATGATCTTGAAGAGATTTGTTGGGCTGCAAGCTTCTCTGGAAGAGACA 600
QY 601 GGAATAATATATATCATGATCTACAGAACTTGTGTAGTCAATCAGAGATCATCG 660
DB 601 GGAATAATATATATCATGATCTACAGAACTTGTGTAGTCAATCAGAGATCATCG 660
QY 601 GGAATAATATATATCATGATCTACAGAACTTGTGTAGTCAATCAGAGATCATCG 660
DB 601 GGAATAATATATATCATGATCTACAGAACTTGTGTAGTCAATCAGAGATCATCG 660
QY 661 ACTCAGTATCATCTGTGATGAGAAACAGGTGTCACTTGAAGGTGGAATGATCAAAAG 720
DB 661 ACTCAGTATCATCTGTGATGAGAAACAGGTGTCACTTGAAGGTGGAATGATCAAAAG 720
QY 721 ACCTGTACAGAGCTTCAAGAAAGAACTTCATCTCACTTGGTTTCTAGACAT 780
DB 721 ACCTGTACAGAGCTTCAAGAAAGAACTTCATCTCACTTGGTTTCTAGACAT 780

DB 721 ACCTGTACAGAGCTTCAAGAAAGAACTTCATCTCACTTGGTTTCTAGACAT 780
QY 781 CTACCTCATCTGAAAGAGAGCAATTAGTACAGAAAGAAATTCAGATGATATTCG 840
DB 781 CTACCTCATCTGAAAGAGAGCAATTAGTACAGAAAGAAATTCAGATGATATTCG 840
QY 841 GTGAACGACAAAGAAACCCCAATCTGATAGTATTCCTTCTTGTGTAAGAGCC 900
DB 841 GTGAACGACAAAGAAACCCCAATCTGATAGTATTCCTTCTTGTGTAAGAGCC 900
QY 901 TGGCTGTGTGTATATGAAGAGATATGTGTGAAGAGAGTACAGTGAATCTACAG 960
DB 901 TGGCTGTGTGTATATGAAGAGATATGTGTGAAGAGAGTACAGTGAATCTACAG 960
QY 901 TGGCTGTGTGTATATGAAGAGATATGTGTGAAGAGAGTACAGTGAATCTACAG 960
DB 901 TGGCTGTGTGTATATGAAGAGATATGTGTGAAGAGAGTACAGTGAATCTACAG 960
QY 961 GGAAGCCATCGAATCCGATCTTGTATGCTGTGTATAGTGAACATTCAGGTGATG 1020
DB 961 GGAAGCCATCGAATCCGATCTTGTATGCTGTGTATAGTGAACATTCAGGTGATG 1020
QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTATGATGATGATGATGATGATGATGATG 1080
DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTATGATGATGATGATGATGATGATGATG 1080
QY 1081 AAGATTATAGCTTATGTAAGAGACAAAGAACTCTCAGATGAGATGATGATATC 1140
DB 1081 AAGATTATAGCTTATGTAAGAGACAAAGAACTCTCAGATGAGATGATGATATC 1140
QY 1141 AAGTTATCTGTATACAGGAGGAGAGTGTATCAGATTCATTTGAAGAAATCTGAAA 1200
DB 1141 AAGTTATCTGTATACAGGAGGAGAGTGTATCAGATTCATTTGAAGAAATCTGAAA 1200
QY 1201 TTTCTTACCTGATCTATGGAATGACATTCATGAAATGAATCCCTCCCTCCAT 1260
DB 1201 TTTCTTACCTGATCTATGGAATGACATTCATGAAATGAATCCCTCCCTCCAT 1260
QY 1261 CACATTGCAACAGATGTTGGGCTTCTGTAAGATTTGGCTTCTGTAAGATTAAGGGAAG 1320
DB 1261 CACATTGCAACAGATGTTGGGCTTCTGTAAGATTTGGCTTCTGTAAGATTAAGGGAAG 1320
QY 1321 ATAAAGGAGAAATCTCTGAAAGCCCAACCTGAAACCTCAACAGCTGAAGAGGCT 1380
DB 1321 ATAAAGGAGAAATCTCTGAAAGCCCAACCTGAAACCTCAACAGCTGAAGAGGCT 1380
QY 1381 TTGATGCTTCTGATTTGTAAGAACTATATGTAAGATTTCAAGAGTGTATGTAAG 1440
DB 1381 TTGATGCTTCTGATTTGTAAGAACTATATGTAAGATTTCAAGAGTGTATGTAAG 1440
QY 1441 AAAATGATGATTAATTAACAAGGCTCAATCAACAAGAGTGAATTTCTCAGC 1500
DB 1441 AAAATGATGATTAATTAACAAGGCTCAATCAACAAGAGTGAATTTCTCAGC 1500
QY 1501 CATCAATCTTATGATCATTTATTTATGACGCAAGAGATGTAAGAGTGAAGAGG 1560
DB 1501 CATCAATCTTATGATCATTTATTTATGACGCAAGAGATGTAAGAGTGAAGAGG 1560
QY 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTGTGCTTAAATGCCATTGAAC 1620
DB 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTGTGCTTAAATGCCATTGAAC 1620
QY 1621 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTGTGCTTAAATGCCATTGAAC 1620
DB 1621 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTGTGCTTAAATGCCATTGAAC 1620
QY 1621 CTGTGTGATTTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAG 1680
DB 1621 CTGTGTGATTTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAG 1680
QY 1681 ATCTTATGCTTCTTATCATGTGCAAGAGCTTAAAGAAAGAAATGAGCTCCAG 1740
DB 1681 ATCTTATGCTTCTTATCATGTGCAAGAGCTTAAAGAAAGAAATGAGCTCCAG 1740
QY 1741 TATGTAGCAACCAATTCAAATGATGCTTAAATTTCCCTTAAGTGTGATCTAT 1800
DB 1741 TATGTAGCAACCAATTCAAATGATGCTTAAATTTCCCTTAAGTGTGATCTAT 1800
QY 1801 AAGAAATTAATATTTCTAATATATTAACCTTGAAGATTTGAACAACCTGAATTTAT 1860
DB 1801 AAGAAATTAATATTTCTAATATATTAACCTTGAAGATTTGAACAACCTGAATTTAT 1860


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Db 661 ACTCAGGTCATCTGTGAGTGAGAACAGGTCCTCACTTGAAGTGGAGTGATCAAAAG 720
Qy 721 ACCCTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTCACTTTGGTTTCTAGACCAT 780
Db 721 ACCCTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTCACTTTGGTTTCTAGACCAT 780
Qy 781 CTACCTCATCTAGAAAGAGAGCAATTAGTAGACACAGAGAAATTGAGATTAATCTAG 840
Db 781 CTACCTCATCTAGAAAGAGAGCAATTAGTAGACACAGAGAAATTGAGATTAATCTAG 840
Qy 841 GTGAAGCAGAAAGAAACCCCAAAATCTGATAGTATTTCCCTTCCCTTGTGATGAAGCC 900
Db 841 GTGAAGCAGAAAGAAACCCCAAAATCTGATAGTATTTCCCTTCCCTTGTGATGAAGCC 900
Qy 901 TGGCTCTGTGTATATAGGGAGATATGTGTGAAAGAAAGCAGTACAGTGAATCTACAG 960
Db 901 TGGCTCTGTGTATATAGGGAGATATGTGTGAAAGAAAGCAGTACAGTGAATCTACAG 960
Qy 961 GGAAGCATCGAATCCGGATCTTGATGCTGTGTATGTAACATTCAGGTGATGGTTGG 1020
Db 961 GGAAGCATCGAATCCGGATCTTGATGCTGTGTATGTAACATTCAGGTGATGGTTGG 1020
Qy 1021 ATCAGGATTCAGTTTCAGATCAGTTAGTATGATTAATTTGAAGTTGAATCTTCGACTCAG 1080
Db 1021 ATCAGGATTCAGTTTCAGATCAGTTAGTATGATTAATTTGAAGTTGAATCTTCGACTCAG 1080
Qy 1081 AAGATTATAGCTTCTAGTGAAGAGCAAGAACTCTCAGATGAGATGATGAGTATATC 1140
Db 1081 AAGATTATAGCTTCTAGTGAAGAGCAAGAACTCTCAGATGAGATGATGAGTATATC 1140
Qy 1141 AAGTTACTGTATCAGGCGAGGAGATGATACAGATTCATTTGAAGAAATCCTGAAA 1200
Db 1141 AAGTTACTGTATCAGGCGAGGAGATGATACAGATTCATTTGAAGAAATCCTGAAA 1200
Qy 1201 TTTCTTCTAGCTGATTTGGAATGCACTTCATGCAATGAAATGAATGCCCTCCCTCAT 1260
Db 1201 TTTCTTCTAGCTGATTTGGAATGCACTTCATGCAATGAAATGAATGCCCTCCCTCAT 1260
Qy 1261 CACATTGCAACAGATGTTGGGCTTCGTGAGAAATTTGGCTTCCTGAAAGATTAAGGGAAG 1320
Db 1261 CACATTGCAACAGATGTTGGGCTTCGTGAGAAATTTGGCTTCCTGAAAGATTAAGGGAAG 1320
Qy 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAATCTCAACAAGCTGAAGAGGCT 1380
Db 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAATCTCAACAAGCTGAAGAGGCT 1380
Qy 1381 TTGATGTTCTGATTTGTAATAAACTATAGTGAATGATTCAGAGAGTCATGTTGAGG 1440
Db 1381 TTGATGTTCTGATTTGTAATAAACTATAGTGAATGATTCAGAGAGTCATGTTGAGG 1440
Qy 1441 AAAATGATGATTAATTAACAAGCTTCACAATCAACAAGAAAGTGAAGCTATTTCTCAGC 1500
Db 1441 AAAATGATGATTAATTAACAAGCTTCACAATCAACAAGAAAGTGAAGCTATTTCTCAGC 1500
Qy 1501 CATCAACTCTTAGTACATTAATTTATAGACGCCAAGAGATGAAAGAGTTGAAAGG 1560
Db 1501 CATCAACTCTTAGTACATTAATTTATAGACGCCAAGAGATGAAAGAGTTGAAAGG 1560
Qy 1561 AAGAAACCCAAAGAAAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCAATTAAGC 1620
Db 1561 AAGAAACCCAAAGAAAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCAATTAAGC 1620
Qy 1621 CTGTGTGTATTTGTCAAGGTTCGACTTAATAATGTTGTCATGTCAGCAAAACAGAGC 1680
Db 1621 CTGTGTGTATTTGTCAAGGTTCGACTTAATAATGTTGTCATGTCAGCAAAACAGAGC 1680
Qy 1681 ATCTTAGGCTGCTTTATAGTGCAAGAGCTAAAGAGTAAGGAAAGGAAAGGAAAGG 1740
Db 1681 ATCTTAGGCTGCTTTATAGTGCAAGAGCTAAAGAGTAAGGAAAGGAAAGGAAAGG 1740
Qy 1741 TATGTAGAACAAACCAATTAATGATTTGCTAATTAATTTCCCTAGTGAAGCTGCTAT 1800
Db 1741 TATGTAGAACAAACCAATTAATGATTTGCTAATTAATTTCCCTAGTGAAGCTGCTAT 1800
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Db 1741 TATGTAGAACAAACCAATTAATGATTTGCTAATTAATTTCCCTAGTGAAGCTGCTAT 1800
Qy 1801 AAGAGAAATTAATTAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
Db 1801 AAGAGAAATTAATTAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
Qy 1861 CATATATCAAGAGAGAAAGAGCTCAATTCACATTAATTTCTCTCTTAATTAAT 1920
Db 1861 CATATATCAAGAGAGAGAAAGAGCTCAATTCACATTAATTTCTCTCTTAATTAAT 1920
Qy 1921 TGACCTACTTGTGTAGTGAATAGTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Db 1921 TGACCTACTTGTGTAGTGAATAGTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Qy 1981 CATCTTTACACCAACTCTTAATTTTAATTAATTTCTACTCTGTCTTAATGAAGTAC 2040
Db 1981 CATCTTTACACCAACTCTTAATTTTAATTAATTTCTACTCTGTCTTAATGAAGTAC 2040
Qy 2041 TTGGTTTTTTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 2100
Db 2041 TTGGTTTTTTTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 2100
Qy 2101 AGACGAGCTTGTCTCTGTATACCAAGCTGAGTGAAGTGAATCTTGCTCACTGCA 2160
Db 2101 AGACGAGCTTGTCTCTGTATACCAAGCTGAGTGAAGTGAATCTTGCTCACTGCA 2160
Qy 2161 AGCTTGCCCTCCCGGGGTTGACACCATTCCTGCTCAGCCTCCCAATTAAGCTTGGCC 2220
Db 2161 AGCTTGCCCTCCCGGGGTTGACACCATTCCTGCTCAGCCTCCCAATTAAGCTTGGCC 2220
Qy 2221 TACAGTCACTTCGCCACACCACTGCTAATTTTGTACTTTTATAGTAGACAGGGTTTC 2280
Db 2221 TACAGTCACTTCGCCACACCACTGCTAATTTTGTACTTTTATAGTAGACAGGGTTTC 2280
Qy 2281 ACCGTGTAGCAGAGATGCTCGATCTCTGACCTGACCTCGATCCGACCTCGGCTCC 2340
Db 2281 ACCGTGTAGCAGAGATGCTCGATCTCTGACCTGACCTCGATCCGACCTCGGCTCC 2340
Qy 2341 CAAAGTGTGGGATTTACAGGCAATGAGCCACCG 2372
Db 2341 CAAAGTGTGGGATTTACAGGCAATGAGCCACCG 2372

RESULT 9
AAV03607
ID AAV03607 standard; cDNA; 2372 BP.
XX
AC AAV03607;
XX
DT 29-APR-1998 (first entry)
XX
DE cDNA sequence of human MDM2.
XX
KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;
KW binding; tumour cell; p53-regulated growth; inhibition;
KW anti-cancer agent; ds.
XX
OS Homo sapiens.
XX
FH Key 312.1787 Location/Qualifiers
FT CDS /*tag= a
FT
PN US5702903-A.
PN
PD 30-DEC-1997.
PD
XX
XX
PF 13-NOV-1995; 95US-00557393.
XX
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
PR 18-MAY-1994; 94US-00245500.
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XX (UJJO) UNIV JOHNS HOPKINS.
 XX
 PI Vogelstein B, Kinzler KW;
 XX
 DR WPI; 1998-076411/07.
 DR P-PSDB; AAM42971.
 XX
 PT Cell containing reporter construct containing human MDM2 and p53 genes -
 PT for identifying compounds that interfere with binding of human MDM2 to
 PT human p53, useful as anti-cancer agents.
 XX
 PS Disclosure; Columns 21-26; 37pp; English.
 XX
 CC The present sequence encodes human MDM2. The MDM2 gene is amplified in
 CC some human tumours. The amplification of this gene is diagnostic of
 CC neoplasia or its potential. It is speculated that the MDM2 protein is a
 CC potential DNA binding protein that functions in the modulation of
 CC expression of other genes and, when present in excess, interferes with
 CC normal constraints on cell growth. A cell containing three recombinant
 CC DNA constructs was produced. These constructs encode a MDM2 protein
 CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
 CC to a transcriptional activation domain, and a reporter gene downstream
 CC from a DNA element which is recognised by the sequence-specific DNA-
 CC binding domain. The cell is used to identify a compound which interferes
 CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour
 CC cells and since binding of MDM2 to p53 appears to allow tumour cells to
 CC escape from p53-regulated growth, compounds that inhibit such binding
 CC would be useful as anti-cancer agents
 CC
 SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
 QY Best Match 100.0%; Score 2372; DB 2; Length 2372;
 QY Query Local Similarity 100.0%; Pred. No. 0;
 QY Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db
 541 GTTCAATGATCTTCTAGAGATTGTTGGCCGCGCAAGCTTCTGTGAAGACACA 600
 QY
 601 GGAATATATATACATGATCTAGAGAACTTGTAGTATGATCAATCAGACAGAAATCATCG 660
 Db
 601 GGAATATATATACATGATCTAGAGAACTTGTAGTATGATCAATCAGACAGAAATCATCG 660
 QY
 661 ACTCAGGTACATCTGTAGTGAAGACAGTGTCACTTGAAGGTGAGATCAAAAG 720
 Db
 661 ACTCAGGTACATCTGTAGTGAAGACAGTGTCACTTGAAGGTGAGATCAAAAG 720
 QY
 721 ACCTTGTAACAAGACTTCAGAAAGAACTTATCTTCAATTTGGTTCTAGACAT 780
 Db
 721 ACCTTGTAACAAGACTTCAGAAAGAACTTATCTTCAATTTGGTTCTAGACAT 780
 QY
 781 CTACCTCATCTAGAAAGAGCAATTTGTGACAGAAAGAAATTCAGATGAATTAATCTG 840
 Db
 781 CTACCTCATCTAGAAAGAGCAATTTGTGACAGAAAGAAATTCAGATGAATTAATCTG 840
 QY
 841 GTGAACGACAAAGAAACGCCCAAACTGTATATTTCCCTTCTTGTATGAAGCC 900
 Db
 841 GTGAACGACAAAGAAACGCCCAAACTGTATATTTCCCTTCTTGTATGAAGCC 900
 QY
 901 TGGCTGTGTGTATTAAGGAGATATGTTGTGAAGAGAGTACAGTAATCTACAG 960
 Db
 901 TGGCTGTGTGTATTAAGGAGATATGTTGTGAAGAGAGTACAGTAATCTACAG 960
 QY
 961 GGAAGCCATGGAATCCGATCTTATGCTGTGTATGAACATTCAGGTATGTTGG 1020
 Db
 961 GGAAGCCATGGAATCCGATCTTATGCTGTGTATGAACATTCAGGTATGTTGG 1020
 QY
 1021 ATCAGATTCAGTTTCAGATCAGTTATGTATGAATTTGAAGTTGATCTTCAGCTCAG 1080
 Db
 1021 ATCAGATTCAGTTTCAGATCAGTTATGTATGAATTTGAAGTTGATCTTCAGCTCAG 1080
 QY
 1081 AAGATTATAGCTTATATGAAGACAAAGAACTTCAGATGAAGATATGAGTATATC 1140
 Db
 1081 AAGATTATAGCTTATATGAAGACAAAGAACTTCAGATGAAGATATGAGTATATC 1140
 QY
 1141 AAGTTACGTGTATCAGCAAGGAGAGTATACAGATTCATTTGAAGAAATCCCTGAA 1200
 Db
 1141 AAGTTACGTGTATCAGCAAGGAGAGTATACAGATTCATTTGAAGAAATCCCTGAA 1200
 QY
 1201 TTTCTTACGTACATATGAAGATGCACTTCATGCAATGAATGAATCCCCCTTCAT 1260
 Db
 1201 TTTCTTACGTACATATGAAGATGCACTTCATGCAATGAATGAATCCCCCTTCAT 1260
 QY
 1261 CACATTGCAACAGATGTTGGCCCTTGTGAAATTTGGCTTCTGAAGATTAAGGAAAG 1320
 Db
 1261 CACATTGCAACAGATGTTGGCCCTTGTGAAATTTGGCTTCTGAAGATTAAGGAAAG 1320
 QY
 1321 ATAAAGGGGAAATCTCTAGAAAGCAATCGGAAATCTCAACCAAGCTGAAAGGGCT 1380
 Db
 1321 ATAAAGGGGAAATCTCTAGAAAGCAATCGGAAATCTCAACCAAGCTGAAAGGGCT 1380
 QY
 1381 TTGATGTTCTGATTTGTAATAAATACTATATGATGATTTCCAGAGAGTCAATGTGTAAG 1440
 Db
 1381 TTGATGTTCTGATTTGTAATAAATACTATATGATGATTTCCAGAGAGTCAATGTGTAAG 1440
 QY
 1441 AAAATGATATTAATTAACAAGCTTCAATCAAGAAAGTGAAGATTTCTCAGC 1500
 Db
 1441 AAAATGATATTAATTAACAAGCTTCAATCAAGAAAGTGAAGATTTCTCAGC 1500
 QY
 1501 CATCAACTTCTAGTACATTTATTTATACAGCAAGAAAGTGAAGATTTGAAGGG 1560
 Db
 1501 CATCAACTTCTAGTACATTTATTTATACAGCAAGAAAGTGAAGATTTGAAGGG 1560
 QY
 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCAATTAAC 1620
 Db
 1561 AAGAAACCAAGACAAAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCAATTAAC 1620
 QY
 1621 CTTGTGTGATTTGTCAAGTGCACCTAAATATGTTGATTCATGCGCAAAACAGAGC 1680

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Db      1621 CTGTGTGATTTTGTCAAGGTGCACTTAAATGGTTGCAATTCATGCGCAAAACAGAC 1680
Qy      1681 ATCTTAGGCTGCTTACATGTCAAAGAGCTAAAGAAAGATAGCCCTGCCCAG 1740
Db      1681 ATCTTAGGCTGCTTACATGTCAAAGAGCTAAAGAAAGATAGCCCTGCCCAG 1740
Qy      1741 TATGTAGACCAACCAATTAATGATGTGCTAATTTTCCCTAGTGAACCTGCTCAT 1800
Db      1741 TATGTAGACCAACCAATTAATGATGTGCTAATTTTCCCTAGTGAACCTGCTCAT 1800
Qy      1801 AAGAGATTAATTAATTTCTAATTAATTAACCTAGGAATTTAGACAACCTGAATTTAT 1860
Db      1801 AAGAGATTAATTAATTTCTAATTAATTAACCTAGGAATTTAGACAACCTGAATTTAT 1860
Qy      1861 CACATTAATCAAGAGAAATGCTCAATTCACATTAATTTCTCTCTTAGTATAT 1920
Db      1861 CACATTAATCAAGAGAAATGCTCAATTCACATTAATTTCTCTCTTAGTATAT 1920
Qy      1921 TGACCTACTTGTGTAGTGAATAGTAATTAATTAATTAATTTGACTGCTTAATGAGAGTAC 1980
Db      1921 TGACCTACTTGTGTAGTGAATAGTAATTAATTAATTAATTTGACTGCTTAATGAGAGTAC 1980
Qy      1981 CATCTTTACACCAACTCTTAATTTAAATTAATTTCTGCTGCTTAATGAGAGTAC 2040
Db      1981 CATCTTTACACCAACTCTTAATTTAAATTAATTTCTGCTGCTTAATGAGAGTAC 2040
Qy      2041 TTGGTTTTTTTTTTCTTAATTAATTAATTAATTAATTAATTAATTTATTTTATTTT 2100
Db      2041 TTGGTTTTTTTTTTCTTAATTAATTAATTAATTAATTAATTAATTTATTTTATTTT 2100
Qy      2101 AGACGAGCTGCTGCTGTATACCAAGGCTGAGAGTGAAGTGAATCTTGAGCTACATGA 2160
Db      2101 AGACGAGCTGCTGCTGTATACCAAGGCTGAGAGTGAAGTGAATCTTGAGCTACATGA 2160
Qy      2161 AGCTCTGCCCTCCCGGGTTGCAACCATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Db      2161 AGCTCTGCCCTCCCGGGTTGCAACCATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Qy      2221 TACAGTCAATCTGCAACCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Db      2221 TACAGTCAATCTGCAACCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Qy      2281 ACCGTTGAGCAGAGTGTCTGATCTCTGACCTGATCCGCGCACTCGGCTGCTC 2340
Db      2281 ACCGTTGAGCAGAGTGTCTGATCTCTGACCTGATCCGCGCACTCGGCTGCTC 2340
Qy      2341 CAAAGTGTGGATTACAGGCAATGAGCCACCG 2372
Db      2341 CAAAGTGTGGATTACAGGCAATGAGCCACCG 2372

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XX      14-FEB-1997; 97US-00801718.
PF      07-APR-1992; 92US-00867840.
XX      23-JUN-1992; 92US-00903103.
PR      07-APR-1993; 93US-00044619.
XX      17-FEB-1995; 95US-00390515.
XX      (UYUO ) UNIT JOHNS HOPKINS.
PI      Kinzler KW, Vogelstein B;
PI      MPI; 1999-152105/13.
DR      P-PSDB; AAW94304.
PT      Inhibiting growth of tumour cells having MDM2 gene amplification - with
PT      MDM2-binding p53 fragment.
XX      Example 1; Col 19-24; 41dp; English.
PS      The present invention describes: (1) a method for inhibiting the growth
CC      of tumour cells which contain a human MDM2 gene amplification, comprising
CC      administering to the cells a DNA molecule that expresses a polypeptide
CC      consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino
CC      acid sequence given in AAW94303, the polypeptide being capable of binding
CC      to human MDM2 (see AAW94304); (2) a method as in (1) where the
CC      polypeptide lacks the homo-oligomerisation domain of p53; and (3) a
CC      method as in (1) where the polypeptide lacks amino acids 138-393 of p53.
CC      The method is useful for treating the following tumour types which have a
CC      MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH), M-20
CC      MFH, L-9 liposarcoma, K17 liposarcoma, K128 liposarcoma, K130
CC      liposarcoma, and OSA-CL MFH. The present sequence encodes human MDM2
XX      Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
SQ
Query Match      100.0%; Score 2372; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GCACCGCGGAGCTTGGCTGCTTGGGGCTGTGTGGCCCTGTGTGCGAAAGATGGA 60
Db      1 GCACCGCGGAGCTTGGCTGCTTGGGGCTGTGTGGCCCTGTGTGCGAAAGATGGA 60
Qy      61 GCAAGAGCGGAGCGCGGAGGCGCGGAGACCCCTCTGACCGAGATCTGCTGCTTTG 120
Db      61 GCAAGAGCGGAGCGCGGAGGCGCGGAGACCCCTCTGACCGAGATCTGCTGCTTTG 120
Qy      121 CAGCGAGAGGACCGTCCCTCCCGGATTAGGCGGAGGCGCGGAGGCGCGGAGGCGCGG 180
Db      121 CAGCGAGAGGACCGTCCCTCCCGGATTAGGCGGAGGCGCGGAGGCGCGGAGGCGCGG 180
Qy      181 GAGAGTGAATGATCCCGAGGCGCGGAGGCGCGGAGGCGCGGAGGCGCGGAGGCGCGG 240
Db      181 GAGAGTGAATGATCCCGAGGCGCGGAGGCGCGGAGGCGCGGAGGCGCGGAGGCGCGG 240
Qy      241 AAGGAACTGGGAGTCTTGAAGGACCCCGGACTCCAGCGGAAACCCCGAGTGTGA 300
Db      241 AAGGAACTGGGAGTCTTGAAGGACCCCGGACTCCAGCGGAAACCCCGAGTGTGA 300
Qy      301 GGAGGAGGGAATGGAATATACCAATGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db      301 GGAGGAGGGAATGGAATATACCAATGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy      361 CACAGATTCAGCTTCGGAACAAAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db      361 CACAGATTCAGCTTCGGAACAAAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy      421 TATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db      421 TATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy      481 TTGGCCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540

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Db 481 TTGGCAGATATATTATGACTAAACGATTATATATGATGAGAGCAACAATATTTATATT 540
Qy 541 GTTCAATGATCTTCTAGAGATTTTGTGGCGTCCAGCTTCTCTGTGAAGAAGCA 600
Db 541 GTTCAATGATCTTCTAGAGATTTTGTGGCGTCCAGCTTCTCTGTGAAGAAGCA 600
Qy 601 GGAATAATATATACCATGATCTACAGAACTTGTGTAGTCAATCAGCAGGAATCATCG 660
Db 601 GGAATAATATATACCATGATCTACAGAACTTGTGTAGTCAATCAGCAGGAATCATCG 660
Qy 661 ACTCAGGATCATCTGTAGTGAAGAAACAGTGTCACTTGAAGGTGGAATCAAAAG 720
Db 661 ACTCAGGATCATCTGTAGTGAAGAAACAGTGTCACTTGAAGGTGGAATCAAAAG 720
Qy 721 ACCTTGTACAGAGCTTCAAGAAAGAAACCTTCACTTCACTTTGGTTTCTTACCAT 780
Db 721 ACCTTGTACAGAGCTTCAAGAAAGAAACCTTCACTTCACTTTGGTTTCTTACCAT 780
Qy 781 CTACCTCATCTGAAGAGAGCAATTTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 CTACCTCATCTGAAGAGAGCAATTTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy 841 GTGAACGACAAAGAAAG 900
Db 841 GTGAACGACAAAGAAAG 900
Qy 901 TGGCTCTGTGTATTAAGAGAGATATGTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 TGGCTCTGTGTATTAAGAGAGATATGTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 960
Qy 961 GAGAGCCATCGAATCCGATCTTGAATGCTGTGTGAAGAGAGAGAGAGAGAGAGAG 1020
Db 961 GAGAGCCATCGAATCCGATCTTGAATGCTGTGTGAAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 ATCAGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1080
Db 1021 ATCAGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1080
Qy 1081 AAGATTATAGCTTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 AAGATTATAGCTTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy 1141 AAGTACTGTGTATCAG 1200
Db 1141 AAGTACTGTGTATCAG 1200
Qy 1201 TTTCTTACGATCTATTTGAAGATCACTTCATGCAATGAATGAATCCCTTCCAT 1260
Db 1201 TTTCTTACGATCTATTTGAAGATCACTTCATGCAATGAATGAATCCCTTCCAT 1260
Qy 1261 CACATTTGCAACGATTTGGGCTTCTGTGAAGATTTGGTCTCTGAAGATAAGAGAG 1320
Db 1261 CACATTTGCAACGATTTGGGCTTCTGTGAAGATTTGGTCTCTGAAGATAAGAGAG 1320
Qy 1321 ATTAAGGGGAATCTCTGAGAAAGCAAACTGAAAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 ATTAAGGGGAATCTCTGAGAAAGCAAACTGAAAGAGAGAGAGAGAGAGAGAGAG 1380
Qy 1381 TTGATGTTCTGATTTGAAGAAAGCTATATGATGATTCAGAGAGTCAATGTTGAG 1440
Db 1381 TTGATGTTCTGATTTGAAGAAAGCTATATGATGATTCAGAGAGTCAATGTTGAG 1440
Qy 1441 AAAATGATGATTAATTTACAAAGCTTCAATCACAAGAAAGTGAAGCTATTTCCAG 1500
Db 1441 AAAATGATGATTAATTTACAAAGCTTCAATCACAAGAAAGTGAAGCTATTTCCAG 1500
Qy 1501 CATCAACTCTGTAGATTTATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 CATCAACTCTGTAGATTTATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Qy 1561 AAGAAACCCAGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1561 AAGAAACCCAGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620

Qy 1621 CTGTGTGATTTTGTCAAGGTGCACTTAAATGTTGATGATTCATGCAAGAGAGAG 1680
Db 1621 CTGTGTGATTTTGTCAAGGTGCACTTAAATGTTGATGATTCATGCAAGAGAGAG 1680
Qy 1681 ATCTTATGAGCTGCTTATACATGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ATCTTATGAGCTGCTTATACATGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 TATGTAGCAACCAATTCAAATGATTTGTGCTTACTTATTTCCCTTATGATCTGAT 1800
Db 1741 TATGTAGCAACCAATTCAAATGATTTGTGCTTACTTATTTCCCTTATGATCTGAT 1800
Qy 1801 AAGAGATTAATATTTCTATATATATATATATATATATATATATATATATATATAT 1860
Db 1801 AAGAGATTAATATTTCTATATATATATATATATATATATATATATATATATATAT 1860
Qy 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCATATAGATTTCTCTTATATATAT 1920
Db 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCATATAGATTTCTCTTATATATAT 1920
Qy 1921 TGACCTACTTGTGTATGAGAGATGATGATTAATTTGATTTGATTTGATTTGATTTG 1980
Db 1921 TGACCTACTTGTGTATGAGAGATGATGATTAATTTGATTTGATTTGATTTGATTTG 1980
Qy 1981 CATCCTTACCAAACTCTAATTTTAAATATATATATATATATATATATATATATAT 2040
Db 1981 CATCCTTACCAAACTCTAATTTTAAATATATATATATATATATATATATATATAT 2040
Qy 2041 TTGGTTTTTTTTTTCTTAAATATATATATATATATATATATATATATATATATAT 2100
Db 2041 TTGGTTTTTTTTTTCTTAAATATATATATATATATATATATATATATATATATAT 2100
Qy 2101 AGACGAGATCTTGTCTGTATACCAAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Db 2101 AGACGAGATCTTGTCTGTATACCAAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Qy 2161 AGCTGTGCTTCCCGGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Db 2161 AGCTGTGCTTCCCGGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Qy 2221 TACAGTCACTGTGCAACCACTGCTTAAATTTTGTATCTTTAGTATGAGAGAGAGTT 2280
Db 2221 TACAGTCACTGTGCAACCACTGCTTAAATTTTGTATCTTTAGTATGAGAGAGAGTT 2280
Qy 2281 ACCGTGTAGGAGAGATGCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCT 2340
Db 2281 ACCGTGTAGGAGAGATGCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCT 2340
Qy 2341 CAAAGTGTGAGATTTACAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2372
Db 2341 CAAAGTGTGAGATTTACAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2372

RESULT 11
AAZ37471
ID AAZ37471 standard; cdna; 2372 BP.
XX
XX AAZ37471;
XX
XX 07-JAN-2000 (first entry)
XX
XX
DE Human sarcoma p53-associated gene.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
XX hyperproliferation; blood cancer; brain cancer; breast cancer;
XX lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
XX restenosis; sr.
XX
XX Homo sapiens.
OS
XX
XX
PN MO9949065-A1.

XX 30-SEP-1999.
 PD 26-MAR-1999; 99MO-US006702.
 XX PF 26-MAR-1999; 98US-00048810.
 XX PR (ISIS-) ISIS PHARM INC.
 XX PI Mirgilla Lf, Nero P, Graham MJ, Moria BP, Cowsett LM;
 XX WPI; 1999-610754/52.
 XX
 XX New antisense compounds used to treat eg. hyperproliferative conditions.
 XX
 PS Example 2; Page 79-81; 157pp; English.
 CC AA237473-237738 represent human mdm2 phosphorothioate oligonucleotides.
 CC AA237471, AA237472, AA237739, AA237740 and AA237741 are used in the
 CC exemplification of the present invention. The present invention describes
 CC novel nucleotide antisense compounds, targeted to the 5' untranslated,
 CC translation termination codon, or 3' untranslated region of a nucleic
 CC acid encoding human mdm2, that modulates expression of human mdm2. The
 CC oligonucleotides mediate their effect by antisense inhibition of
 CC hyperproliferative gene expression. The antisense compound is used to
 CC treat an animal having a disease or condition associated with mdm2,
 CC particularly a hyperproliferative condition, more particularly cancer,
 CC especially of the blood, brain, breast, lung or soft tissue, or
 CC psoriasis, fibrosis, atherosclerosis or restenosis
 CC
 SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2372; DB 2; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTGCTTCTGGGCGCTGTGCGCCGTGTGTGGAAGATGGA 60
 DB 1 GCACCGCGGAGCTTGGCTGCTTCTGGGCGCTGTGCGCCGTGTGTGGAAGATGGA 60
 QY 61 GCAGAGCCGAGCCGAGGCGGCGCGGACCCCTGTGACCGAGATCTCTGCTTTG 120
 DB 61 GCAGAGCCGAGCCGAGGCGGCGCGGACCCCTGTGACCGAGATCTCTGCTTTG 120
 QY 121 CAGCCAGAGACACCGTCTCTCCCGGATTAATGCGTGAAGGCCAGTGGCCCG 180
 DB 121 CAGCCAGAGACACCGTCTCTCCCGGATTAATGCGTGAAGGCCAGTGGCCCG 180
 QY 181 GAGAGTGAATGATCCCGAGGCGCAGGCGCTGTGCTTCCGAGATGATCCCGCTG 240
 DB 181 GAGAGTGAATGATCCCGAGGCGCAGGCGCTGTGCTTCCGAGATGATCCCGCTG 240
 QY 241 AAGGAACTGGGAGCTTTGAGGGAACCCCGACTCCAGCGGAGAAACCCCGATGTA 300
 DB 241 AAGGAACTGGGAGCTTTGAGGGAACCCCGACTCCAGCGGAGAAACCCCGATGTA 300
 QY 301 GGAGCAGGCAAAATGTGCAATACCAATGTCTGTACTTATGATGATGATGATGAT 360
 DB 301 GGAGCAGGCAAAATGTGCAATACCAATGTCTGTACTTATGATGATGATGATGAT 360
 QY 361 CACGATTCGAGCTTCGGAACAAGAGACCCGTGTGAGCAAAAGCATTTGCTTTGAAGT 420
 DB 361 CACGATTCGAGCTTCGGAACAAGAGACCCGTGTGAGCAAAAGCATTTGCTTTGAAGT 420
 QY 421 TATTAAGTCTGTGTGTCACAAAAGACACTTATATGATAAGAGGTTCTTTTATC 480
 DB 421 TATTAAGTCTGTGTGTCACAAAAGACACTTATATGATAAGAGGTTCTTTTATC 480
 QY 481 TTGGCCAGTATTTATGACTAAACGATTTATGATGAGAGCAACAATATGATAT 540
 DB 481 TTGGCCAGTATTTATGACTAAACGATTTATGATGAGAGCAACAATATGATAT 540
 QY 541 GTTCAATGATCTTAGAGATTTGTTGGCGTCAAGCTTCTGTGAAAGAGCA 600

DB 541 GTTCAATGATCTTAGAGATTTGTTGGCGTCAAGCTTCTGTGAAAGAGCA 600
 QY 601 GGAATAATATACCATGATCTACAGAACTTGATGATGATGATGATGATGATGAT 660
 DB 601 GGAATAATATACCATGATCTACAGAACTTGATGATGATGATGATGATGATGAT 660
 QY 661 ACTCAGTATCATCTGTAGTGAACAAGGTGACCTTGAAGTGGAGTGAATCAAAAG 720
 DB 661 ACTCAGTATCATCTGTAGTGAACAAGGTGACCTTGAAGTGGAGTGAATCAAAAG 720
 QY 721 ACCCTGACAAAGCTTCAGAAAGAACTTCATCTTCATGTTGTTTACAGCAT 780
 DB 721 ACCCTGACAAAGCTTCAGAAAGAACTTCATCTTCATGTTGTTTACAGCAT 780
 QY 781 CTACCTCATCTAGAAAGAGAGCAATTAAGTGAACAGAAAGAAATTCAGATTAATCTG 840
 DB 781 CTACCTCATCTAGAAAGAGAGCAATTAAGTGAACAGAAAGAAATTCAGATTAATCTG 840
 QY 841 GTGAACGACAAAGAAAGCCCAATCTGATGATTTTCCCTTCTTGTGATGAAGCC 900
 DB 841 GTGAACGACAAAGAAAGCCCAATCTGATGATTTTCCCTTCTTGTGATGAAGCC 900
 QY 901 TGGCTCTGTGTATTAAGGAGATATGTTGAAAGAGAGTACAGTGAATCTACAG 960
 DB 901 TGGCTCTGTGTATTAAGGAGATATGTTGAAAGAGAGTACAGTGAATCTACAG 960
 QY 961 GGAGCCCATCGAATCCGATCTTGAATGCTGTGATGATGAATGATGATGATGATG 1020
 DB 961 GGAGCCCATCGAATCCGATCTTGAATGCTGTGATGATGAATGATGATGATGATG 1020
 QY 1021 ATCAGATTCAGTTTCAGATCAGTTTATGATGATTTGAAGTGAATCTTCAGACTCAG 1080
 DB 1021 ATCAGATTCAGTTTCAGATCAGTTTATGATGATTTGAAGTGAATCTTCAGACTCAG 1080
 QY 1081 AAGATTATAGCTTATGTAAGAAAGCAAGAACTCTGATGAAGTATGATGATATC 1140
 DB 1081 AAGATTATAGCTTATGTAAGAAAGCAAGAACTCTGATGAAGTATGATGATATC 1140
 QY 1141 AAGTTACTGTATACAGGCAAGGAGAGTATGATGATGATGATGATGATGATGAT 1200
 DB 1141 AAGTTACTGTATACAGGCAAGGAGAGTATGATGATGATGATGATGATGATGAT 1200
 QY 1201 TTTCTTACGATGATTTGGAATGCACTTCATGCAATGAATGAATGATGATGATGAT 1260
 DB 1201 TTTCTTACGATGATTTGGAATGCACTTCATGCAATGAATGAATGATGATGATGAT 1260
 QY 1261 CACATTTGACAGATGTTGGGCTTCGTGAGAAATTTGCTTCTGAAGTAAAGGAAAG 1320
 DB 1261 CACATTTGACAGATGTTGGGCTTCGTGAGAAATTTGCTTCTGAAGTAAAGGAAAG 1320
 QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGCTGAAGAGGCT 1380
 DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGCTGAAGAGGCT 1380
 QY 1381 TTGATGTTCTGATTTGTAATAAACTATATGATGATTTCAAGAGTCAATGTTGAGG 1440
 DB 1381 TTGATGTTCTGATTTGTAATAAACTATATGATGATTTCAAGAGTCAATGTTGAGG 1440
 QY 1441 AAAATGATGATTAATTAACAAGCTTCACATCAAGAAAGTGAAGCTATTTCTCAGC 1500
 DB 1441 AAAATGATGATTAATTAACAAGCTTCACATCAAGAAAGTGAAGCTATTTCTCAGC 1500
 QY 1501 CATCAACTTATGATGATTTATTTATGACGCAAGAGATGTAAGAGTTGAAGGG 1560
 DB 1501 CATCAACTTATGATGATTTATTTATGACGCAAGAGATGTAAGAGTTGAAGGG 1560
 QY 1561 AAGAAACCAAGACAAAGAGAGAGTGTGATCTAGTTTCCCTTAATGCAATGTAAC 1620
 DB 1561 AAGAAACCAAGACAAAGAGAGAGTGTGATCTAGTTTCCCTTAATGCAATGTAAC 1620
 QY 1621 CTGTGATATTTGCAAGTGCACCTAAAAATGTTGATGATGATGATGATGATGATG 1680

XX Hannon GJ, Beach DH;
 XX WPI: 2000-40055/34.
 DR P-PSDB: AA96567.
 XX
 PT New method for increasing the proliferative capacity of cell lines
 PT comprising administering agents reversibly activating telomerase activity
 PT and reversibly inactivating Rb/INK4 and/or p53 pathways useful in
 PT treating age related diseases.

XX Claim 5; Page 119-120; 123pp; English.

XX This cDNA, designated hEST2, is a human telomerase catalytic subunit
 CC homologous to yeast EST2 and Euploies p123. hEST2 is a member of the
 CC reverse transcriptase family of enzymes. The invention concerns methods
 CC and reagents for extending the life-span, e.g. the number of mitotic
 CC divisions, of a cell. The method relies on activation of a telomerase
 CC activity and inhibition of one or both of a retinoblastoma (Rb)/INK4
 CC pathway or a p53 pathway. Phosphorylation of Rb by cyclin-dependent
 CC kinases, cdk4 and cdk6, releases the cells into the division cycle.
 CC Binding of INK4 family members, e.g. the tumour suppressor p16INK4a,
 CC inhibits kinase activity and results in growth arrest. Rb inactivators
 CC can selectively and reversibly inactivate an Rb/INK4 pathway, especially
 CC an Rb/p16INK4a pathway. The oncoprotein MDM2 is a cellular inhibitor of
 CC Rb/E2F function and the p53 tumour suppressor and can also be used in the
 CC method. Other molecules which can be used include cdk4 or cdk6 mutants.
 CC In particular, a cdk4 mutant is one which differs from at one or more of
 CC residues K22, R24, H95 and/or D97. Additional constructs include a
 CC papilloma virus E7 protein, or other viral oncoprotein which bypasses Rb
 CC and/or p53. Antisense constructs of the Rb and p16INK4a genes may also be
 CC used. The methods are useful for increasing the proliferative capacity of
 CC cells. The cells are subsequently of use in pharmaceutical and cosmetic
 CC preparations used to treat conditions related to (premature) ageing, e.g.
 CC macular degeneration and arteriosclerosis. The cells can also be used to
 CC replace tumour cell lines in vitro and for studies on biochemical and
 CC physiological aspects of growth and differentiation. Long lived
 CC (immortal) cells could also be of use in the production of normal or
 CC genetically engineered biotechnology products

XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 2372; DB 3; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCCGAGCTTGGCTGCTTCTGGGGCCCTGTGTGCGCTGTGTGCGAAAGATGA 60
 DB 1 GCACCGCCGAGCTTGGCTGCTTCTGGGGCCCTGTGTGCGCTGTGTGCGAAAGATGA 60
 QY 61 GCAAGAACCCGAGCCGAGGGGCGCGGACCCCTGTGACCGAATCCCTGTGCTTTG 120
 DB 61 GCAAGAACCCGAGCCGAGGGGCGCGGACCCCTGTGACCGAATCCCTGTGCTTTG 120
 QY 121 CAGCCAGAGACGCTGCTCCCTCCGCGATTAGTGCCTGACGAGCGCCAGTGCCTG 180
 DB 121 CAGCCAGAGACGCTGCTCCCTCCGCGATTAGTGCCTGACGAGCGCCAGTGCCTG 180
 QY 121 CAGCCAGAGACGCTGCTCCCTCCGCGATTAGTGCCTGACGAGCGCCAGTGCCTG 180
 DB 121 CAGCCAGAGACGCTGCTCCCTCCGCGATTAGTGCCTGACGAGCGCCAGTGCCTG 180
 QY 181 GAGAGTGAATATATCCCGAGGCGCGGCGCTGCTTCCGCGATGATGATCCCGG 240
 DB 181 GAGAGTGAATATATCCCGAGGCGCGGCGCTGCTTCCGCGATGATGATCCCGG 240
 QY 181 GAGAGTGAATATATCCCGAGGCGCGGCGCTGCTTCCGCGATGATGATCCCGG 240
 DB 181 GAGAGTGAATATATCCCGAGGCGCGGCGCTGCTTCCGCGATGATGATCCCGG 240
 QY 241 AAGGAAATCTGGGAGATCTTGAAGGACCCCGACTCCAGCGGAAACCCCGGATG 300
 DB 241 AAGGAAATCTGGGAGATCTTGAAGGACCCCGACTCCAGCGGAAACCCCGGATG 300
 QY 301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACTTGTGATGCTGTGTACCACT 360
 DB 301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACTTGTGATGCTGTGTACCACT 360
 QY 361 CACAGATTCACGCTTCGAAACAAGACCTCTGTTAGACCAAGCATTTGCTTTGAAGT 420
 DB 361 CACAGATTCACGCTTCGAAACAAGACCTCTGTTAGACCAAGCATTTGCTTTGAAGT 420

QY 421 TATTAAAGTCTGTGTGTCACAAAAGACCTTATCTATGAAGAGGTTCTTTTATC 480
 DB 421 TATTAAAGTCTGTGTGTCACAAAAGACCTTATCTATGAAGAGGTTCTTTTATC 480
 QY 481 TTGGCCAGTAT 540
 DB 481 TTGGCCAGTAT 540
 QY 541 GTTCAAATGATCTTCTAGAGATTTGTTGGCGCCAGCTTCTGTGTGAAGACACA 600
 DB 541 GTTCAAATGATCTTCTAGAGATTTGTTGGCGCCAGCTTCTGTGTGAAGACACA 600
 QY 601 GGAATAAT 660
 DB 601 GGAATAAT 660
 QY 661 ACTCAGGATCATCTGTAGTGAAGACAGGTGTCACCTTGAAGGTGGAGTATCAAAAG 720
 DB 661 ACTCAGGATCATCTGTAGTGAAGACAGGTGTCACCTTGAAGGTGGAGTATCAAAAG 720
 QY 721 ACCTGTACAGAGCTTCAGGAAGAAACCTTATCTTACATTTGGTTCTAGACCAT 780
 DB 721 ACCTGTACAGAGCTTCAGGAAGAAACCTTATCTTACATTTGGTTCTAGACCAT 780
 QY 781 CTACCTCATCTAGAGAGAGACCAATTTAGTGAACAGAAAGAAATTCAGATGAATATCTG 840
 DB 781 CTACCTCATCTAGAGAGAGACCAATTTAGTGAACAGAAAGAAATTCAGATGAATATCTG 840
 QY 841 GTGAACGACAAAGAAAGACCAAAATCTGATATATTTCCCTTCTTATGAAGACC 900
 DB 841 GTGAACGACAAAGAAAGACCAAAATCTGATATATTTCCCTTCTTATGAAGACC 900
 QY 901 TGCGCTGTGTAT 960
 DB 901 TGCGCTGTGTAT 960
 QY 961 GGAAGCCATTCAGATCCGATCTTGAATGCTGTATGATGAACATTCAGATGATGTTGG 1020
 DB 961 GGAAGCCATTCAGATCCGATCTTGAATGCTGTATGATGAACATTCAGATGATGTTGG 1020
 QY 1021 ATCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1080
 DB 1021 ATCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1080
 QY 1081 AAGATTATAGCTTATAGTGAAGACCAAGAACTCTCAGATGAAGATGATGATATC 1140
 DB 1081 AAGATTATAGCTTATAGTGAAGACCAAGAACTCTCAGATGAAGATGATGATATC 1140
 QY 1141 AAGTTACTGTGTATCAGGCAAGGAGAGATGATGATGATGATGATGATGATGAT 1200
 DB 1141 AAGTTACTGTGTATCAGGCAAGGAGAGATGATGATGATGATGATGATGATGAT 1200
 QY 1201 TTTCTTATGCTGAT 1260
 DB 1201 TTTCTTATGCTGAT 1260
 QY 1261 CACATTGCAAGATGTTGGGCGCTTGTGGAATTTGCTTCTGTAAGATTAAGGGAAG 1320
 DB 1261 CACATTGCAAGATGTTGGGCGCTTGTGGAATTTGCTTCTGTAAGATTAAGGGAAG 1320
 QY 1321 ATAAAGGGAATCTCTGAGAAAGCAATCTGAAACCTCAACACAACTGAAAGGCT 1380
 DB 1321 ATAAAGGGAATCTCTGAGAAAGCAATCTGAAACCTCAACACAACTGAAAGGCT 1380
 QY 1381 TTGATGTTCTGATTTGTAATAAACTATATGATGATTTCAAGAGATCATGTGTTGAG 1440
 DB 1381 TTGATGTTCTGATTTGTAATAAACTATATGATGATTTCAAGAGATCATGTGTTGAG 1440
 QY 1441 AAAATGATATATAATTAACAAGCTTCAATCAAGAAAGTGAAGCTATATCTCAGC 1500
 DB 1441 AAAATGATATATAATTAACAAGCTTCAATCAAGAAAGTGAAGCTATATCTCAGC 1500

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QY 1501 CATCACTTCTAGTACATTTATTTATAGACCCAGAGAAGTGAAGATTGAAAGG 1560
DB 1501 CATCACTTCTAGTACATTTATTTATAGACCCAGAGAAGTGAAGATTGAAAGG 1560
QY 1561 AAGAAACCCAGAGCAAGAGAGAGTGTGGAATCTAGTTGCCCTTAATGCCATTGAAC 1620
DB 1561 AAGAAACCCAGAGCAAGAGAGAGTGTGGAATCTAGTTGCCCTTAATGCCATTGAAC 1620
QY 1621 CTGTGTGATTTGTCAAGGTCCGACCTAAAGATGTGCAATGCCATGCGCAAAACAGGAC 1680
DB 1621 CTGTGTGATTTGTCAAGGTCCGACCTAAAGATGTGCAATGCCATGCGCAAAACAGGAC 1680
QY 1681 ATCTTAGGCTCTGCTTACATGTGCAAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
DB 1681 ATCTTAGGCTCTGCTTACATGTGCAAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
QY 1741 TATGTAGACCAACCAATTCAAATGATGTGCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
DB 1741 TATGTAGACCAACCAATTCAAATGATGTGCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
QY 1801 AAGAGATTAATATTTCTTACATATTAACCTTAGAATTTAGACAACCTGAAATTTAT 1860
DB 1801 AAGAGATTAATATTTCTTACATATTAACCTTAGAATTTAGACAACCTGAAATTTAT 1860
QY 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTCTTAGTATAT 1920
DB 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTCTTAGTATAT 1920
QY 1921 TGACCTACTTTGATGTGAATAGTAATACTTAATATTTGACTTGAATATAGTAC 1980
DB 1921 TGACCTACTTTGATGTGAATAGTAATACTTAATATTTGACTTGAATATAGTAC 1980
QY 1981 CATCTTTACACCACTCTTAATTTAAATTTTACTCTGCTTAAATGAAAGTAC 2040
DB 1981 CATCTTTACACCACTCTTAATTTAAATTTTACTCTGCTTAAATGAAAGTAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAATATGTAATAGACATTTAAATGTAACCTTATTTTTTTT 2100
DB 2041 TTGGTTTTTTTTTTCTTAATATGTAATAGACATTTAAATGTAACCTTATTTTTTTT 2100
QY 2101 AGACCGAGTCTTGTCTGTGTACCCAGGCTGAGTGAAGTGTGATCTTGGCTCACTGCA 2160
DB 2101 AGACCGAGTCTTGTCTGTGTACCCAGGCTGAGTGAAGTGTGATCTTGGCTCACTGCA 2160
QY 2161 AGCTTGCCTCTCCCGGGTTCGACCACTTCTCTGCTCAGCCTCCCAATTAAGCTTGGC 2220
DB 2161 AGCTTGCCTCTCCCGGGTTCGACCACTTCTCTGCTCAGCCTCCCAATTAAGCTTGGC 2220
QY 2221 TACAGTCATCTGSCACCACTGGGTAATTTTTTGTACTTTTATGAGAGACAGGTTTC 2280
DB 2221 TACAGTCATCTGSCACCACTGGGTAATTTTTTGTACTTTTATGAGAGACAGGTTTC 2280
QY 2281 ACCGTGTTAGCCAGATGTGTGATCTCTGACCTGATCCGCCACTCGGCTCC 2340
DB 2281 ACCGTGTTAGCCAGATGTGTGATCTCTGACCTGATCCGCCACTCGGCTCC 2340
QY 2341 CAAAGTCTGGGATTAACAGGCATGAGCCACCG 2372
DB 2341 CAAAGTCTGGGATTAACAGGCATGAGCCACCG 2372

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RESULT 14

AAE80625 standard; cDNA; 2372 BP.

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XX AA80625;
XX
XX 02-MAY-2001 (first entry)
XX
XX Human mdm2 cDNA.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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OS Homo sapiens.
XX
XX US6184212-B1.
XX
XX 06-FEB-2001.
XX
XX 26-MAR-1999; 99US-00280805.
XX
XX 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM;
XX WPI; 2001-190948/19.
XX
XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
XX acid molecule encoding human mdm-2 useful for modulating the expression
XX of human mdm-2 and reducing hyperproliferation of human cells.
XX
XX Example 2; Col 43-46; 77pp; English.
XX
XX The present invention relates to an antisense compound 8-30 nucleobases
XX in length targeted to nucleobases 1-308 of the 5' untranslated region,
XX 1776-1806 of the translation termination codon region or 1818-2370 of the
XX 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
XX The invention is useful for reducing hyperproliferation of human cells,
XX modulating the expression of mdm2 in human cells or tissues or in vitro.
XX The hyperproliferative disorder includes cancer or psoriasis
XX
XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

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Query Match 100.0%; Score 2372; DB 4; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCACCGCGGACCTTGGCTCTTCTGGGCTGTGTGCGCCCTGTGTGCGAAATGGA 60
DB 1 GCACCGCGGACCTTGGCTCTTCTGGGCTGTGTGCGCCCTGTGTGCGAAATGGA 60
QY 61 GCAGAGCGGACCGGAGGCGGCGGACCCCTTGAACGAGATCTTGGCTTTG 120
DB 61 GCAGAGCGGACCGGAGGCGGCGGACCCCTTGAACGAGATCTTGGCTTTG 120
QY 121 CAGCAGAGACGACCGTCCCTCCCGGATTAAGTGCCTAGCAGGCGCCAGTCCGCGCG 180
DB 121 CAGCAGAGAGACCGTCCCTCCCGGATTAAGTGCCTAGCAGGCGCCAGTCCGCGCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGGAGGCGGCTGTGCTTCCGCAATGATCCCGGTG 240
DB 181 GAGAGTGAATGATCCCGAGGCGGAGGCGGCTGTGCTTCCGCAATGATCCCGGTG 240
QY 241 AAGGAACTGGGGAGCTTTGAGGGAACCCCGGACCTCAAGCGGAAACCCCGGATGAGTA 300
DB 241 AAGGAACTGGGGAGCTTTGAGGGAACCCCGGACCTCAAGCGGAAACCCCGGATGAGTA 300
QY 301 GGAGCAGGCAATGTGCAATACCAATGTCATGTAAGTGTGCTGTACCACT 360
DB 301 GGAGCAGGCAATGTGCAATACCAATGTCATGTAAGTGTGCTGTACCACT 360
QY 361 CACAGATTCAGCTTCCGGAACAAGAGACCTGTGTAGACCAAGCATTTGCTTTGAAGT 420
DB 361 CACAGATTCAGCTTCCGGAACAAGAGACCTGTGTAGACCAAGCATTTGCTTTGAAGT 420
QY 421 TATTAAGTCTGTGTGCACAAAAAGACATTAATATGAAAGAGGTTCTTTTATTC 480
DB 421 TATTAAGTCTGTGTGCACAAAAAGACATTAATATGAAAGAGGTTCTTTTATTC 480
QY 481 TTGGCCAGTATATTAATGCTAAACGATTAATGATGAGAGCAACATATTTGATAT 540
DB 481 TTGGCCAGTATATTAATGCTAAACGATTAATGATGAGAGCAACATATTTGATAT 540
QY 541 GTTCAAAAGATCTTAGAAGATTTGTTGGCGTCCCAAGCTTCTGTGAAAGAGCACA 600

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Db 541 GTTCAATGATCTTCTAGAGATTTGTTGGCGGCCAAGCTTCTGTGAAAGAGACA 600
Qy 601 GGAATAATATATCCATGATCTACAGAACTTGTAATGTGTAATCAGAGAAATCATTCG 660
Db 601 GGAATAATATATCCATGATCTACAGAACTTGTAATGTGTAATCAGAGAAATCATTCG 660
Qy 661 ACTCAGGATCATCTGTAGTGAAGACAGGTGTCACTTGAAGTGGAGTATCAAAAG 720
Db 661 ACTCAGGATCATCTGTAGTGAAGACAGGTGTCACTTGAAGTGGAGTATCAAAAG 720
Qy 721 ACCTTGTAACAAGACCTTCAGAGAGAAACCTTCATCTTCAATTTGGTTTCTAGACCAT 780
Db 721 ACCTTGTAACAAGACCTTCAGAGAGAAACCTTCATCTTCAATTTGGTTTCTAGACCAT 780
Qy 781 CTACCTCATCTAGAGAGAGACCAATTAAGTGAACAGAGAAATTCAGATTAATTCG 840
Db 781 CTACCTCATCTAGAGAGAGACCAATTAAGTGAACAGAGAAATTCAGATTAATTCG 840
Qy 841 GTGAACGACAAAGAAAGCCCAAAATCTGATAGTATTCCTTCCCTTCTTGATGAAAGCC 900
Db 841 GTGAACGACAAAGAAAGCCCAAAATCTGATAGTATTCCTTCCCTTCTTGATGAAAGCC 900
Qy 901 TGGCTCTGTGTATTAAGGAGATATGTTGTAAGAAAGCAGTGAATCTACAG 960
Db 901 TGGCTCTGTGTATTAAGGAGATATGTTGTAAGAAAGCAGTGAATCTACAG 960
Qy 961 GGAGGCCATCGAATCCGATCTTGATGCTGTGTGAAGAACATTCAGTGAATGGTTGG 1020
Db 961 GGAGGCCATCGAATCCGATCTTGATGCTGTGTGAAGAACATTCAGTGAATGGTTGG 1020
Qy 1021 ATCAGGATTCAGTTTCAATCAGATCAGTTAGTGAATTTGAAGTTGAATCTCTCGACTAG 1080
Db 1021 ATCAGGATTCAGTTTCAATCAGATCAGTTAGTGAATTTGAAGTTGAATCTCTCGACTAG 1080
Qy 1081 AAGATTATAGCCTTAGTAAGAGAGACAAAGAACTTCAGATGAAGATGAAGTATATC 1140
Db 1081 AAGATTATAGCCTTAGTAAGAGAGACAAAGAACTTCAGATGAAGATGAAGTATATC 1140
Qy 1141 AAGTTACGTGTATACAGCAGGAGAGAGATGATACAGATTCATTTGAAGAAATCCTGAA 1200
Db 1141 AAGTTACGTGTATACAGCAGGAGAGAGATGATACAGATTCATTTGAAGAAATCCTGAA 1200
Qy 1201 TTTCTTGAATGATGATGAAATGACCTTCATGCAATGAAATGAAATGAAATGAAATGAA 1260
Db 1201 TTTCTTGAATGATGATGAAATGACCTTCATGCAATGAAATGAAATGAAATGAAATGAA 1260
Qy 1261 CACATTCGACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCTGAAGTAAAGGAAAG 1320
Db 1261 CACATTCGACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCTGAAGTAAAGGAAAG 1320
Qy 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGTGAAGAGGCT 1380
Db 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAATACTCAACAAGTGAAGAGGCT 1380
Qy 1381 TTGATGTTCTGATTTGTAATAAACTATAGTAATGATTCAGAGAGTCAATGTGAGG 1440
Db 1381 TTGATGTTCTGATTTGTAATAAACTATAGTAATGATTCAGAGAGTCAATGTGAGG 1440
Qy 1441 AAAATGATGATTAATTAACAAGCTTCACATCAACAAGAAAGTGAAGCTATTCACG 1500
Db 1441 AAAATGATGATTAATTAACAAGCTTCACATCAACAAGAAAGTGAAGCTATTCACG 1500
Qy 1501 CATCACTTCTAGTACATTAATTAAGACCAAGAGATGTAAGAGGTTGAAAGG 1560
Db 1501 CATCACTTCTAGTACATTAATTAAGACCAAGAGATGTAAGAGGTTGAAAGG 1560
Qy 1561 AAGAAACCAAGACAAAGAGAGAGTGAATCTAGTTGGCCCTTAATGCAATTGAAC 1620
Db 1561 AAGAAACCAAGACAAAGAGAGAGTGAATCTAGTTGGCCCTTAATGCAATTGAAC 1620
Qy 1621 CTGTGTGATTTGTCAAGGTCGACTAAATATGTTGCAATTCAGCAAGAC 1680
Db 1621 CTGTGTGATTTGTCAAGGTCGACTAAATATGTTGCAATTCAGCAAGAC 1680
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Db 1621 CTGTGTGATTTGTCAAGGTCGACTAAATATGTTGCAATTCAGCAAGAC 1680
Qy 1681 ATCTTATGCGCCTGCTTACATATGTCGAAAGAGCTAAAGAAAGAAATTAAGCCTGCCAG 1740
Db 1681 ATCTTATGCGCCTGCTTACATATGTCGAAAGAGCTAAAGAAAGAAATTAAGCCTGCCAG 1740
Qy 1741 TATGTAGCAACCAATTAATGATGCTTAATTTCCCTAGTGAAGCTGTCTAT 1800
Db 1741 TATGTAGCAACCAATTAATGATGCTTAATTTCCCTAGTGAAGCTGTCTAT 1800
Qy 1801 AAGGAATTAATATTTCTAATCTATATACCTTGAAGATTTAGCAACCTGAATTTAT 1860
Db 1801 AAGGAATTAATATTTCTAATCTATATACCTTGAAGATTTAGCAACCTGAATTTAT 1860
Qy 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTTATATAT 1920
Db 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTTATATAT 1920
Qy 1921 TGACCTTACTTGTAGTGAAGTGAATTAATCTATATATTTGACTTGAATATAGT 1980
Db 1921 TGACCTTACTTGTAGTGAAGTGAATTAATCTATATATTTGACTTGAATATAGT 1980
Qy 1981 CATCTTTACCAACCTCTTAATTTTAATTAATTTCTAATCTGTCTTAAATGAAGATAC 2040
Db 1981 CATCTTTACCAACCTCTTAATTTTAATTAATTTCTAATCTGTCTTAAATGAAGATAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAATATATATATGATGATTAATTAATTAATTAATTTT 2100
Db 2041 TTGGTTTTTTTTTTCTTAATATATATATGATGATTAATTAATTAATTAATTTT 2100
Qy 2101 AGACGAGTCTTGTCTGTTTACCAGAGCTGAGAGTGAAGTGAATCTTGCTGCTAC 2160
Db 2101 AGACGAGTCTTGTCTGTTTACCAGAGCTGAGAGTGAAGTGAATCTTGCTGCTAC 2160
Qy 2161 AGCTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Db 2161 AGCTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Qy 2221 TACAGTCACTGTCACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Db 2221 TACAGTCACTGTCACACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Qy 2281 ACCGTGTTAGCAGAGATGCTGATCTCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
Db 2281 ACCGTGTTAGCAGAGATGCTGATCTCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
Qy 2341 CAAAGTCTGGGATTTACAGGATGAGCCACG 2372
Db 2341 CAAAGTCTGGGATTTACAGGATGAGCCACG 2372

RESULT 15
AAd07530 standard; DNA; 2372 BP.
AAd07530;
10-AUG-2001 (first entry)
XX
XX Human p-53 associated mdm2 gene.
XX
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; de.
XX
XX Homo sapiens.
XX
XX US6238921-B1.
XX
XX PD 29-MAY-2001.
XX
XX PF 26-MAR-1998; 98US-00048910.
XX
XX PR 26-MAR-1998; 98US-00048810.
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XX	(ISIS-) ISIS PHARM INC.
XX	PA
XX	PI Miraglia LJ, Nero P, Graham MJ, Monia BP;
XX	DR WPI, 2001-366477/38.
XX	PT New oligonucleotides 16506, 16507, 16518, 16520, 16521, 16522 and 16524,
XX	PT which inhibits human mdm2 expression, useful for inhibiting, diagnosing
XX	PT or treating abnormal proliferative conditions associated with mdm2.
XX	PS Example 2; Col 19-24; 19pp; English.
XX	CC The present invention relates to compositions and methods for modulating
CC	CC the expression of human mdm2 gene, a naturally present cellular gene
CC	CC implicated in abnormal cell proliferation and tumour formation. The
CC	CC invention also provides antisense oligonucleotides which are targeted to
CC	CC the mdm2 gene and are capable of inhibiting the expression of mdm2 gene.
CC	CC The oligonucleotides are useful in diagnostics, therapeutics, prophylaxis
CC	CC and as research reagents. They are especially useful for inhibiting,
CC	CC diagnosing and treating abnormal proliferative conditions associated with
CC	CC mdm2. The method is useful for detecting and determining the role of mdm2
CC	CC expression in various cell functions and physiological processes and
CC	CC conditions, and for diagnosing conditions associated with mdm2
CC	CC expression. The present sequence is p-53 associated mdm2 gene from human
XX	Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
XX	Query Match 100.0%; Score 2372; DB 4; Length 2372;
XX	Best Local Similarity 100.0%; Pred. No. 0;
XX	Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GCACCCGCGGAGCTTGGCTCTTCTGGGGCCGTGTGCGCCCTGTGTGCGAAAGATGGA 60
DB	1 GCACCGCGCGAGCTTGGCTCTTCTGGGGCCGTGTGCGCCCTGTGTGCGAAAGATGGA 60
QY	61 GCAGAAAGCCGAGCCCGAGGGGGCGCGCAGCCCTCTGACCGAGATCCTGCTGCTTGC 120
DB	61 GCAGAAAGCCGAGCCCGAGGGGGCGCGCAGCCCTCTGACCGAGATCCTGCTGCTTGC 120
QY	121 CAGCCAGGAGCAGCGCTCCCTCCCGAGTTAGTGCCTGAGAGGCCCAAGTCCCTGGCCCG 180
DB	121 CAGCCAGGAGCAGCGCTCCCTCCCGAGTTAGTGCCTGAGAGGCCCAAGTCCCTGGCCCG 180
QY	181 GAGAGTGAATGATCCCGGAGGCCCGAGGGCGTGTGCTTCCGCAATGATGATCCCGGTG 240
DB	181 GAGAGTGAATGATCCCGGAGGCCCGAGGGCGTGTGCTTCCGCAATGATGATCCCGGTG 240
QY	241 AAGGAACTGGGGAGCTTTGAGGAGACCCCGAATCCCAAGCGGAAACCCCGAGATGTTGA 300
DB	241 AAGGAACTGGGGAGCTTTGAGGAGACCCCGAATCCCAAGCGGAAACCCCGAGATGTTGA 300
QY	301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACTTACTGATGTGTCTGTAAACACTT 360
DB	301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACTTACTGATGTGTCTGTAAACACTT 360
QY	361 CACAGATTCGAGCTTCGGAACAAGAGACCTGTGTTAGACCAAAAGCATTTGTTGAAGT 420
DB	361 CACAGATTCGAGCTTCGGAACAAGAGACCTGTGTTAGACCAAAAGCATTTGTTGAAGT 420
QY	421 TATTAAATCTGTGTGTGTCACAAAAGACACTTATATCTATGAAAGAGTTCTTTTATATC 480
DB	421 TATTAAATCTGTGTGTGTCACAAAAGACACTTATATCTATGAAAGAGTTCTTTTATATC 480
QY	481 TTGGCAGTATATTTATGACTTAAAGCATTTATATGATGAGAGCAACAATTTGATATTT 540
DB	481 TTGGCAGTATATTTATGACTTAAAGCATTTATATGATGAGAGCAACAATTTGATATTT 540
QY	541 GTTCAAAATGATCTTCTAGAGATTTGTGTGGCGTCCAAAGCTTCTCTGTGAAGAGACACA 600
DB	541 GTTCAAAATGATCTTCTAGAGATTTGTGTGGCGTCCAAAGCTTCTCTGTGAAGAGACACA 600
QY	601 GGAATAATATATCAATGATCTTACAGGAATCTGTAGTACTCAATGACAGAAATCATCGG 660

Db	601	GGAAAATATTAATCAATGATCTTACAGGAACTTGGTAGTAACTCAATCAGCAGAAATCATCCG	660
Qy	661	ACTCAGGTACATCTGTGTGATGAGAAACAGGTGTCACTTGAAGTGGAGTATCAAAAG	720
Db	661	ACTCAGGTACATCTGTGTGATGAGAAACAGGTGTCACTTGAAGTGGAGTATCAAAAG	720
Qy	721	ACCTGTACAGAGCTTCAGGAAAGAAACCTTCATCTCACTTGGTGTCTAGACCAT	780
Db	721	ACCTGTACAGAGCTTCAGGAAAGAAACCTTCATCTCACTTGGTGTCTAGACCAT	780
Qy	781	CTACTCTATCTAGAAAGAGACCAATTAGTGAACAAGAAATTCAGATGAATTAATCTG	840
Db	781	CTACTCTATCTAGAAAGAGACCAATTAGTGAACAAGAAATTCAGATGAATTAATCTG	840
Qy	841	GTGAACGACAAAGAAAACGCCAACAATCTGATAGTATTCCTTCCCTTATGAAAGCC	900
Db	841	GTGAACGACAAAGAAAACGCCAACAATCTGATAGTATTCCTTCCCTTATGAAAGCC	900
Qy	901	TGGCTCTGTGTATATAAGGAGATATGTTGTGAAGAAGCAGTAGACGTAATCTACAG	960
Db	901	TGGCTCTGTGTATATAAGGAGATATGTTGTGAAGAAGCAGTAGACGTAATCTACAG	960
Qy	961	GGAGGCCATCGAATCCGGATCTTGATGCTGGGTGAAGTGAACATTCAAGTATTTGGTGG	1020
Db	961	GGAGGCCATCGAATCCGGATCTTGATGCTGGGTGAAGTGAACATTCAAGTATTTGGTGG	1020
Qy	1021	ATCAGAAATTCAGTTTCAGATCAGTTTGTGTAGAAATTTGAAGTTGAATCTCTGCATCAG	1080
Db	1021	ATCAGAAATTCAGTTTCAGATCAGTTTGTGTAGAAATTTGAAGTTGAATCTCTGCATCAG	1080
Qy	1081	AAGATTTATAGCCTTAGTGAAGAAAGAAAGAACTCTCAGATGAAGATGATAGTATATTC	1140
Db	1081	AAGATTTATAGCCTTAGTGAAGAAAGAAAGAACTCTCAGATGAAGATGATAGTATATTC	1140
Qy	1141	AAGTTTACTGTATACAGCAGGGAGAGTGTACAGATTCATTGGAAGAGATCTGAAA	1200
Db	1141	AAGTTTACTGTATACAGCAGGGAGAGTGTACAGATTCATTGGAAGAGATCTGAAA	1200
Qy	1201	TTTCCCTTAGCAGCTAATTGGAATGCACTTCATGAAATGAATATATTCCTTCCAT	1260
Db	1201	TTTCCCTTAGCAGCTAATTGGAATGCACTTCATGAAATGAATATATTCCTTCCAT	1260
Qy	1261	CACATTCGAAACAGATGTTGGGCCCTCTGTGTGAAATTTGGCTTCTGGAAGTAAAGGAAG	1320
Db	1261	CACATTCGAAACAGATGTTGGGCCCTCTGTGTGAAATTTGGCTTCTGGAAGTAAAGGAAG	1320
Qy	1321	ATTAAGGGGAAATCTTGAGAAAGCCAACTGAAAACTCAACAAGCTGAAGAGGCT	1380
Db	1321	ATTAAGGGGAAATCTTGAGAAAGCCAACTGAAAACTCAACAAGCTGAAGAGGCT	1380
Qy	1381	TTGATGTTCCGTGATTTGTAATAAACTATAGTGAATGATTCAGAGAGTCATGTGTGAAG	1440
Db	1381	TTGATGTTCCGTGATTTGTAATAAACTATAGTGAATGATTCAGAGAGTCATGTGTGAAG	1440
Qy	1441	AAATATGATGATTAATAATTACCAAGCTTCACAATCAACAAGAAAGTGAAGACTATCTCAGC	1500
Db	1441	AAATATGATGATTAATAATTACCAAGCTTCACAATCAACAAGAAAGTGAAGACTATCTCAGC	1500
Qy	1501	CATCAACTTCTAGTAGCATTAATTTATAGCAGCCCAAGAAAGTGTGAAGAGTTTGAAGGG	1560
Db	1501	CATCAACTTCTAGTAGCATTAATTTATAGCAGCCCAAGAAAGTGTGAAGAGTTTGAAGGG	1560
Qy	1561	AAAGAAACCAAGAAAGAAAGAGGTGTGAATCTAATTTGCCCTTAATGCCATTGAAC	1620
Db	1561	AAAGAAACCAAGAAAGAAAGAGGTGTGAATCTAATTTGCCCTTAATGCCATTGAAC	1620
Qy	1621	CTTGTGTGATTTGTCAAGTGTGACCTTAATAATGTTGCAATTTGTCATGTGCAAAAAGAGAC	1680
Db	1621	CTTGTGTGATTTGTCAAGTGTGACCTTAATAATGTTGCAATTTGTCATGTGCAAAAAGAGAC	1680
Qy	1681	ATCTTATGCGCTGTTTACATGTGCAAGAAAGCTTAAGAAAGAAATTAAGCCTTGCCAG	1740

Db 1681 ATCTTATGCGCTGCTTTACATGTGCAGAAAGACTAAAGAAAAAGAAATTAAGCCCTGCCAG 1740
QY 1741 TATGTAGACAAACCAATTCAAATGATGTGTACTTATTTCCCTAGTGAACCTGTCTAT 1800
Db 1741 TATGTAGACAAACCAATTCAAATGATGTGTACTTATTTCCCTAGTGAACCTGTCTAT 1800
QY 1801 AAGAGATTTATATTTCTAATCTAATTAACCTAGAAATTTAGACAAACCTGAATTTAT 1860
Db 1801 AAGAGATTTATATTTCTAATCTAATTAACCTAGAAATTTAGACAAACCTGAATTTAT 1860
QY 1861 CACATATATCAAAAGTGAGAAAAATGCTCAATTCACATAGATTTCTCTCTTTAGATAT 1920
Db 1861 CACATATATCAAAAGTGAGAAAAATGCTCAATTCACATAGATTTCTCTCTTTAGATAT 1920
QY 1921 TGACCTTCTTTGTAGAGGAAATAGTAATTAATTAATTTGACTGGAATATGTAGCT 1980
Db 1921 TGACCTTCTTTGTAGAGGAAATAGTAATTAATTAATTTGACTGGAATATGTAGCT 1980
QY 1981 CATCCTTTACACCAACTCCTAATTTTAAATATTTCTACTGCTTAAATGAGAAATAC 2040
Db 1981 CATCCTTTACACCAACTCCTAATTTTAAATATTTCTACTGCTTAAATGAGAAATAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAATATATGATATGACATTTAAATGTAACTTATATTTTTT 2100
Db 2041 TTGGTTTTTTTTTTCTTAATATATGATATGACATTTAAATGTAACTTATATTTTTT 2100
QY 2101 AGACCGAGTCTTGCTGTGTACCCAGGCTGAGAGTGCAGTGGTGAATCTTGGCTCACTGCA 2160
Db 2101 AGACCGAGTCTTGCTGTGTACCCAGGCTGAGAGTGCAGTGGTGAATCTTGGCTCACTGCA 2160
QY 2161 AGCTTGCCCTCCCGGGTTGCGACATTTCTGTGCTCAGCCTCCCAATTAGCTTGSCC 2220
Db 2161 AGCTTGCCCTCCCGGGTTGCGACATTTCTGTGCTCAGCCTCCCAATTAGCTTGSCC 2220
QY 2221 TACAGTATCTGCCACACACCTGGCTAATTTTTTGTACTTTTATAGAGACAGGGTTTC 2280
Db 2221 TACAGTATCTGCCACACACCTGGCTAATTTTTTGTACTTTTATAGAGACAGGGTTTC 2280
QY 2281 ACCGTGTAGCCAGATGTGTCTCGATCTCTGACCTCGTGAATCCGCCACTCGGCTCC 2340
Db 2281 ACCGTGTAGCCAGATGTGTCTCGATCTCTGACCTCGTGAATCCGCCACTCGGCTCC 2340
QY 2341 CAAAGTGTGGGATTTACAGCATGAGCCACCG 2372
Db 2341 CAAAGTGTGGGATTTACAGCATGAGCCACCG 2372

Search completed: August 4, 2006, 12:25:52
Job time : 1495 secs

241 AAGAACTGGGAGTCTTGAAGGACCCCGACCTCAAGCGGAAAAACCCGGATGTGA 300
| | | | |
Db 241 AAGAACTGGGAGTCTTGAAGGACCCCGACCTCAAGCGGAAAAACCCGGATGTGA 300
Qy 301 GGAGAGGCAAAATGTGCATATCAACATGTCTGTAACCTAAGTGTGTACCACT 360
| | | | |
Db 301 GGAGAGGCAAAATGTGCATATCAACATGTCTGTAACCTAAGTGTGTACCACT 360
Qy 361 CACAGATCCGAGCTTCGGAACAAGAGACCCGTGTAACCAAGCAATTCCTTTGAAGT 420
| | | | |
Db 361 CACAGATCCGAGCTTCGGAACAAGAGACCCGTGTAACCAAGCAATTCCTTTGAAGT 420
Qy 421 TATTAAAGTCTGTGTGCACAAAAAGACACTTATATATGAAGAAGTCTTTTATATC 480
| | | | |
Db 421 TATTAAAGTCTGTGTGCACAAAAAGACACTTATATATGAAGAAGTCTTTTATATC 480
Qy 481 TTGGCAGATATATATGAATAACGATATATATGATGAAGCAACATATTTGATAT 540
| | | | |
Db 481 TTGGCAGATATATATGAATAACGATATATATGATGAAGCAACATATTTGATAT 540
Qy 541 GTTCAAAATGATCTTGAAGATTTGTTGGCTGCCAAGCTTCTGTGGAAGAAGCA 600
| | | | |
Db 541 GTTCAAAATGATCTTGAAGATTTGTTGGCTGCCAAGCTTCTGTGGAAGAAGCA 600
Qy 601 GGAATATATATACATGATCTACAGAACTTGTGTATGTCATGACAGATCATCG 660
| | | | |
Db 601 GGAATATATATACATGATCTACAGAACTTGTGTATGTCATGACAGATCATCG 660
Qy 661 ACTCAGATATCTGTGAGTGAACAAGGTGTACCTTGAAGGTGGAGTATCAAAAG 720
| | | | |
Db 661 ACTCAGATATCTGTGAGTGAACAAGGTGTACCTTGAAGGTGGAGTATCAAAAG 720
Qy 721 ACCTGTCAAAAGCTTCAGAAAGAAACCTTCATCTTCAATTTGTTTACACAT 780
| | | | |
Db 721 ACCTGTCAAAAGCTTCAGAAAGAAACCTTCATCTTCAATTTGTTTACACAT 780
Qy 781 CTACCTCATCTGAAGAGAGCAATTAGTGAACAAGAAAAATTCAATGATTAATCTG 840
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RESULT 2

AR009781 LOCUS AR009781 2372 bp DNA linear PAT 04-DEC-1998
DEFINITION AR009781 Sequence 2 from patent US 5756455.
ACCESSION AR009781
VERSION AR009781.1 GI:3968586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (baees 1 to 2372)
AUTHORS Kinzler, K.W. and Vogelstein, B.
TITLE Amplification of human MDM2 gene in human tumors
JOURNAL Patent: US 5756455-A 2 26-MAY-1998;
FEATURES
source 1.2372
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Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
AR028963
LOCUS AR028963 2372 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5858976.
ACCESSION AR028963
VERSION AR028963.1 GI:5940936
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burrell, M., Hill, D.E., Kinzler, K.W. and Vogelstein, B.
TITLE Methods for inhibiting interaction of human MDM2 and p53
JOURNAL Patent: US 5858976-A 2 12-JUN-1999;
FEATURES
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION	Sequence 1 from patent US 6238921.		linear
ACCESSION	AR154584		
VERSION	AR154584.1	GI:15122637	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2372)		
TITLE	Mitraglia, L.J., Nero, P., Graham, M.J. and Monia, B.P.		
JOURNAL	Antisense oligonucleotide modulation of human mdm2 expression		
FEATURES	Patent: US 6238921-A 1 29-MAY-2001;		
SOURCE	Location/Qualifiers		
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RESULT 5
BD073962 2372 bp DNA linear PAT 27-AUG-2002
LOCUS BD073962
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073962
VERSION BD073962.1 GI:22619565
KEYWORDS JP 2001513996-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 2372)
AUTHORS Chen, J., Agrawal, S. and Zhang, R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 1 11-SEP-2001;
HYBRIDON INC
COMMENT OS unidentified
PN JP 2001513996-A/1
PD 11-SEP-2001
PF 18-AUG-1998 US 2000507794
PR 22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
JIANDDONG CHEN, SUDHIR AGRAWAL, RUIWEN ZHANG
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CC Topology: linear;
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LOCUS	BD138075	Antisense modulation of human MDM2 expression.	
DEFINITION	BD138075	GI:23233020	
ACCESSION	BD138075.1	GI:23233020	
VERSION	JP 2002508944-A/1.		
KEYWORDS	unidentified		
SOURCE	unidentified		
ORGANISM	unclassified sequences.		
REFERENCE	1 (bases 1 to 2372)		
AUTHORS	Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.		
JOURNAL	Antisense modulation of human MDM2 expression Patent: JP 2002508944-A 1 26-MAR-2002; ISIS PHARMACEUTICALS INC		
COMMENT	OS Unidentified PN JP 2002508944-A/1 PD 26-MAR-2002 PF 26-MAR-1999 JP 2000536025 PI 26-MAR-1998 US 09/048810 LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M		
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Qy      1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCACATGATTTCTTCTTTAGATATAT 1920
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BD233925
LOCUS      2372 bp DNA linear PAT 17-JUL-2003
DEFINITION Method and reagent of enhancing growth capability and preventing
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ACCESSION  BD233925
VERSION     BD233925.1 GI:33043695
KEYWORDS    JP 2002530436-A/2.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE   1 (bases 1 to 2372)
            Hannon,G.J. and Beach,D.H.
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            Patent: JP 2002530436-A 2 17-SEP-2002;
            GENETICA INC
COMMENT     OS Homo sapiens (human)
            PN JP 2002530436-A/2
            PD 17-SEP-2002 JP 2000584049
            PE 24-NOV-1999 JP 2000584049
            PR 25-NOV-1998 US 60/109,891, 17-FEB-1999 US 60/120549 PI
            PC A61K35/12,A61K7/00,A61K38/22,A61K45/00,A61K48/00,A61P43/00, PC
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            PC C12N15/09,A61K37/24,C12N15/00
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Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
111727
LOCUS 111727 2372 bp DNA linear PAT 26-JUL-1995

DEFINITION Sequence 1 from Patent US 5411860.
ACCESSION 111727
VERSION 111727.1 GI:309479
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Vogelstein, B. and Kinzler, K. W.
TITLE Amplification of human MDM2 gene in human tumors
JOURNAL Patent: US 5411860-A 1 02-May-1995;
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Matches 2372; Conservative 0; Mismatches 0; Indels. 0; Gaps 0;
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112226
LOCUS 112226 2372 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 1 from patent US 5420263.
ACCESSION 112226
VERSION 112226.1 GI:909724
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burrell,M., Hill,D.E., Kinzler,K.W. and Vogelstein,B.
TITLE Amplification of human MDM2 gene in human tumors
JOURNAL Patent: US 5420263-A 1 30-MAY-1995;
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DEFINITION Sequence 1 from patent US 5519118.
ACCESSION 121256
VERSION 121256.1 GI:1601610
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
Vogelstein, B. and Kinzler, K.
TITLE Human MDM2 protein involved in human tumors
JOURNAL Patent: US 5519118-A 1 21-MAY-1996;
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RESULT 11
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DEFINITION Sequence 2 from patent US 5550023.
ACCESSION 125341 GI:1605211
VERSION 125341.1
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2372)
AUTHORS Kinzler, K.W. and Vogelstein, B.
TITLE Amplification of human MDW2 gene in human tumors
JOURNAL Patent: US 5550023-A 2 27-AUG-1996;
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DEFINITION Sequence 2 from patent US 5606044.
ACCESSION 136472
VERSION 136472.1 GI:2086985
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burrell, M., Hill, D.E., Kinzler, K.W. and Vogelstein, B.
TITLE Kits for detecting amplification of human MDM2
JOURNAL Patent: US 5606044-A 2 25-FEB-1997;
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ACCESSION 140222
VERSION 140222.1 GI:2083227
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burrell,M., Hill,D.E., Kinzler,K.W. and Vogelstein,B.
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DEFINITION Sequence 2 from patent US 6399755.
ACCESSION AR212312
VERSION AR212312.1 GI:21515852
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SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Kinzler, K.W. and Vogelstein, B.
TITLE Products for inhibiting expression of human MDX2
JOURNAL Patent: US 6399755-A 2 04-JUN-2002;
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LOCUS AR214399 2372 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 43 from patent US 6407062.
ACCESSION AR214399
VERSION AR214399.1 GI:23312052
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Sheri,C.J., Quelle,D., Rousset,M.F., Zindy,F. and Weber,J.D.
TITLE ARF-p19, a novel regulator of the mammalian cell cycle
JOURNAL Patent: US 6407062-A 43 18-JUN-2002;
St. Jude Children's Research Hospital; Memphis, TN
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	2372	100.0	2372	US-09-956-425-7	Sequence 7, Appl1
3	2372	100.0	2372	US-09-851-771A-1	Sequence 1, Appl1
4	2372	100.0	2372	US-09-541-848-1	Sequence 1, Appl1
5	2372	100.0	2372	US-09-873-367C-450	Sequence 450, App
6	2372	100.0	2372	US-09-966-724-1	Sequence 1, Appl1
7	2372	100.0	2372	US-10-007-926A-121	Sequence 121, App
8	2372	100.0	2372	US-10-005-344-1	Sequence 1, Appl1
9	2372	100.0	2372	US-10-422-536-136	Sequence 136, App
10	2372	100.0	2372	US-10-232-951-34	Sequence 34, App
11	2372	100.0	2372	US-10-052-482-173	Sequence 173, App
12	2372	100.0	2372	US-10-489-802-7	Sequence 7, Appl1
13	2372	100.0	2372	US-10-723-860-2235	Sequence 2235, App
14	2372	100.0	2372	US-10-843-641A-450	Sequence 450, App
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09752983
; Patent No. US20010016575A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
; APPLICANT: Graham, Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 271
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,983
; FILING DATE: 02-Jan-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/280,805
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Licata, Jane Massey
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-810-1515
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: Nucleic Acid

STRANDEDNESS: Single
TOPOLOGY: Unknown
ANTI-SENSE: No
PUBLICATION INFORMATION:
AUTHORS: Oliner, J.D.
AUTHORS: Kinzler, K.W.
AUTHORS: Melzer, P.S.
AUTHORS: George, D.L.
AUTHORS: Vogelstein, B.
TITLE: Amplification of a gene encoding a
p53-associated protein in human sarcomas
JOURNAL: Nature
VOLUME: 358
ISSUE: 6381
PAGES: 80-83
DATE: 02-JUL-1992
US-09-752-983-1
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 Db 2341 CAAAGTGTGGGATTAACAGGCATGAGCCACCG 2372

RESULT 2
 US-09-956-425-7
 ; Sequence 7, Application US/09956425
 ; Patent No. US2002045192A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kriwacki, Richard
 ; APPLICANT: Bothner, Brian
 ; APPLICANT: Lewis, William
 ; TITLE OF INVENTION: Aft and Hdm2 Interaction Domains and Method of Use Thereof
 ; FILE REFERENCE: 1340/1/035
 ; CURRENT APPLICATION NUMBER: US/09-956,425
 ; CURRENT FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 2372
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-956-425-7

Query Match 100.0%; Score 2372; DB 3; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCGAAAGATGA 60
 Db 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCGAAAGATGA 60
 Qy 61 GCAAGAACCCGAGCCGAGGGGGCGCGGACCCCTTGAACCGAGATCTGCTGCTTGG 120
 Db 61 GCAAGAACCCGAGCCGAGGGGGCGCGGACCCCTTGAACCGAGATCTGCTGCTTGG 120
 Qy 121 CAGCCAGAGACGCGTCCCTCCCGGATTAAGTGCCTAGAGGCGCCAGTGGCCCTGGCCG 180
 Db 121 CAGCCAGAGACGCGTCCCTCCCGGATTAAGTGCCTAGAGGCGCCAGTGGCCCTGGCCG 180

Qy 181 GAGAGTGAATGATCCCCGAGGGCCGAGGGCGTGTGCTTCCGCAATGATCAGTCCCGTG 240
 Db 181 GAGAGTGAATGATCCCCGAGGGCCGAGGGCGTGTGCTTCCGCAATGATCAGTCCCGTG 240
 Qy 241 AAGGAACCTGGGAGTCTTTGAGGAGCCCCCGACCTCCAAAGCGGAAACCCTGGATGTGA 300
 Db 241 AAGGAACCTGGGAGTCTTTGAGGAGCCCCCGACCTCCAAAGCGGAAACCCTGGATGTGA 300
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 Db 301 GGAGAGGCAAAATGTCGAATACCAACATGTCTGTACTTCTATGATGTGTGTATACCACT 360
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 Db 361 CACAGATTCAGCTTCGGAACAAAGAGCCCTGGTATGACCAAGCAATGCTTTGAAAT 420
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 Db 421 TATTAAGTCTGTGTGTGACCAAAAAGACATTAATATATGAAAGAGTCTTTTATATC 480
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 Db 481 TTGGCCAGTATATTAATGACTAAACGATTAATGATGAGAGCAACAATATGATAT 540
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 Db 541 GTTCAAATGATCTTGTAGAGATTTGTTGGGTGCGCAAGCTTCTGTGAAAGAGCA 600
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 Db 601 GGAATATATATACATGATCTTACAGAACTTGTGTGTATCAATACAGCAGAAATCATCG 660
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 Db 661 ACTCAGTACATCTGTGATGAGAAACAGGTGTACCTTGAAAGTGGAGTATCAAAAG 720
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 Db 721 AACTGTACAAAGCTTGTAGAGAGAAACCTTCACTTCACTTGTGTTCTTACACAT 780
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 Db 781 CTACCTCATCTGAGAGAGACCAATTTAGTGAACAGAGAAATTCAGATGAATATCTG 840
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 Db 841 GTGAACGACAAAGAAACGCGCAAAATGTGATGATTTCCCTTTCTTTGATGAAGCC 900
 Qy 901 TGGCTCTGTGTATTAAGGAGATATGTGTGAAGAAAGACGTGACGTGAATCTACG 960
 Db 901 TGGCTCTGTGTATTAAGGAGATATGTGTGAAGAAAGACGTGACGTGAATCTACG 960
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 Db 961 GGAGCCCATGCAATCCGATCTTGTGCTGTGTGATGAGCAATTCAGGTGATGGTGG 1020
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 Db 1021 ATCAGATTCAGTTTCAATCAATCAATTTAGTGAATTTGAAGTGAATCTCTGACTAG 1080
 Qy 1081 AAGATTAAGCTTATAGTGAAGAGCAAGAACTTCAGATGAAGATGATGATATATC 1140
 Db 1081 AAGATTAAGCTTATAGTGAAGAGCAAGAACTTCAGATGAAGATGATGATATATC 1140
 Qy 1141 AAGTTACTGTGTATCAGGAGGAGAGTGAATACATTTCAATTTGAAGAAATCTGAAA 1200
 Db 1141 AAGTTACTGTGTATCAGGAGGAGAGTGAATACATTTCAATTTGAAGAAATCTGAAA 1200
 Qy 1201 TTTCTTACTGACTATTTGAATGACATCTATGCAATGAATGAATCCCCCTTCAT 1260
 Db 1201 TTTCTTACTGACTATTTGAATGACATCTATGCAATGAATGAATCCCCCTTCAT 1260
 Qy 1261 CACATGCAACAGATGTTGGGCGCTTGTGTGAGATTTGGCTTCTGAAATGAAGGAAAG 1320

181 GAGAGTGAATATCCCGAGGCGTGTGCTTCCGAGTATGATCCCGCTG 240
181 GAGAGTGAATATCCCGAGGCGTGTGCTTCCGAGTATGATCCCGCTG 240
241 AAGGAACTGGGAGTCTTGAAGGACCCCGACTCGAAGCGGAAACCCCGAGTGA 300
241 AAGGAACTGGGAGTCTTGAAGGACCCCGACTCGAAGCGGAAACCCCGAGTGA 300
301 GGAGCAGGAAATGTGCAATACCAATGCTGTACTGTGAGTGTGTAACCACT 360
301 GGAGCAGGAAATGTGCAATACCAATGCTGTACTGTGAGTGTGTAACCACT 360
361 CACAGATTCAGCTTCGGAACAAGAGCCCTGTTAGACCAAGCCATGCTTTGAAT 420
361 CACAGATTCAGCTTCGGAACAAGAGCCCTGTTAGACCAAGCCATGCTTTGAAT 420
421 TTTTAAAGTCTGTGTGTCACAAAAGACCTTATATGAAAGGTTCTTTTATC 480
421 TTTTAAAGTCTGTGTGTCACAAAAGACCTTATATGAAAGGTTCTTTTATC 480
481 TTGGCAGATATTTATGATTAACGATTAATGATGAGAGCAACATATTTATAT 540
481 TTGGCAGATATTTATGATTAACGATTAATGATGAGAGCAACATATTTATAT 540
541 GTTCAATGATCTTCTAGAGAGATTTGTTGGCTGCCAAGCTTCTGTGAAGAGACA 600
541 GTTCAATGATCTTCTAGAGAGATTTGTTGGCTGCCAAGCTTCTGTGAAGAGACA 600
601 GGAATAATATATACATGATCTACAGGAACTTGTGTAGTCAATCAGCAGATCCG 660
601 GGAATAATATATACATGATCTACAGGAACTTGTGTAGTCAATCAGCAGATCCG 660
661 ACTCAGTATCTGTGATGAGAGACAGGTGTCACTTGAAGTGGAGATCAAAAG 720
661 ACTCAGTATCTGTGATGAGAGACAGGTGTCACTTGAAGTGGAGATCAAAAG 720
721 ACCTGTACAGAGCTTCAAGAGAGAACTTCACTTCACTTGTGTGAGACAT 780
721 ACCTGTACAGAGCTTCAAGAGAGAACTTCACTTCACTTGTGTGAGACAT 780
781 CTACCTCATCTAGAGAGAGAGATTTAGTGAACAAGAAATTCAGATGATATCTG 840
781 CTACCTCATCTAGAGAGAGAGATTTAGTGAACAAGAAATTCAGATGATATCTG 840
841 GTGAACGACAAAGAAACCCCAAAATCTGATATGATTTCCCTTCTTGAAGAGCC 900
841 GTGAACGACAAAGAAACCCCAAAATCTGATATGATTTCCCTTCTTGAAGAGCC 900
901 TGGCTCTGTGTATTAAGGAGATATGTTGAAAGAGCAGTACAGTGAATCTACG 960
901 TGGCTCTGTGTATTAAGGAGATATGTTGAAAGAGCAGTACAGTGAATCTACG 960
961 GGAGCCCATCGATCCGATCTTGAATGCTGTGAAGTGAATCAGGATGATGGTGG 1020
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1021 ATCAGAGTTCAGTTTCAGATGATTTAGTGAATTTGAAGTGAATCTCGACTCG 1080
1021 ATCAGAGTTCAGTTTCAGATGATTTAGTGAATTTGAAGTGAATCTCGACTCG 1080
1081 AAGATTATAGCTTGTGTAAGAGAGACAACTCTCAGATGAAGATGATGATATC 1140
1081 AAGATTATAGCTTGTGTAAGAGAGACAACTCTCAGATGAAGATGATGATATC 1140
1141 AAGTTACTGTGTATCAGGAGGAGAGATGATACAGATTCATTTGAAGAGATCTGAAA 1200
1141 AAGTTACTGTGTATCAGGAGGAGAGATGATACAGATTCATTTGAAGAGATCTGAAA 1200
1201 TTTCTTACTGATCTATTTGAAGATGATGATGATGATGATGATGATGATGATGAT 1260
1201 TTTCTTACTGATCTATTTGAAGATGATGATGATGATGATGATGATGATGATGAT 1260
1261 CACATTGCAACGATGTTGGGCTTCGTGAGATTTGCTTCTGTAAGTAAAGGAAAG 1320

1261 CACATTGCAACGATGTTGGGCTTCGTGAGATTTGCTTCTGTAAGTAAAGGAAAG 1320
1321 ATTAAGGGGAAATCTCTGAGAAAGCAACCTGAAATCTCAACAGCTGAAGAGGCT 1380
1321 ATTAAGGGGAAATCTCTGAGAAAGCAACCTGAAATCTCAACAGCTGAAGAGGCT 1380
1381 TTGATGTTCTGATTTGTAAGAAATCTATGTAATGATGATGATGATGATGATGAT 1440
1381 TTGATGTTCTGATTTGTAAGAAATCTATGTAATGATGATGATGATGATGATGAT 1440
1441 AAAATGATGATTAATTAACAAGCTTCAATCAACAAGAAAGTGAAGATATCTCAGC 1500
1441 AAAATGATGATTAATTAACAAGCTTCAATCAACAAGAAAGTGAAGATATCTCAGC 1500
1501 CATCACTTCTAGTATGATTTATTAAGAGCCCAAGAGATGTAAGAGTTGAAAGG 1560
1501 CATCACTTCTAGTATGATTTATTAAGAGCCCAAGAGATGTAAGAGTTGAAAGG 1560
1561 AAGAAACCAAGACAAAGAGAGAGTGGATTTAGTTGGCCCTTAATGCCATTGAC 1620
1561 AAGAAACCAAGACAAAGAGAGAGTGGATTTAGTTGGCCCTTAATGCCATTGAC 1620
1621 CTGTGTGATTTGTCAAGGTGCACTTAAATGTTGCTCATGTCAGCAAAACAGAC 1680
1621 CTGTGTGATTTGTCAAGGTGCACTTAAATGTTGCTCATGTCAGCAAAACAGAC 1680
1681 ATCTTATGCTCTGCTTTACATGTCGAAAGAGCTTAAAGAAAGAAAGTAAAGCTG 1740
1681 ATCTTATGCTCTGCTTTACATGTCGAAAGAGCTTAAAGAAAGAAAGTAAAGCTG 1740
1741 TATGTAGACAACTTCAATGATTTGCTTAACTTATTTCCCTGATGATGATGATGAT 1800
1741 TATGTAGACAACTTCAATGATTTGCTTAACTTATTTCCCTGATGATGATGATGAT 1800
1801 AAGAGATATATATTTCTAATGATTAACCTTAAAGATTTGAGACAACTGAAATTTAT 1860
1801 AAGAGATATATATTTCTAATGATTAACCTTAAAGATTTGAGACAACTGAAATTTAT 1860
1861 CACATATATCAAGTGAAGAAATGCTCAATTCAGATGATTTCTCTTATGATATAT 1920
1861 CACATATATCAAGTGAAGAAATGCTCAATTCAGATGATTTCTCTTATGATATAT 1920
1921 TGAACCTTGTGTGATGAGATGATGATGATGATGATGATGATGATGATGATGAT 1980
1921 TGAACCTTGTGTGATGAGATGATGATGATGATGATGATGATGATGATGATGAT 1980
1981 CATCTTACCAACTCTTAAATTTAAATTTCTACTGCTTAAATGAGAGATC 2040
1981 CATCTTACCAACTCTTAAATTTAAATTTCTACTGCTTAAATGAGAGATC 2040
2041 TTGGTTTTTTTTCTTAAATTTGATATGATTTTAAATTTGATTTATTTTATTTT 2100
2041 TTGGTTTTTTTTCTTAAATTTGATATGATTTTAAATTTGATTTATTTTATTTT 2100
2101 AGACCGAGCTTGTCTGTGTTACCAAGCTGAGTGAAGTGAATCTTGGCTCACTGCA 2160
2101 AGACCGAGCTTGTCTGTGTTACCAAGCTGAGTGAAGTGAATCTTGGCTCACTGCA 2160
2161 AGCTGTGCTTCCCGGGGTGCACTTCTCCTCCTCAAGCTTCAATTTAGCTTGGC 2220
2161 AGCTGTGCTTCCCGGGGTGCACTTCTCCTCCTCAAGCTTCAATTTAGCTTGGC 2220
2221 TACAGTCACTGTCACACACCTGCTAATTTTGTATCTTTTATGAGAGAGGTTTC 2280
2221 TACAGTCACTGTCACACACCTGCTAATTTTGTATCTTTTATGAGAGAGGTTTC 2280
2281 ACCGTGTTAGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
2281 ACCGTGTTAGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2340
2341 CAAAGTGTGGGATTTACAGGAGTGAACCG 2372

Db 2341 CAAAGTCTGGATTACAGCATGAGCCACCG 2372

RESULT 4

US-09-541-848-1

Sequence 1, Application US/09541848

Publication No. US2003019765A1

GENERAL INFORMATION:

APPLICANT: CHEN, Jiandong

APPLICANT: AGRAM, Sudhir

APPLICANT: ZHANG, Ruiwen

TITLE OF INVENTION: MD-M2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES

FILE REFERENCE: 29924/98057C

CURRENT FILING DATE: US/09/541,848

PRIOR APPLICATION NUMBER: 09/383,507

PRIOR FILING DATE: 1999-08-26

PRIOR APPLICATION NUMBER: 09/073,567

PRIOR FILING DATE: 1998-05-06

PRIOR APPLICATION NUMBER: 08/916,834

PRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 51

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 1

LENGTH: 2372

TYPE: DNA

ORGANISM: Homo sapiens

US-09-541-848-1

Query Match 100.0%; Score 2372; DB 3; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCCGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGTGCGAAAGATGA 60

DB 1 GCACCGCCGAGCTTGGCTGCTTCTGGGGCCCTGTGTGTGCGAAAGATGA 60

QY 61 GCAAGAACCCGAGCCGAGGGGCGCGGACCCCTGACCGAGATCCTGTGCTTTG 120

DB 61 GCAAGAACCCGAGCCGAGGGGCGCGGACCCCTGACCGAGATCCTGTGCTTTG 120

QY 121 CAGCCAGAGACACCGCTCCCTCCCGGATTAAGTGCCTAGAGCGCCAGTGCCTGCGCCG 180

DB 121 CAGCCAGAGACACCGCTCCCTCCCGGATTAAGTGCCTAGAGCGCCAGTGCCTGCGCCG 180

QY 121 CAGCCAGAGACACCGCTCCCTCCCGGATTAAGTGCCTAGAGCGCCAGTGCCTGCGCCG 180

DB 121 CAGCCAGAGACACCGCTCCCTCCCGGATTAAGTGCCTAGAGCGCCAGTGCCTGCGCCG 180

QY 181 GAGATTTGAAATGATCCCGAGGCGCGAGGCGGTGCTTCCGAGTGAATGCTCCCGTG 240

DB 181 GAGATTTGAAATGATCCCGAGGCGCGAGGCGGTGCTTCCGAGTGAATGCTCCCGTG 240

QY 181 GAGATTTGAAATGATCCCGAGGCGCGAGGCGGTGCTTCCGAGTGAATGCTCCCGTG 240

DB 181 GAGATTTGAAATGATCCCGAGGCGCGAGGCGGTGCTTCCGAGTGAATGCTCCCGTG 240

QY 241 AAGGAACTGGGAGATCTTTGAGGAGCCCGGACTCCAAGCGGAAACCCCGATGTGA 300

DB 241 AAGGAACTGGGAGATCTTTGAGGAGCCCGGACTCCAAGCGGAAACCCCGATGTGA 300

QY 241 AAGGAACTGGGAGATCTTTGAGGAGCCCGGACTCCAAGCGGAAACCCCGATGTGA 300

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DB 301 GGAGCAGGCAAAATGTGCAATACCAATGTCTGTACTTATGATGATGCTGTAAACCACT 360

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DB 361 CACAAATTCGAGCTTCGAAACAAAGAGACCTGTGTAGACCAAGCCATTTGGAAGT 420

QY 361 CACAAATTCGAGCTTCGAAACAAAGAGACCTGTGTAGACCAAGCCATTTGGAAGT 420

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QY 421 TATTAAGCTGTGTGTGACAAAGAAAGACCTTATCTATGAAAGAGTTCTTTTATC 480

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DB 481 TTGGCCAGTATATTAATGACTAAACGATTAATGATGAGAGCAACAATATTTATAT 540

QY 481 TTGGCCAGTATATTAATGACTAAACGATTAATGATGAGAGCAACAATATTTATAT 540

DB 481 TTGGCCAGTATATTAATGACTAAACGATTAATGATGAGAGCAACAATATTTATAT 540

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DB 541 GTTCAAATGATCTTTAGAGAGATTTGTTGGCGTGCAGGCTTCTCTGTGAAGAGCACA 600

QY 601 GAAATATATATACATGATCTTACAGAACTTGTGATGATCAATCAGAGGATCATCG 660

DB 601 GAAATATATATATACATGATCTTACAGAACTTGTGATGATCAATCAGAGGATCATCG 660

QY 661 ACTCAGATACATCTGTAG 720

DB 661 ACTCAGATACATCTGTAG 720

QY 661 ACTCAGATACATCTGTAG 720

DB 661 ACTCAGATACATCTGTAG 720

QY 721 ACCTTGTACAGAGCTTCAG 780

DB 721 ACCTTGTACAGAGCTTCAG 780

QY 721 ACCTTGTACAGAGCTTCAG 780

DB 721 ACCTTGTACAGAGCTTCAG 780

QY 781 CTACCTCATCTAG 840

DB 781 CTACCTCATCTAG 840

QY 781 CTACCTCATCTAG 840

DB 781 CTACCTCATCTAG 840

QY 841 GTGAACGCAAAAGAAAG 900

DB 841 GTGAACGCAAAAG 900

QY 841 GTGAACGCAAAAG 900

DB 841 GTGAACGCAAAAG 900

QY 901 TGAGCTGTGTGTATATAGAGAGAGATGTTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 960

DB 901 TGAGCTGTGTGTATATAGAGAGAGATGTTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 960

QY 901 TGAGCTGTGTGTATATAGAGAGAGATGTTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 960

DB 901 TGAGCTGTGTGTATATAGAGAGAGATGTTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 960

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DB 961 GAGCGCATGCAATCCGATCTTATGCTGTGTATGATGAAATTCAGTGAATGTTGG 1020

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QY 1081 AAGATTTAGGCTTATGAG 1140

DB 1081 AAGATTTAGGCTTATGAG 1140

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DB 1141 AAGTTACTGTATCAGGAG 1200

QY 1141 AAGTTACTGTATCAGGAG 1200

DB 1141 AAGTTACTGTATCAGGAG 1200

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QY 1201 TTTCTTATGCTGATCTATTTGAG 1260

DB 1201 TTTCTTATGCTGATCTATTTGAG 1260

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QY 1321 ATAAAGGGGAAATCTTGAAG 1380

DB 1321 ATAAAGGGGAAATCTTGAAG 1380

QY 1381 TTGATGTTCTGATTTGAG 1440

DB 1381 TTGATGTTCTGATTTGAG 1440

QY 1381 TTGATGTTCTGATTTGAG 1440

DB 1381 TTGATGTTCTGATTTGAG 1440

QY 1441 AAAATGATGATTAATTTACAG 1500

DB 1441 AAAATGATGATTAATTTACAG 1500

QY 1441 AAAATGATGATTAATTTACAG 1500

DB 1441 AAAATGATGATTAATTTACAG 1500

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DB 1501 CATCACTTCTAGTATGATTTATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560

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QY 1561 AAGAAACCAAG 1620

DB 1561 AAGAAACCAAG 1620

QY 1621 CTGTGTATTTGTCAAG 1680

DB 1621 CTGTGTATTTGTCAAG 1680

QY 1621 CTGTGTATTTGTCAAG 1680

DB 1621 CTGTGTATTTGTCAAG 1680

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DB 1681 ATCTTATGAGCTGCTTATCATGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740

1681 ATCTTATGCGCTCTTACATGTCAGAAAGAGCTAAAGAAAGAAATAGCCCTGCGCAG 1740
1741 TATGTAGACAAACCAATTCAAATGATGTGTACTTATTTCCCTGAGTGAACCTGTCTAT 1800
1741 TATGTAGACAAACCAATTCAAATGATGTGTACTTATTTCCCTGAGTGAACCTGTCTAT 1800
1801 AAGAGATATATATATTTCTACTATATTAACCTAGGAATTTAGACAACTGAATTTAT 1860
1801 AAGAGATATATATATTTCTACTATATTAACCTAGGAATTTAGACAACTGAATTTAT 1860
1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCATAGATTTCTCTCTTTAGTAAAT 1920
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1921 TGACCTACTTTGGTATGAGAAATAGTAATTAATTAATTTGACTTGAATATGTAAGCT 1980
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1981 CATCTTTACACCACTCTCTAATTTTAAATTTTCTACTGCTGCTTAAATGAGAGTAC 2040
1981 CATCTTTACACCACTCTCTAATTTTAAATTTTCTACTGCTGCTTAAATGAGAGTAC 2040
2041 TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGGG 2100
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2101 AAGACGAGTCTGCTCTGTTTACCAGGCTGAGAGTGAAGTGTATCTTGGCTCACTGCA 2160
2101 AAGACGAGTCTGCTCTGTTTACCAGGCTGAGAGTGAAGTGTATCTTGGCTCACTGCA 2160
2161 AGCTGCGCCTCCCGGGGTTGCGACATTTCTGCTGCTGACCTCCCATTTAGCTTGGCC 2220
2161 AGCTGCGCCTCCCGGGGTTGCGACATTTCTGCTGCTGACCTCCCATTTAGCTTGGCC 2220
2221 TACAGTCACTGTCACACACACCTGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
2221 TACAGTCACTGTCACACACACCTGCTAATTTTGTACTTTAGTAGAGACAGGGTTTC 2280
2281 ACCGTTTACGCGAGATGCTGATCTCTGATCTCTGATCTGATCTGATCTGATCTGATCTG 2340
2281 ACCGTTTACGCGAGATGCTGATCTCTGATCTCTGATCTGATCTGATCTGATCTGATCTG 2340
2341 CAAAGTCTGGAGTTTACAGGCAATGAGCCACCG 2372
2341 CAAAGTCTGGAGTTTACAGGCAATGAGCCACCG 2372

RESULT 5
US-09-873-367C-450
Sequence 450, Application US/09873367C
GENERAL INFORMATION:
APPLICANT: Young, Paul
APPLICANT: Soppet, Daniel
APPLICANT: Endres, Gregory
APPLICANT: Augustus, Meena
APPLICANT: Ebner, Reinhard
APPLICANT: Carter, Kenneth
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
PRIOR FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: U.S. 60/245,084
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 1067

SOFTWARE: PatentIn version 3.0
SEQ ID NO 450
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
US-09-873-367C-450

Query Match
Best Local Similarity 100.0%; Pred No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCAACGCGGAGCTTGGCTGCTCTTCTGAGGCTGTGTGAGGCTGTGTGCGAAGATGA 60
1 GCAACGCGGAGCTTGGCTGCTCTTCTGAGGCTGTGTGAGGCTGTGTGCGAAGATGA 60
61 GCAAGAGCCGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
61 GCAAGAGCCGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
121 CAGCCAGAGGACCCGCT 180
121 CAGCCAGAGGACCCGCT 180
181 GAGAGTGAATGATCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
181 GAGAGTGAATGATCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
241 AAGGAACTGGGAGAGCTTGAAGGAGCCCGAGCTCCAGCGGAGGAGGAGGAGGAGGAGG 300
241 AAGGAACTGGGAGAGCTTGAAGGAGCCCGAGCTCCAGCGGAGGAGGAGGAGGAGGAGG 300
301 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
301 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
361 CACAGATTCACCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
361 CACAGATTCACCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
421 TATTAAGTCTGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
421 TATTAAGTCTGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
481 TTGGCAGATATTTATGACTTAAACGATTAATGATGAGAGGAGGAGGAGGAGGAGGAG 540
481 TTGGCAGATATTTATGACTTAAACGATTAATGATGAGAGGAGGAGGAGGAGGAGGAG 540
541 GTTCAAAATGATCTTCTAGAGGATTTGTTGGGCTGCGAAGCTTCTCTGGAAGAGCACA 600
541 GTTCAAAATGATCTTCTAGAGGATTTGTTGGGCTGCGAAGCTTCTCTGGAAGAGCACA 600
601 GGAAGAT 660
601 GGAAGAT 660
661 ACTCAGATCACTGTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
661 ACTCAGATCACTGTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
721 ACCCTGTACAAAGGCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
721 ACCCTGTACAAAGGCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
781 CTACCTCATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
781 CTACCTCATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
841 GTGAAGCAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
841 GTGAAGCAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
901 TGGCTCTGTGATATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
901 TGGCTCTGTGATATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960

Db 901 TGGCTGTGTGTAATGAAGAGATATGTGTGAAGAAGACGTAGCAGTATCTACAG 960
Qy 961 GAGCGCATCGAATCCGATCTTGATGCTGTGTGAATGAACATTCAGGTATGGTGG 1020
Db 961 GAGCGCATCGAATCCGATCTTGATGCTGTGTGAATGAACATTCAGGTATGGTGG 1020
Qy 1021 ATCAGATTCAGTTTCAGATCAGTTTGAATTTGAAGTTGAATCTCTGACTGAG 1080
Db 1021 ATCAGATTCAGTTTCAGATCAGTTTGAATTTGAAGTTGAATCTCTGACTGAG 1080
Qy 1081 AAGATTATAGCTTGTGTGAAGAAGACAAGAACTCTCAGATGAATATGATGATATTC 1140
Db 1081 AAGATTATAGCTTGTGTGAAGAAGACAAGAACTCTCAGATGAATATGATGATATTC 1140
Qy 1141 AAGTACTGTGTATCAGGACGGGAGAGATGATACAGATTCATTGAGAAGATCTGAAA 1200
Db 1141 AAGTACTGTGTATCAGGACGGGAGAGATGATACAGATTCATTGAGAAGATCTGAAA 1200
Qy 1201 TTTCTTGTAGCTGATTTGGAATGCACTTCATGCAATGAAATGAAATCCCTTCAT 1260
Db 1201 TTTCTTGTAGCTGATTTGGAATGCACTTCATGCAATGAAATGAAATCCCTTCAT 1260
Qy 1261 CACATTCGACAGATGTTGGGCTCTTGTGTGAATTTGGTCTCTGATGATGAAGGAAA 1320
Db 1261 CACATTCGACAGATGTTGGGCTCTTGTGTGAATTTGGTCTCTGATGATGAAGGAAA 1320
Qy 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACAGCTGAAGGAGCT 1380
Db 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACAGCTGAAGGAGCT 1380
Qy 1381 TTGATGTTCTGTATTTGTAATTAATCTATATGATGATTCAGAGAGTCATGTGTTGAG 1440
Db 1381 TTGATGTTCTGTATTTGTAATTAATCTATATGATGATTCAGAGAGTCATGTGTTGAG 1440
Qy 1441 AAAATGATGATTAATTTACACAAGCTTCACATTCACAGAAAGTGAAGCTATTTCCAGC 1500
Db 1441 AAAATGATGATTAATTTACACAAGCTTCACATTCACAGAAAGTGAAGCTATTTCCAGC 1500
Qy 1501 CATCAACTTCTAGTACATTTATTTATGACGACCAAGAGATGTAAGAGTTGAAAAGG 1560
Db 1501 CATCAACTTCTAGTACATTTATTTATGACGACCAAGAGATGTAAGAGTTGAAAAGG 1560
Qy 1561 AAGAAACCCAGACAAAGAGAGTGTGAATCTAGTTGCCCTTAATGCCATTGAAC 1620
Db 1561 AAGAAACCCAGACAAAGAGAGTGTGAATCTAGTTGCCCTTAATGCCATTGAAC 1620
Qy 1621 CTGTGTGTATTTGTCAAGGTCACTTAATAAATGTTGCTTGTCAATGCAAAACAGGAC 1680
Db 1621 CTGTGTGTATTTGTCAAGGTCACTTAATAAATGTTGCTTGTCAATGCAAAACAGGAC 1680
Qy 1681 ATCTATGAGCTGCTTTTACATGTGCAAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
Db 1681 ATCTATGAGCTGCTTTTACATGTGCAAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
Qy 1741 TATGTAGACAACTTCAATGATGTTGCTAATTTTCCCTAGTTGACCTGTCTAT 1800
Db 1741 TATGTAGACAACTTCAATGATGTTGCTAATTTTCCCTAGTTGACCTGTCTAT 1800
Qy 1801 AAGAGATTAATTAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
Db 1801 AAGAGATTAATTAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
Qy 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATTAATTTCTTCTTTAGATATAT 1920
Db 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATTAATTTCTTCTTTAGATATAT 1920
Qy 1921 TGACCTACTTGTGTGTGTGAATGTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Db 1921 TGACCTACTTGTGTGTGTGAATGTAATTAATTAATTAATTAATTAATTAATTAAT 1980
Qy 1981 CATCTTTACACCACTCTTAATTTTAATTAATTTTACTCTGTCTTAATGAAGATAC 2040
Db 1981 CATCTTTACACCACTCTTAATTTTAATTAATTTTACTCTGTCTTAATGAAGATAC 2040

Qy 2041 TTGGTTTTTTTTTTCTTAATATGATATGACATTTAATGTAATTAATTTTGTG 2100
Db 2041 TTGGTTTTTTTTTTCTTAATATGATATGACATTTAATGTAATTAATTTTGTG 2100
Qy 2101 AGACCGAGTCTTGTCTCTGTTTACCAGAGCTGAGAGTGCAGTGGGTATCTTGGCTAC 2160
Db 2101 AGACCGAGTCTTGTCTCTGTTTACCAGAGCTGAGAGTGCAGTGGGTATCTTGGCTAC 2160
Qy 2161 AGCTGTGCTCCCGGGGTTGCAACATTCCTGCTCAGCTCCCAATAGCTGGCC 2220
Db 2161 AGCTGTGCTCCCGGGGTTGCAACATTCCTGCTCAGCTCCCAATAGCTGGCC 2220
Qy 2221 TACAGTATCTGCCACACACACCTGCTAATTTTGTATCTTTAGTAGAGACAGGTTTC 2280
Db 2221 TACAGTATCTGCCACACACACCTGCTAATTTTGTATCTTTAGTAGAGACAGGTTTC 2280
Qy 2281 ACCGTGTTAGCCAGAGTGTCTGATCTCTGACCTGTGATTCGCCCACTCGGCTTC 2340
Db 2281 ACCGTGTTAGCCAGAGTGTCTGATCTCTGACCTGTGATTCGCCCACTCGGCTTC 2340
Qy 2341 CAAGTGTGGGATTTACAGCATGAGCCAGC 2372
Db 2341 CAAGTGTGGGATTTACAGCATGAGCCAGC 2372

RESULT 6
US-09-966-724-1
Sequence 1, Application US/09966724
Publication No. US20040170971A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G ST., N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966,724
FILING DATE: 01-Oct-2001
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/044,619
FILING DATE: 2001-10-01
APPLICATION NUMBER: US 07/867,840
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,40148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-966-724-1

Query Match 100.0%; Score 2372; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGCGAGCTTGGCTTCTTGGGGCCCTGTGTGACCTGTGTGTGCGAAAGATGA 60
DB 1 GCACCGCGCGAGCTTGGCTTCTTGGGGCCCTGTGTGACCTGTGTGTGCGAAAGATGA 60
QY 61 GGAAGAGCGCGAGCGCGAGCGCGCGAGCGCGCGAGCGCGAGCGCGAGCGCGAGCGCG 120
DB 61 GGAAGAGCGCGAGCGCGAGCGCGCGAGCGCGCGAGCGCGCGAGCGCGAGCGCGAGCG 120
QY 121 CAGCGAGAGCAGCGCGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCG 180
DB 121 CAGCGAGAGCAGCGCGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCG 180
QY 181 GAGAGTGAATGATCCCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAG 240
DB 181 GAGAGTGAATGATCCCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAG 240
QY 241 AAGAGAACTGGGGAAGCTTGGAGGAGCGCGCGAGCGCGAGCGCGAGCGCGAGCGCG 300
DB 241 AAGAGAACTGGGGAAGCTTGGAGGAGCGCGCGAGCGCGAGCGCGAGCGCGAGCGCG 300
QY 301 GAGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCG 360
DB 301 GAGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCG 360
QY 361 CACAGATTCAGCGCTTGGAGGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCG 420
DB 361 CACAGATTCAGCGCTTGGAGGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCG 420
QY 421 TATTAAGCTGTGGTGCACAAAAGACACTTAATCTAAGAAAGGTTCTTTTATTC 480
DB 421 TATTAAGCTGTGGTGCACAAAAGACACTTAATCTAAGAAAGGTTCTTTTATTC 480
QY 481 TTGGCAGATATTTATGACTAAGATTAATGATGAGAGAGCAACAATATTGATAT 540
DB 481 TTGGCAGATATTTATGACTAAGATTAATGATGAGAGAGCAACAATATTGATAT 540
QY 541 GTTCAATGATCTTGAAGAGATTTGTTGGCGTCCAGCTTCTCTGGAAGAGACACA 600
DB 541 GTTCAATGATCTTGAAGAGATTTGTTGGCGTCCAGCTTCTCTGGAAGAGACACA 600
QY 601 GGAAGAAATATATCATGATCTACAGAGAACTTGTGTAGTCAATCAGCAGATCATGG 660
DB 601 GGAAGAAATATATCATGATCTACAGAGAACTTGTGTAGTCAATCAGCAGATCATGG 660
QY 661 ACTGAGTATCTGTGTGAGTGAAGACAGGTGCACCTTGAAGGTGGAGTATCAAAAG 720
DB 661 ACTGAGTATCTGTGTGAGTGAAGACAGGTGCACCTTGAAGGTGGAGTATCAAAAG 720
QY 721 ACCCTGTACAGAGCTTCAAGAGAGAACTTCACTTCACTTCACTTCACTTCACTT 780
DB 721 ACCCTGTACAGAGCTTCAAGAGAGAACTTCACTTCACTTCACTTCACTTCACTT 780
QY 781 CTAACCTCATCTGAAGAGAGCAATTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 CTAACCTCATCTGAAGAGAGCAATTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 GTGAAGCAGCAAG 900

DB 841 GTGAAGCAGCAAG 900
QY 901 TGGCTCTGTGTGTATTAAGGAGATGTGTGGAAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 TGGCTCTGTGTGTATTAAGGAGATGTGTGGAAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GGAAGCGCATGAGATCCGAGTCTTGAATGCGGTGTAGTGAACATTCAGGTGATGG 1020
DB 961 GGAAGCGCATGAGATCCGAGTCTTGAATGCGGTGTAGTGAACATTCAGGTGATGG 1020
QY 1021 ATCAGAGATTCAGTTTCAAGATCAGTTTGAAGATTTGAAGTGAATCTCTGACTCAG 1080
DB 1021 ATCAGAGATTCAGTTTCAAGATCAGTTTGAAGATTTGAAGTGAATCTCTGACTCAG 1080
QY 1081 AAGATTAATGCTTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1140
DB 1081 AAGATTAATGCTTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1140
QY 1141 AAGTATCTGTGTATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1141 AAGTATCTGTGTATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 TTTCTTGTAGCTGATTAATGAGAGATCAGTTTCAAGATGAATGAGATCCCTCCAT 1260
DB 1201 TTTCTTGTAGCTGATTAATGAGAGATCAGTTTCAAGATGAATGAGATCCCTCCAT 1260
QY 1261 CACATTCAGCAAGATGTGGGCTTCTGTGAGAGATTTGGCTTCGTAAGATTAAGGAG 1320
DB 1261 CACATTCAGCAAGATGTGGGCTTCTGTGAGAGATTTGGCTTCGTAAGATTAAGGAG 1320
QY 1321 AATAAGGGGAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 1380
DB 1321 AATAAGGGGAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 1380
QY 1381 TTGATGTTCTGATTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1381 TTGATGTTCTGATTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 AAAATGATGATTAATTAACAGAGCTTCAATCAAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 AAAATGATGATTAATTAACAGAGCTTCAATCAAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 CATCACTTGTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1560
DB 1501 CATCACTTGTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1560
QY 1561 AAGAAACCCAG 1620
DB 1561 AAGAAACCCAG 1620
QY 1621 CTTGTGTATTTGTCAAGGTGCACTTAATAATGTTGATTCATGAGCAAAAGAGAG 1680
DB 1621 CTTGTGTATTTGTCAAGGTGCACTTAATAATGTTGATTCATGAGCAAAAGAGAG 1680
QY 1681 ATCTTATGCTGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 ATCTTATGCTGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 TATGTAGCAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800
DB 1741 TATGTAGCAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800
QY 1801 AAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1860
DB 1801 AAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1860
QY 1861 CACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
DB 1861 CACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
QY 1921 TGACCTACTTGTGTAGTGAATGAGATTAATTAATTAATTAATTAATTAATTA 1980

Db 1921 TGACCTACTTGTAGTAGGAATAGTAATCTACTAATTAATTTGAATGTAATATGTAAGCT 1980
Qy 1981 CATCTTTTACACCAACTCTTAATTTTAAATATTTCTACTCTGTCTTAATGAGAAGTAC 2040
Db 1981 CATCTTTTACACCAACTCTTAATTTTAAATATTTCTACTCTGTCTTAATGAGAAGTAC 2040
Qy 2041 TTGGTTTTTTTTTTCTTAATATATATATATATGACATTTAAATGTAATATTTTTTTTGG 2100
Db 2041 TTGGTTTTTTTTTTCTTAATATATATATATATGACATTTAAATGTAATATTTTTTTTGG 2100
Qy 2101 AGACCGAGTCTTGTCTGTCTTACCAAGGCTGAGAGTGAATGGTGTACTTTGGCTACATGCA 2160
Db 2101 AGACCGAGTCTTGTCTGTCTTACCAAGGCTGAGAGTGAATGGTGTACTTTGGCTACATGCA 2160
Qy 2161 AGCTGTGCTTCCCGGGGTTGACACATTTCTCTGCTCAGGCTCCCAATTAAGTTGGCC 2220
Db 2161 AGCTGTGCTTCCCGGGGTTGACACATTTCTCTGCTCAGGCTCCCAATTAAGTTGGCC 2220
Qy 2221 TACAGTCACTGACACACACCTGGCTAATTTTTTTGTAATTTTATAGAGACAGGGTTTC 2280
Db 2221 TACAGTCACTGACACACACCTGGCTAATTTTTTTGTAATTTTATAGAGACAGGGTTTC 2280
Qy 2281 ACCGTGTAGGACGAGATGCTCTGCATCTCTGACCTCGTGAATCCGCCACCTCGGCTCC 2340
Db 2281 ACCGTGTAGGACGAGATGCTCTGCATCTCTGACCTCGTGAATCCGCCACCTCGGCTCC 2340
Qy 2341 CAAAGTGTGGGATTATACAGGACATGAGCCACCG 2372
Db 2341 CAAAGTGTGGGATTATACAGGACATGAGCCACCG 2372

RESULT 7

US-10-007-926A-121
; Sequence 121, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOUIGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: mouse double minute 2, human homolog of;
; US-10-007-926A-121

Query Match 100.0%; Score 2372; DB 7; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCACGCGCGAGCTTGGCTGTTTGGGGCTGTGTGGCTGTGTGTGCGAAAAGATGGA 60
Db 1 GCACGCGCGAGCTTGGCTGTTTGGGGCTGTGTGGCTGTGTGTGCGAAAAGATGGA 60
Qy 61 GCAGAGCCGAGCCGAGGGGCGCGGAGACCCCTCTTACCGAGATCTGTGCTTTGG 120
Db 61 GCAGAGCCGAGCCGAGGGGCGCGGAGACCCCTCTTACCGAGATCTGTGCTTTGG 120
Qy 121 CAGCAGAGACGATCCCTCCCGGATTAGTGCATGACAGGCGCCAGTGCCTGGCCG 180

Db 121 CAGCAGAGACGATCCCTCCCGGATTAGTGCATGACAGGCGCCAGTGCCTGGCCG 180
Qy 181 GAGAGTGAATGATCCCCAGAGCCCAAGGCGTCGTGCTCCGACGATGATGATCCCGTGG 240
Db 181 GAGAGTGAATGATCCCCAGAGCCCAAGGCGTCGTGCTCCGACGATGATGATCCCGTGG 240
Qy 241 AAGGAAACTGGGAGTCTTGAAGGACCCCGCATCTCAAGCGCGAAAACCCCGATGGTGA 300
Db 241 AAGGAAACTGGGAGTCTTGAAGGACCCCGCATCTCAAGCGCGAAAACCCCGATGGTGA 300
Qy 301 GGAGCAGGCAATGTGCAATTCGAAATGCTGTGTAACCTAGATGATGATGATGATGATGAT 360
Db 301 GGAGCAGGCAATGTGCAATTCGAAATGCTGTGTAACCTAGATGATGATGATGATGATGAT 360
Qy 361 CACAGATTCGAGCTTGGGAAACAAGACCCGTTGAACCAAGCCATGCTTTTGAAGT 420
Db 361 CACAGATTCGAGCTTGGGAAACAAGACCCGTTGAACCAAGCCATGCTTTTGAAGT 420
Qy 421 TATTAAAGTCTGTGTGTCACAAAAGACACTTATATATGATAAAGAGGTTCTTTTATTC 480
Db 421 TATTAAAGTCTGTGTGTCACAAAAGACACTTATATATGATAAAGAGGTTCTTTTATTC 480
Qy 481 TTGGCAGTATATATGACTTAAAGATTAATATGATGAGAACCAACATATTTGTAATTT 540
Db 481 TTGGCAGTATATATGACTTAAAGATTAATATGATGAGAACCAACATATTTGTAATTT 540
Qy 541 GTTCAATGATCTTGAAGATTTGTTGGCGTGGCCAAAGCTTCTGTGTGAAGAGCACA 600
Db 541 GTTCAATGATCTTGAAGATTTGTTGGCGTGGCCAAAGCTTCTGTGTGAAGAGCACA 600
Qy 601 GAAAAATATATACATGATCTTACAGAACTTGTATGATGATGATGATGATGATGATGATG 660
Db 601 GAAAAATATATACATGATCTTACAGAACTTGTATGATGATGATGATGATGATGATGATG 660
Qy 661 ACTCAGTACATCTGTGATGAGAACAGGTGTCACTTGAAGGTGGAGTATCAAAAG 720
Db 661 ACTCAGTACATCTGTGATGAGAACAGGTGTCACTTGAAGGTGGAGTATCAAAAG 720
Qy 721 ACCCTGTACAAAGAGCTTACAGAAACCTTCACTTCACTTGTGTTCTTACAGCAT 780
Db 721 ACCCTGTACAAAGAGCTTACAGAAACCTTCACTTCACTTGTGTTCTTACAGCAT 780
Qy 781 CTACCTCATCTAGAAAGAGACCAATTAAGTGAACAGAAATTCAGATGAATATATCTG 840
Db 781 CTACCTCATCTAGAAAGAGACCAATTAAGTGAACAGAAATTCAGATGAATATATCTG 840
Qy 841 GTGAACGACAAAGAAACGCCACAAATCTGATGATTTCCCTTCTTGTGATGAAGCC 900
Db 841 GTGAACGACAAAGAAACGCCACAAATCTGATGATTTCCCTTCTTGTGATGAAGCC 900
Qy 901 TGGCTGTGTGTATTAAGGAGATGTGTGTAAGAGAGAGTGCATGATTTACAG 960
Db 901 TGGCTGTGTGTATTAAGGAGATGTGTGTAAGAGAGTGCATGATTTACAG 960
Qy 961 GGAGCCCATGCAATCCGATCTTGAATGCTGTGTATGTAACATTCAGGTATGGTTGG 1020
Db 961 GGAGCCCATGCAATCCGATCTTGAATGCTGTGTATGTAACATTCAGGTATGGTTGG 1020
Qy 1021 ATCAGATTCAGTTTCAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 ATCAGATTCAGTTTCAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Qy 1081 AAGATTAATAGCTTAAGTAAAGGACAAAGACTTCAGATGAATATATATGATGATGAT 1140
Db 1081 AAGATTAATAGCTTAAGTAAAGGACAAAGACTTCAGATGAATATATATGATGATGAT 1140
Qy 1141 AAGTACTGTGTATCAGGACGGGAGATGATACGATTTCAATTTGAAGAGATCTTGAAA 1200
Db 1141 AAGTACTGTGTATCAGGACGGGAGATGATACGATTTCAATTTGAAGAGATCTTGAAA 1200
Qy 1201 TTTCTTAGCTGACTTATGAAATGCACTTCAATGCAATGAAATGAAATCCCTTTCAT 1260

Db 1201 TTTCCTTACGCTGATTTAGGAAATGCACTTCATGCAATGAAATGCCCTTCAT 1260
Qy 1261 CACATTGCAACAGATTTGGGCTTCGTGAGAAATGGCTTCGTAAGATTAAGGGAAG 1320
Db 1261 CACATTGCAACAGATTTGGGCTTCGTGAGAAATGGCTTCGTAAGATTAAGGGAAG 1320
Qy 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGAGAAATCTCAACAGCTGAGAGGCT 1380
Db 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGAGAAATCTCAACAGCTGAGAGGCT 1380
Qy 1381 TTGATGCTTCTGATTTGTAAGAAATCTATAGTAATCTTCAGAGAGTCAATGTTGAG 1440
Db 1381 TTGATGCTTCTGATTTGTAAGAAATCTATAGTAATCTTCAGAGAGTCAATGTTGAG 1440
Qy 1441 AAAATGATGATTAATTAACAGAGCTTCAATCAAGAAAGTGAAGCTATTCACAG 1500
Db 1441 AAAATGATGATTAATTAACAGAGCTTCAATCAAGAAAGTGAAGCTATTCACAG 1500
Qy 1501 CATCAACTTCTAGTAGCATTTATTAAGAGCCCAAGAGATGTAAGAGTTGAAAGG 1560
Db 1501 CATCAACTTCTAGTAGCATTTATTAAGAGCCCAAGAGATGTAAGAGTTGAAAGG 1560
Qy 1561 AAGAAACCCAGAGCAAGAGAGAGTGTGAATCTAGTTGCCCTTAATGCCATTGAAC 1620
Db 1561 AAGAAACCCAGAGCAAGAGAGAGTGTGAATCTAGTTGCCCTTAATGCCATTGAAC 1620
Qy 1621 CTGATGATTTGTCAAGAGTGCACCTTAATTAATGTTGATTTGCCATGCGAAGAC 1680
Db 1621 CTGATGATTTGTCAAGAGTGCACCTTAATTAATGTTGATTTGCCATGCGAAGAC 1680
Qy 1681 ATCTATGAGCTGCTTTATCATGTCAGAAAGCTAAAGAAAGAAAGAAAGTACCAG 1740
Db 1681 ATCTATGAGCTGCTTTATCATGTCAGAAAGCTAAAGAAAGAAAGTACCAG 1740
Qy 1741 TATGAGACCAACCAATTCATTAATGTTGCTAATTTCCCTAGTTGACCTGTCTAT 1800
Db 1741 TATGAGACCAACCAATTCATTAATGTTGCTAATTTCCCTAGTTGACCTGTCTAT 1800
Qy 1801 AAGAAATATATATTTCTAATATTAACCTTAGAAATTTAGACAACTGAAATTTAT 1860
Db 1801 AAGAAATATATATTTCTAATATTAACCTTAGAAATTTAGACAACTGAAATTTAT 1860
Qy 1861 CACATATATCAAAAGTGAAGAAATGCTCAATCACTAGATTTCTCTTAAATATAT 1920
Db 1861 CACATATATCAAAAGTGAAGAAATGCTCAATCACTAGATTTCTCTTAAATATAT 1920
Qy 1921 TGACCTACTTGTGTAGTGAATGTAATTAATTAATTTGAATTTGATGATGAGT 1980
Db 1921 TGACCTACTTGTGTAGTGAATGTAATTAATTAATTTGAATTTGATGATGAGT 1980
Qy 1981 CATCTTTACCAACTCTCTAATTTTAAATTTCTACTGCTCTTAAATGAGAATAC 2040
Db 1981 CATCTTTACCAACTCTCTAATTTTAAATTTCTACTGCTCTTAAATGAGAATAC 2040
Qy 2041 TTGTTTTTTTTTTCTTAAATGTAATTAATTAATTAATTAATTTTATTTTAT 2100
Db 2041 TTGTTTTTTTTTTCTTAAATGTAATTAATTAATTAATTTTATTTTATTTTAT 2100
Qy 2101 AGACGAGTCTGCTCTGTTACCCAGAGCTGAGTCAAGTGTGATCTTGCTCACTGA 2160
Db 2101 AGACGAGTCTGCTCTGTTACCCAGAGCTGAGTCAAGTGTGATCTTGCTCACTGA 2160
Qy 2161 AGCTTGTGCTTCCCGGGTTCGACCAATTTCTGCTCAAGCTCCCAATAGCTGAGC 2220
Db 2161 AGCTTGTGCTTCCCGGGTTCGACCAATTTCTGCTCAAGCTCCCAATAGCTGAGC 2220
Qy 2221 TACAGTCACTGTCACACACCTGGCTAATTTTGTACTTTTAAAGAGAGGGTTTC 2280
Db 2221 TACAGTCACTGTCACACACCTGGCTAATTTTGTACTTTTAAAGAGAGGGTTTC 2280
Qy 2281 ACCGTTTACGAGAGATGTTCTGATCTCTGACCTCGATCCGCCCACTCGGCTCC 2340
Db 2281 ACCGTTTACGAGAGATGTTCTGATCTCTGACCTCGATCCGCCCACTCGGCTCC 2340

Qy 2341 CAAAGTGTGGATTTACAGAGATGAGCCAGC 2372
Db 2341 CAAAGTGTGGATTTACAGAGATGAGCCAGC 2372

RESULT 8
US-10-005-344-1
; Sequence 1, Application US/10005344
; Publication No. US20030203862A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia
; APPLICANT: Pamela Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Brett P. Monia
; APPLICANT: Erich Kolier
; APPLICANT: Mingyi Chiang
; APPLICANT: Mano Manoharan
; TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
; FILE REFERENCE: ISPH-0622
; CURRENT APPLICATION NUMBER: US/10/005,344
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 09/048,810
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/280,805
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 379
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (312) ... (1787)
US-10-005-344-1

Query Match 100.0%; Score 2372; DB 7; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCGCCGAGCTTGGCTGCTTCTGAGGCTGTGTGAGGCTGTGTGAGAAATGGA 60
Db 1 GCACCGCCGAGCTTGGCTGCTTCTGAGGCTGTGTGAGGCTGTGTGAGAAATGGA 60
Qy 61 GCAGAGCCGAGCCGAGGAGGCGCGGAGCCCTGACCGAGATCTGCTGCTTTCG 120
Db 61 GCAGAGCCGAGCCGAGGAGGCGCGGAGCCCTGACCGAGATCTGCTGCTTTCG 120
Qy 121 CAGCCAGAGACCGCTCCCTCCCGGATTAAGTGTGCTGACGAGCGCCAGTGCCGCG 180
Db 121 CAGCCAGAGACCGCTCCCTCCCGGATTAAGTGTGCTGACGAGCGCCAGTGCCGCG 180
Qy 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTGCTTCCGAGTATGATCCCGCG 240
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Qy 241 AAGGAACTGGGAGATCTTGAAGGAGCCCGGACTCAAGCGGAAACCCCGATGTGA 300
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Qy 301 GAGAGCAAGATGTGCAATACCAATGATGCTGATCTGATGATGCTGTACCACT 360
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Qy 361 CACAGATTCAGCTTCGGAACAAGAGACCTGGTTAGACAAAGCATTTGTTGAAGT 420
Db 361 CACAGATTCAGCTTCGGAACAAGAGACCTGGTTAGACAAAGCATTTGTTGAAGT 420
Qy 421 TATTAAGTCTGTGTGTGCACAAAAAGACATTAATATGAAAGAGGTTCTTTTATC 480
Db 421 TATTAAGTCTGTGTGTGCACAAAAAGACATTAATATGAAAGAGGTTCTTTTATC 480

481 TTGGCCAGTATATATATGACTAAACGATATATATGATGAGAGCAACACATATTTGATATTT 540
481 TTGGCCAGTATATATATGACTAAACGATATATATGATGAGAGCAACACATATTTGATATTT 540
541 GTTCAATGATCTTCTAGAGAGATTTTGGCGTGCAGAGCTTCTCTGTGAAGAAGACA 600
541 GTTCAATGATCTTCTAGAGAGATTTTGGCGTGCAGAGCTTCTCTGTGAAGAAGACA 600
601 GGAAAAATATATCAATGATCTTCAAGAGAGCTTGTGTGTGATGATGAGAGAGATATATG 660
601 GGAAAAATATATCAATGATCTTCAAGAGAGCTTGTGTGTGATGATGAGAGAGATATATG 660
661 ACTCAGGATCATCTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
661 ACTCAGGATCATCTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
721 ACCTTGTACAGAGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
721 ACCTTGTACAGAGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
781 CTACCTCATCTAG 840
781 CTACCTCATCTAG 840
841 GTGAACGACAAAG 900
841 GTGAACGACAAAG 900
901 TGGCTCTGTGTAT 960
901 TGGCTCTGTGTAT 960
961 GGAAGCCATCCAG 1020
961 GGAAGCCATCCAG 1020
1021 ATCAGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 1080
1021 ATCAGAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 1080
1081 AAGATTATAGCTTATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1081 AAGATTATAGCTTATAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
1141 AAGTACTGTGTATCAG 1200
1141 AAGTACTGTGTATCAG 1200
1201 TTTCTTGTAGTATCAG 1260
1201 TTTCTTGTAGTATCAG 1260
1261 CACATTTGCAAG 1320
1261 CACATTTGCAAG 1320
1321 ATAAAGGGGAAATCTCTGAG 1380
1321 ATAAAGGGGAAATCTCTGAG 1380
1331 ATAAAGGGGAAATCTCTGAG 1380
1331 ATAAAGGGGAAATCTCTGAG 1380
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1441 AAAATGAT 1500
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1501 CATCAACTCTAGTAT 1560
1501 CATCAACTCTAGTAT 1560
1561 AAGAAACCAAG 1620
1561 AAGAAACCAAG 1620

1561 AAGAAACCAAG 1620
1561 AAGAAACCAAG 1620
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1621 CTGTGTGATTTGTCAAG 1680
1681 ATCTTATGAG 1740
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1801 AAGAGAT 1860
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1861 AAGAGAT 1920
1861 AAGAGAT 1920
1921 TGACCTACTTGTATGAG 1980
1921 TGACCTACTTGTATGAG 1980
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1981 CATCTTATACAG 2040
2041 TTGGTTTTTTTTTTCTTAAATATATATATATATATATATATATATATATATATATAT 2100
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2101 AGACGAGCTTGTCTCTGTATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
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2161 AGCTTGCCCTCCCGGAG 2220
2161 AGCTTGCCCTCCCGGAG 2220
2221 TACAGTATCTGAG 2280
2221 TACAGTATCTGAG 2280
2281 ACCGTGTTAG 2340
2281 ACCGTGTTAG 2340
2341 CAAAGTGTGGAGATTAAG 2372
2341 CAAAGTGTGGAGATTAAG 2372

RESULT 9
US-10-422-536-136
; Sequence 136, Application US/10422536
; Publication No. US20040014100a1
; GENERAL INFORMATION:
; APPLICANT: Kinsella, James
; APPLICANT: Lorens, James
; APPLICANT: Pray, Todd
; APPLICANT: Bennett, Mark
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR INHIBITING
; FILE REFERENCE: A-71433-1/AMP-CYO
; CURRENT APPLICATION NUMBER: US/10/422,536
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/187,130
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/800,770

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/ PRIOR FILING DATE: 2001-03-06
/ PRIOR APPLICATION NUMBER: US 10/232,758
/ PRIOR FILING DATE: 2002-08-30
/ NUMBER OF SEQ ID NOS: 168
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 136
/ LENGTH: 2372
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-422-536-136

Query Match      100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGAGCTTGGCTCTTCTGGGCTGTGTGCGCTGTGTGTGGAAGATGGA 60
DB 1 GCACCGCGGAGAGCTTGGCTCTTCTGGGCTGTGTGCGCTGTGTGTGGAAGATGGA 60
QY 61 GCAGAGAGCGAGAGCGCGAGAGCGCGAGAGCGCGAGAGCGCGAGAGCGCGAGAG 120
DB 61 GCAGAGAGCGAGAGCGCGAGAGCGCGAGAGCGCGAGAGCGCGAGAGCGCGAGAG 120
QY 121 CAGCCAGAGAGAGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 121 CAGCCAGAGAGAGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 181 GAGAGTGGAGATATATCCCGAGAGCGCGAGAGCGCGAGAGCGCGAGAGCGCGAG 240
DB 181 GAGAGTGGAGATATATCCCGAGAGCGCGAGAGCGCGAGAGCGCGAGAGCGCGAG 240
QY 241 AAGGAACTGGGAGAGCTTGGAGAGAGCGCGAGAGCGCGAGAGCGCGAGAGCGCGAG 300
DB 241 AAGGAACTGGGAGAGCTTGGAGAGAGCGCGAGAGCGCGAGAGCGCGAGAGCGCGAG 300
QY 301 GAGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 GAGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 CACAGATTCAGAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 CACAGATTCAGAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 TATTAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATC 480
DB 421 TATTAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATC 480
QY 481 TTGGCAGATATATATATATATATATATATATATATATATATATATATATATATAT 540
DB 481 TTGGCAGATATATATATATATATATATATATATATATATATATATATATATATAT 540
QY 541 GTTCAATGATCTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 GTTCAATGATCTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 GGAATAATATATATATATATATATATATATATATATATATATATATATATATATAT 660
DB 601 GGAATAATATATATATATATATATATATATATATATATATATATATATATATATAT 660
QY 661 ACTCAGATATATATATATATATATATATATATATATATATATATATATATATATAT 720
DB 661 ACTCAGATATATATATATATATATATATATATATATATATATATATATATATATAT 720
QY 721 ACCTTGATATATATATATATATATATATATATATATATATATATATATATATATAT 780
DB 721 ACCTTGATATATATATATATATATATATATATATATATATATATATATATATATAT 780
QY 781 CTAACCTATATATATATATATATATATATATATATATATATATATATATATATATAT 840
DB 781 CTAACCTATATATATATATATATATATATATATATATATATATATATATATATATAT 840
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DB 841 GTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
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DB 841 GTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 TGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
DB 901 TGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
QY 961 GAGAGCGAGATATATATATATATATATATATATATATATATATATATATATATATAT 1020
DB 961 GAGAGCGAGATATATATATATATATATATATATATATATATATATATATATATATAT 1020
QY 1021 ATCAGAGATATATATATATATATATATATATATATATATATATATATATATATAT 1080
DB 1021 ATCAGAGATATATATATATATATATATATATATATATATATATATATATATATAT 1080
QY 1081 AAGATTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1140
DB 1081 AAGATTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1140
QY 1141 AAGTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1200
DB 1141 AAGTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1200
QY 1201 TTTCTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1260
DB 1201 TTTCTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1260
QY 1261 CACATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1261 CACATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1321 ATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 ATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 TTGATGTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1440
DB 1381 TTGATGTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1440
QY 1441 AAAATGATATATATATATATATATATATATATATATATATATATATATATATATATAT 1500
DB 1441 AAAATGATATATATATATATATATATATATATATATATATATATATATATATATATAT 1500
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DB 1501 CATCACTTCTATATATATATATATATATATATATATATATATATATATATATATATAT 1560
QY 1561 AAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1561 AAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 CTTGTGTATATATATATATATATATATATATATATATATATATATATATATATATAT 1680
DB 1621 CTTGTGTATATATATATATATATATATATATATATATATATATATATATATATATAT 1680
QY 1681 ATCTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1740
DB 1681 ATCTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1740
QY 1741 TATGTAGACACCAATATATATATATATATATATATATATATATATATATATATATATAT 1800
DB 1741 TATGTAGACACCAATATATATATATATATATATATATATATATATATATATATATATAT 1800
QY 1801 AAGAGATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1860
DB 1801 AAGAGATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1860
QY 1861 CACATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1920
DB 1861 CACATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1920
QY 1921 TGACCTATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
DB 1921 TGACCTATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
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QY 1981 CATCTTACGACCACTCTAATTTTAAATATTTCTACTGCTTAAATGAGAGTAC 2040
DB 1981 CATCTTACGACCACTCTAATTTTAAATATTTCTACTGCTTAAATGAGAGTAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAAATATATATATGACATTTAAATGTAATTTTATTTT 2100
DB 2041 TTGGTTTTTTTTTTCTTAAATATATATATGACATTTAAATGTAATTTTATTTT 2100
QY 2101 AGACCGAGCTCTGCTGCTTACCCGAGCTGAGTGCATGATGCTTGTGCTACATGCA 2160
DB 2101 AGACCGAGCTCTGCTGCTTACCCGAGCTGAGTGCATGATGCTTGTGCTACATGCA 2160
QY 2161 AGCTGTGCTCTCCCGGGTTCGACACATTTCTCTGCTCAGCTTCCCAATTAAGTTGSCC 2220
DB 2161 AGCTGTGCTCTCCCGGGTTCGACACATTTCTCTGCTCAGCTTCCCAATTAAGTTGSCC 2220
QY 2221 TACAGTCATCTGCCACCAACACCTGGCTAATTTTGTACTTTAGTAGAGACAGGTTTC 2280
DB 2221 TACAGTCATCTGCCACCAACACCTGGCTAATTTTGTACTTTAGTAGAGACAGGTTTC 2280
QY 2281 ACCGTGTAGCCAGATGCTCTCCATCTCTGACTCTGATCCGCCACCTCGGCTCC 2340
DB 2281 ACCGTGTAGCCAGATGCTCTCCATCTCTGACTCTGATCCGCCACCTCGGCTCC 2340
QY 2341 CAAAGTCTGGGATTTACAGGACATGAGCCACCG 2372
DB 2341 CAAAGTCTGGGATTTACAGGACATGAGCCACCG 2372

RESULT 10

US-10-232-951-34
; Sequence 34, Application US/10232951
; Publication No. US20040043386A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Todd
; APPLICANT: Wong, Brian
; APPLICANT: Bennett, Mark
; APPLICANT: Parlati, Francesco
; APPLICANT: Rigel Pharmaceuticals, Incorporated
; TITLE OF INVENTION: Methods and Compositions for Functional Ubiquitin
; FILE REFERENCE: 021044-006800US
; CURRENT APPLICATION NUMBER: US/10/232,951
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: E3 ubiquitin ligating agent mouse double minute 2
; OTHER INFORMATION: (mdm2) homolog full length protein isoform, mouse
; OTHER INFORMATION: p53-binding protein (MDM2) homolog, transcript
; OTHER INFORMATION: variant MDM2, transformed 3T3 cell double minute 2,
; US-10-232-951-34

Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCTGTGTGGCCCTGTGTGTGCGAAAAGTGA 60
DB 1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCTGTGTGGCCCTGTGTGTGCGAAAAGTGA 60
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DB 61 GCAAGAGCCGAGCCGAGGGGGGCGCGACCCCTGACCGAGATCTGTGCTTTCG 120
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DB 121 CAGCCAGAGACACGCTCCCTCCCGGATTAATGCTGACAGGCGCCAGTGCCTGCGCCG 180

DB 121 CAGCCAGAGACACGCTCCCTCCCGGATTAATGCTGACAGGCGCCAGTGCCTGCGCCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCCAGAGCGTGTGCTTCGCGAGTATGATGCCGCTG 240
DB 181 GAGAGTGAATGATCCCGAGGCGCCAGAGCGTGTGCTTCGCGAGTATGATGCCGCTG 240
QY 241 AAGGAACTGGGAGTCTTGAAGGAGCCCGGACTCCAGAGCGGAAAAACCCGAGTGTGA 300
DB 241 AAGGAACTGGGAGTCTTGAAGGAGCCCGGACTCCAGAGCGGAAAAACCCGAGTGTGA 300
QY 301 GGACAGGCAAAATGTGCAATACCAATGTCTGTAACCTACTGATGAGTGTCTTAACACT 360
DB 301 GGACAGGCAAAATGTGCAATACCAATGTCTGTAACCTACTGATGAGTGTCTTAACACT 360
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DB 361 CACAGATTCGAGCTTGGGAAACAGAGACCCCTGTTAGACCAAGCCATYGGCTTTGAAGT 420
QY 421 TATTAAGTCTGTGTGTCACAAAAAGACATTAATATGAAAGAGGTTCTTTTATTC 480
DB 421 TATTAAGTCTGTGTGTCACAAAAAGACATTAATATGAAAGAGGTTCTTTTATTC 480
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QY 541 GTTCAAAATGATCTTGAAGATTTGTTGGCGTGGCCAGGCTCTGTGTGAAGAGCACA 600
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QY 601 GAAAAATATATACCATGATCTTACAGAACTTGTATGATGATCAAGCAGGAATCATCGG 660
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DB 1201 TTTCTTACTGACTATTTGAAGATGCACTTCAATGCAATGAAGTATCCCTCTCAT 1260

QY 1261 CACATTGCAACAGATGTTGGGCTTCGTGAGAAATGGCTTCCTGAAGATTAAGGGAAG 1320
DB 1261 CACATTGCAACAGATGTTGGGCTTCGTGAGAAATGGCTTCCTGAAGATTAAGGGAAG 1320
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DB 1321 ATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAAAACTCAACAACTGGAAGGGCT 1380
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DB 1381 TTGATGTCCTGATGTAATAAACTATGTAATGTAATGTAATGTAATGTAATGTAATG 1440
QY 1441 AAAATGATGATTAATTAACAAGCTTCACATCAACAAGAAAGTGAAGTATTCACAC 1500
DB 1441 AAAATGATGATTAATTAACAAGCTTCACATCAACAAGAAAGTGAAGTATTCACAC 1500
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DB 1501 CATCAACTTCAGTAGAGATTAATTAAGCAGCCAAAGAGATGTAAGAGTTGAAAGG 1560
QY 1561 AAGAAACCCCAACAAAGAGAGAGTGTGAATCTAGTTGCCCTTAATGCCATTGAAC 1620
DB 1561 AAGAAACCCCAACAAAGAGAGAGTGTGAATCTAGTTGCCCTTAATGCCATTGAAC 1620
QY 1621 CTGTGTGATTTGTCAAGGTGACCTAAATGTTGATGTCATGTCATGTCATGTCATG 1680
DB 1621 CTGTGTGATTTGTCAAGGTGACCTAAATGTTGATGTCATGTCATGTCATGTCATG 1680
QY 1681 ATCTTAGGCTCTGCTTACATGTCAGAAAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
DB 1681 ATCTTAGGCTCTGCTTACATGTCAGAAAGAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
QY 1741 TATGTAAGCAACCAATCAATGATGTCCTAATCTTAATCCCTAGTTGACCTGTCTAT 1800
DB 1741 TATGTAAGCAACCAATCAATGATGTCCTAATCTTAATCCCTAGTTGACCTGTCTAT 1800
QY 1801 AAGAAATTAATTAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1860
DB 1801 AAGAAATTAATTAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1860
QY 1861 CACATATATCAAAAGTGAAGAAATGCTCAATCAGATAGATTTCTTCTTTAGTAAAT 1920
DB 1861 CACATATATCAAAAGTGAAGAAATGCTCAATCAGATAGATTTCTTCTTTAGTAAAT 1920
QY 1921 TGACCTACTTGGTAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1980
DB 1921 TGACCTACTTGGTAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1980
QY 1981 CATCTTTTACCAACTCTTAATTTTAAATTAATTTCTACTCTGTCTTAATGAGAATAC 2040
DB 1981 CATCTTTTACCAACTCTTAATTTTAAATTAATTTCTACTCTGTCTTAATGAGAATAC 2040
QY 2041 TTGGTTTTTTTTTTCTTAATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 2100
DB 2041 TTGGTTTTTTTTTTCTTAATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 2100
QY 2101 AGACCGAGTCTTGTCTGTACCAAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2160
DB 2101 AGACCGAGTCTTGTCTGTACCAAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2160
QY 2161 AGCTTGCCTCTCCCGGGTTCGACATCTCTGCTCAAGCTTCCCAATTAAGCTTGGC 2220
DB 2161 AGCTTGCCTCTCCCGGGTTCGACATCTCTGCTCAAGCTTCCCAATTAAGCTTGGC 2220
QY 2221 TACAGTCAATGTCACCAACCTGCTAATTTTGTACTTTTGTAGTAGAGACAGGTTTC 2280
DB 2221 TACAGTCAATGTCACCAACCTGCTAATTTTGTACTTTTGTAGTAGAGACAGGTTTC 2280
QY 2281 ACCGTGTTAGCGAGATGTCGTGATCTCTGACCTGTGATCCGCCACTCGGCTTC 2340
DB 2281 ACCGTGTTAGCGAGATGTCGTGATCTCTGACCTGTGATCCGCCACTCGGCTTC 2340
QY 2340 ACCGTGTTAGCGAGATGTCGTGATCTCTGACCTGTGATCCGCCACTCGGCTTC 2340

QY 2341 CAAAGTGTGGGATTAACAGCATGAGCCACCG 2372
DB 2341 CAAAGTGTGGGATTAACAGCATGAGCCACCG 2372

RESULT 11
US-10-052-482-173
; Sequence 173, Application US/10052482
; Publication No. US20040072264A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71087/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/052,482
; PRIORITY FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: Patencin version 3.1
; SEQ ID NO 173
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-482-173

Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAACCGCGGAGCTTGGCTGCTTCTGAGGCTGTGTGCTGTGTGCGAAAGATGGA 60
DB 1 GCAACCGCGGAGCTTGGCTGCTTCTGAGGCTGTGTGCTGTGTGCGAAAGATGGA 60
QY 61 GCAACCGCGGAGCTTGGCTGCTTCTGAGGCTGTGTGCTGTGTGCGAAAGATGGA 120
DB 61 GCAACCGCGGAGCTTGGCTGCTTCTGAGGCTGTGTGCTGTGTGCGAAAGATGGA 120
QY 121 CAGCAGAGAGCAGCTTCCCTCCCGGATTAAGTGAAGAGGCGCCAGTCCCTGCGCCG 180
DB 121 CAGCAGAGAGCAGCTTCCCTCCCGGATTAAGTGAAGAGGCGCCAGTCCCTGCGCCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTGTGTGCTGTGTGCGAGTGAATGAT 240
DB 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTGTGTGCTGTGTGCGAGTGAATGAT 240
QY 241 AAGGAACTGGGAGATCTTGAAGGACCCCGCATCTCAAGCGGAAACCCCGGATGTA 300
DB 241 AAGGAACTGGGAGATCTTGAAGGACCCCGCATCTCAAGCGGAAACCCCGGATGTA 300
QY 301 GGAGCAGGCAATGTCATATACCAATGTCATGTCATGTCATGTCATGTCATGTCATG 360
DB 301 GGAGCAGGCAATGTCATATACCAATGTCATGTCATGTCATGTCATGTCATGTCATG 360
QY 361 CACAGATTCAGCTTCGAAACAAAGAGACCTGCTGTAACCAAAAGCATTTGTAAGT 420
DB 361 CACAGATTCAGCTTCGAAACAAAGAGACCTGCTGTAACCAAAAGCATTTGTAAGT 420
QY 421 TATTAAGTCTGTGTGTCACAAAGAGACCTGCTGTAACCAAAAGCATTTGTAAGT 480
DB 421 TATTAAGTCTGTGTGTCACAAAGAGACCTGCTGTAACCAAAAGCATTTGTAAGT 480
QY 481 TTGGCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
DB 481 TTGGCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540
QY 541 GTTCAATGATCTTTAGAGATTTGTTGGCTGTCAGAGCTTCTGTGTAAGAGCACA 600
DB 541 GTTCAATGATCTTTAGAGATTTGTTGGCTGTCAGAGCTTCTGTGTAAGAGCACA 600
QY 601 GGAATAAT 660

Db 601 GGAATATATACCATGATCTACAGAACTGGTAGTAGTCAATCAGAGAAATCATCGG 660
Qy 661 ACTCAGGACATCTGTGAGTGAAGCAGGTGACCTTGAAGGTGGAGTATCAAAAG 720
Db 661 ACTCAGGACATCTGTGAGTGAAGCAGGTGACCTTGAAGGTGGAGTATCAAAAG 720
Qy 721 ACCTGTACAGAGCTTCAGAGAGAAACCTTCATCTTCACTTGGTTCTAGACCAT 780
Db 721 ACCTGTACAGAGCTTCAGAGAGAAACCTTCATCTTCACTTGGTTCTAGACCAT 780
Qy 781 CTACCTCATCTAGAGAGAGAGCAATTAAGTGAAGAGAGAAATTCAGATGATATCTG 840
Db 781 CTACCTCATCTAGAGAGAGAGCAATTAAGTGAAGAGAGAAATTCAGATGATATCTG 840
Qy 841 GTGAACGCAAGAAAGAAAGCCCAATCTGATGATATTCCTTCTTCTTGAAGAAC 900
Db 841 GTGAACGCAAGAAAGAAAGCCCAATCTGATGATATTCCTTCTTCTTGAAGAAC 900
Qy 901 TGGCTCTGTGTATTAAGGAGATATGTGTAAGAGAGAGTGAAGTATCTAG 960
Db 901 TGGCTCTGTGTATTAAGGAGATATGTGTAAGAGAGAGTGAAGTATCTAG 960
Qy 961 GGAAGCCATCGAATCCGATCTTGATGCTGTGTAAGTGAAGTATCTAG 1020
Db 961 GGAAGCCATCGAATCCGATCTTGATGCTGTGTAAGTGAAGTATCTAG 1020
Qy 1021 ATCAGGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1080
Db 1021 ATCAGGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 1080
Qy 1081 AAGATTATAGCTTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 AAGATTATAGCTTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy 1141 AAGATTATAGCTTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1141 AAGATTATAGCTTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Qy 1201 TTTCTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db 1201 TTTCTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Qy 1261 CACATTGCAAG 1320
Db 1261 CACATTGCAAG 1320
Qy 1321 ATAAAGGGGAAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 ATAAAGGGGAAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Qy 1381 TTGATGTTCTGTATGTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 TTGATGTTCTGTATGTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Qy 1441 AAAATGATGATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 AAAATGATGATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Qy 1501 CATCACTTCTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 CATCACTTCTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Qy 1561 AAGAAACCCAG 1620
Db 1561 AAGAAACCCAG 1620
Qy 1621 CTGTGTGTATTTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 1621 CTGTGTGTATTTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Qy 1681 ATCTTATGAGCTGTCTTATGATGCAAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ATCTTATGAGCTGTCTTATGATGCAAGAGAGAGAGAGAGAGAGAGAGAG 1740

Db 1681 ATCTTATGAGCTGTCTTATGATGCAAGAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 TATGTAGACCAACCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 TATGTAGACCAACCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Qy 1801 AAGAGAAATTAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 AAGAGAAATTAATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Qy 1861 CACATATATCAAG 1920
Db 1861 CACATATATCAAG 1920
Qy 1921 TGACCTACTTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 TGACCTACTTGTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Qy 1981 CATCTTACCAACCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Db 1981 CATCTTACCAACCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Qy 2041 TTGCTTTTCTTTCTTTAAATATGATATGATATGATATGATATGATATGAT 2100
Db 2041 TTGCTTTTCTTTCTTTAAATATGATATGATATGATATGATATGATATGAT 2100
Qy 2101 AGACGAGATCTTGTCTGTATACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Db 2101 AGACGAGATCTTGTCTGTATACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Qy 2161 AGCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220
Db 2161 AGCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220
Qy 2221 TACAGTATCTGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 2280
Db 2221 TACAGTATCTGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 2280
Qy 2281 ACCGTGTAG 2340
Db 2281 ACCGTGTAG 2340
Qy 2341 CAAAGTGTGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2372
Db 2341 CAAAGTGTGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2372

RESULT 12
US-10-489-802-7
; Sequence 7, Application US/10489802
; Publication No. US20040248198A1
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital, Inc.
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Art and Hdm2 Interaction Domains and
; TITLE OF INVENTION: Method of Use Thereof
; FILE REFERENCE: 44158/243642
; CURRENT APPLICATION NUMBER: US/10/489,802
; PRIOR FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: US 09/956,425
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FaSeq for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-489-802-7

Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	GCACCCGCGAGCTTGGCTGCTTCTGGGGCTGTGTGCGCTGTGTGCGAAAGATGGA	60	
Db	1	GCACCCGCGAGCTTGGCTGCTTCTGGGGCTGTGTGCGCTGTGTGCGAAAGATGGA	60	
Qy	61	GCAAGAGCCGAGCCGAGGGGGCGCGGACCCCTCTGACCGAGATCTGTGCTTTG	120	
Db	61	GCAAGAGCCGAGCCGAGGGGGCGCGGACCCCTCTGACCGAGATCTGTGCTTTG	120	
Qy	121	CAGCCGAGGACCCGCTCCCTCCCGGATTAAGTGTGCGAGCGCCAGTGCCTGCGCG	180	
Db	121	CAGCCGAGGACCCGCTCCCTCCCGGATTAAGTGTGCGAGCGCCAGTGCCTGCGCG	180	
Qy	181	GAGAGTGAATATCCCGGAGCGCGGCGGTGTGCTTCCGAGATGCAATGCCCCG	240	
Db	181	GAGAGTGAATATCCCGGAGCGCGGCGGTGTGCTTCCGAGATGCAATGCCCCG	240	
Qy	241	AGGAAACTGGGGAGCTTGTAGGGGACCCCGGACTCCAGCGGAAACCCCGGATGTA	300	
Db	241	AGGAAACTGGGGAGCTTGTAGGGGACCCCGGACTCCAGCGGAAACCCCGGATGTA	300	
Qy	301	GGAGCAGGCAATGTGCAATACCAATGTGTACCTAATGATGCTGTAAACCACT	360	
Db	301	GGAGCAGGCAATGTGCAATACCAATGTGTACCTAATGATGCTGTAAACCACT	360	
Qy	361	CACAGATTCAGCTTCGGAACAAGAACCTGTGTAGACCAAGCAATGCTTTGAAT	420	
Db	361	CACAGATTCAGCTTCGGAACAAGAACCTGTGTAGACCAAGCAATGCTTTGAAT	420	
Qy	421	TATTAAGCTGTGGTGTGCAAAAAAGACCTTAATACATGAAAGAGTCTTTTATC	480	
Db	421	TATTAAGCTGTGGTGTGCAAAAAAGACCTTAATACATGAAAGAGTCTTTTATC	480	
Qy	481	TTGGCCAGTAATTAATGACTAAACGATTAATGATGAGAAAGCAACAATATGTAAT	540	
Db	481	TTGGCCAGTAATTAATGACTAAACGATTAATGATGAGAAAGCAACAATATGTAAT	540	
Qy	541	GTTCAAAATGATCTTGAAGAGATTTGTTGGCGTGCAGCTTCCTGTGAAGAGCACA	600	
Db	541	GTTCAAAATGATCTTGAAGAGATTTGTTGGCGTGCAGCTTCCTGTGAAGAGCACA	600	
Qy	601	GGAATAATATATACATGATCTACAGGAACCTGTGTAGTACATGACGAGATCATGCG	660	
Db	601	GGAATAATATATACATGATCTACAGGAACCTGTGTAGTACATGACGAGATCATGCG	660	
Qy	661	ACTCAGTACATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTGTATCAAAAG	720	
Db	661	ACTCAGTACATCTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGTGTATCAAAAG	720	
Qy	721	ACCTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTCACATTTGGTTCTAGACAT	780	
Db	721	ACCTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTCACATTTGGTTCTAGACAT	780	
Qy	781	CTACCTCATCTAGAGAGAGCAATTAAGTGAACAGAAAGAAATTCAGATGAATATCTG	840	
Db	781	CTACCTCATCTAGAGAGAGCAATTAAGTGAACAGAAAGAAATTCAGATGAATATCTG	840	
Qy	841	GTAAGCACAAGAAAGCCCAATATCTGATGATTTCCCTTCCTTTGATGAAGCC	900	
Db	841	GTAAGCACAAGAAAGCCCAATATCTGATGATTTCCCTTCCTTTGATGAAGCC	900	
Qy	901	TGGCTCTGTGTATTAAGGAGATATGTGTGAAGAGAGAGTACAGTGTATCTACAG	960	
Db	901	TGGCTCTGTGTATTAAGGAGATATGTGTGAAGAGAGAGTACAGTGTATCTACAG	960	
Qy	961	GGAAGCAGATCCGATCTTGAATGCTGTGATGATGATGATGATGATGATGATGATG	1020	
Db	961	GGAAGCAGATCCGATCTTGAATGCTGTGATGATGATGATGATGATGATGATGATG	1020	
Qy	1021	ATCAGAGTTCAGTTCAATCAGTATGATGATGATGATGATGATGATGATGATGATG	1080	
Db	1021	ATCAGAGTTCAGTTCAATCAGTATGATGATGATGATGATGATGATGATGATGATG	1080	

Qy	1081	AAAGATTATAGCCTTAGTGAAGAGGACAAGAACTCTCAGATGAAGATGATGATATATC	1140	
Db	1081	AAAGATTATAGCCTTAGTGAAGAGGACAAGAACTCTCAGATGAAGATGATGATATATC	1140	
Qy	1141	AAAGTACTGTATACAGGAGGGAGAGTGTATACAGATTCATTTGAAGAGATCTGA	1200	
Db	1141	AAAGTACTGTATACAGGAGGGAGAGTGTATACAGATTCATTTGAAGAGATCTGA	1200	
Qy	1201	TTTCTTACCTGATCTATTTGAAGATGCACTTCATGCAATGAATGAATCCCCCTTCAT	1260	
Db	1201	TTTCTTACCTGATCTATTTGAAGATGCACTTCATGCAATGAATGAATCCCCCTTCAT	1260	
Qy	1261	CACATTCGACAGATGTTGGGCGCTTCGGAAGAAATGGCTTCCTGAGATGAAGGAAAG	1320	
Db	1261	CACATTCGACAGATGTTGGGCGCTTCGGAAGAAATGGCTTCCTGAGATGAAGGAAAG	1320	
Qy	1321	ATPAAGGGGAATCTCTGAGAAAGCCAACTGGAAGAACTCAACAAGCTGAAGAGGCT	1380	
Db	1321	ATPAAGGGGAATCTCTGAGAAAGCCAACTGGAAGAACTCAACAAGCTGAAGAGGCT	1380	
Qy	1381	TTGATGTTCTGATTTGTAAGAACTATAGTAATGATTCAGAGATCATGTGTGAGG	1440	
Db	1381	TTGATGTTCTGATTTGTAAGAACTATAGTAATGATTCAGAGATCATGTGTGAGG	1440	
Qy	1441	AAAATGATGATTAATTAACAAGCTTCACATCAACAAGAGTGAAGCTATTCACAG	1500	
Db	1441	AAAATGATGATTAATTAACAAGCTTCACATCAACAAGAGTGAAGCTATTCACAG	1500	
Qy	1501	CATCAACTCTAGTACATTTATTAAGAGCCAGAAAGATGGAAGAGTTGAAGAGG	1560	
Db	1501	CATCAACTCTAGTACATTTATTAAGAGCCAGAAAGATGGAAGAGTTGAAGAGG	1560	
Qy	1561	AGAAACCCAGACAAAGAGAGAGTGTGAATCTAGTTGCCCTTAATGCAATTTGAAC	1620	
Db	1561	AGAAACCCAGACAAAGAGAGAGTGTGAATCTAGTTGCCCTTAATGCAATTTGAAC	1620	
Qy	1621	CTTGTGTATTTGTCAAGGTGCACTTAAGATGTTGTCATTTCCATGACCAAGAC	1680	
Db	1621	CTTGTGTATTTGTCAAGGTGCACTTAAGATGTTGTCATTTCCATGACCAAGAC	1680	
Qy	1681	ATCTATGGCCGCTTCAATGAGAAAGACCTTAAGAAAGAAATGAGCCCTGCCAG	1740	
Db	1681	ATCTATGGCCGCTTCAATGAGAAAGACCTTAAGAAAGAAATGAGCCCTGCCAG	1740	
Qy	1741	TATGTAGCAACCAATTCATATGATTTGCTAATTTCCCTAGTTGACCTGTCTAT	1800	
Db	1741	TATGTAGCAACCAATTCATATGATTTGCTAATTTCCCTAGTTGACCTGTCTAT	1800	
Qy	1801	AAAGAAATTAATTAATTTCTAATATATAACCTAGGAATTTAGACAACCTGAATTTAT	1860	
Db	1801	AAAGAAATTAATTAATTTCTAATATATAACCTAGGAATTTAGACAACCTGAATTTAT	1860	
Qy	1861	CACATATATCAAGAGAGAAATGCTCAATTCATATGATTTCTTCTTTAGATATAT	1920	
Db	1861	CACATATATCAAGAGAGAAATGCTCAATTCATATGATTTCTTCTTTAGATATAT	1920	
Qy	1921	TGACCTACTTGGTGTGAGAAATAGTAATCTTATATATTTGAATGATGATGATG	1980	
Db	1921	TGACCTACTTGGTGTGAGAAATAGTAATCTTATATATTTGAATGATGATGATG	1980	
Qy	1981	CATCTTTACACCAACTCTTAATTTTAATATTTCTGCTGTAAATGAGAATGAC	2040	
Db	1981	CATCTTTACACCAACTCTTAATTTTAATATTTCTGCTGTAAATGAGAATGAC	2040	
Qy	2041	TTGGTTTTTTTTTTCTTAATATATGATATGACATTTAATGATATTTATTTTGTG	2100	
Db	2041	TTGGTTTTTTTTTTCTTAATATATGATATGACATTTAATGATATTTATTTTGTG	2100	
Qy	2101	AGACGAGTCTTGTCTGTATCCAGGCTGAGATGCAATGAGTGTATCTTGGCTCACTGA	2160	
Db	2101	AGACGAGTCTTGTCTGTATCCAGGCTGAGATGCAATGAGTGTATCTTGGCTCACTGA	2160	

QY 2161 AGCTCTGCCCTCCCGGGTTGCAACATTTCTCTGCTCCAGCCTCCCAATTAGCTTGGCC 2220
DB 2161 AGCTCTGCCCTCCCGGGTTGCAACATTTCTCTGCTCCAGCCTCCCAATTAGCTTGGCC 2220
QY 2221 TAGAGTATCTGCGCAACACACCTGGCTAATTTTGTACTTTTGTATAGAGACAGGTTTC 2280
DB 2221 TAGAGTATCTGCGCAACACACCTGGCTAATTTTGTACTTTTGTATAGAGACAGGTTTC 2280
QY 2281 ACCGTTTGGCAGGATGGTCTGATCTCTGATCCTGATCCGCCACCTCGGCTCC 2340
DB 2281 ACCGTTTGGCAGGATGGTCTGATCTCTGATCCTGATCCGCCACCTCGGCTCC 2340
QY 2341 CAAAGTCTGGGATTACAGGATAGCCACCG 2372
DB 2341 CAAAGTCTGGGATTACAGGATAGCCACCG 2372

RESULT 13
US-10-723-860-2235
; Sequence 2235, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natsasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882, 0193, NUS01
; CURRENT APPLICATION NUMBER: US/10/723, 860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429, 739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2235
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2235

Query Match 100.0%; Score 2372; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTGGCTGCTTCTGGGGCTGTGAGGCCCTGTGTCGAAAGATGGA 60
DB 1 GCACCGCGGAGCTGGCTGCTTCTGGGGCTGTGAGGCCCTGTGTCGAAAGATGGA 60
QY 61 GCAGAGACCGAGCCCGAGGGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTTCG 120
DB 61 GCAGAGACCGAGCCCGAGGGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTTCG 120
QY 121 CAGCCAGAGACACCGTCCCTCCCGGATTAATGTCGTAAGAGCGCCAGTCCCTGACCCG 180
DB 121 CAGCCAGAGACACCGTCCCTCCCGGATTAATGTCGTAAGAGCGCCAGTCCCTGACCCG 180
QY 181 GAGAGTGAATATATCCCGAGGCGGAGGCGCTGCTCCCGAGATGACATCCCGCG 240
DB 181 GAGAGTGAATATATCCCGAGGCGGAGGCGCTGCTCCCGAGATGACATCCCGCG 240
QY 241 AAGAAACTGGGAGATCTTGAAGGACCCCGACTCCAGCGGAAACCCCGAGATGTA 300
DB 241 AAGAAACTGGGAGATCTTGAAGGACCCCGACTCCAGCGGAAACCCCGAGATGTA 300
QY 301 GGAGAGGCAAAATGTGCAATACCAATGTGTGACTTAATGATGCTGTAAACCACT 360
DB 301 GGAGAGGCAAAATGTGCAATACCAATGTGTGACTTAATGATGCTGTAAACCACT 360
QY 361 CACAGATTCAGACTTCGGAACAAGAGACCTGTGTTAGACCAAGACCATGCTTTGAAT 420
DB 361 CACAGATTCAGACTTCGGAACAAGAGACCTGTGTTAGACCAAGACCATGCTTTGAAT 420
QY 421 TATTAAGTCTGTGTGTCACAAAAGACATTAATGTAAGAGAGTTCTTTTATTC 480

DB 421 TATTAAGTCTGTGTGTCACAAAAGACATTAATGTAAGAGAGTTCTTTTATTC 480
QY 481 TTGGCAGATATATATGACTTAAAGATTAATGTAAGAGCAACAATATGTAATTT 540
DB 481 TTGGCAGATATATATGACTTAAAGATTAATGTAAGAGCAACAATATGTAATTT 540
QY 541 GTTCAAAATGATCTTCTAGAGATTTGTTGGCGTCCAGGCTTCTGTGTAAGAGACA 600
DB 541 GTTCAAAATGATCTTCTAGAGATTTGTTGGCGTCCAGGCTTCTGTGTAAGAGACA 600
QY 601 GGAAATATATACATGATCTAGAGAACTTGTAATGTAATGTAATGTAATGTAATGTA 660
DB 601 GGAAATATATACATGATCTAGAGAACTTGTAATGTAATGTAATGTAATGTAATGTA 660
QY 661 ACTCAGGATCATCTGTGAGTGAAGACAGTGTCACTTGAAGTGGAGATCAAAAG 720
DB 661 ACTCAGGATCATCTGTGAGTGAAGACAGTGTCACTTGAAGTGGAGATCAAAAG 720
QY 721 ACCTTGTAACAAGCTTCAGAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACAT 780
DB 721 ACCTTGTAACAAGCTTCAGAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACAT 780
QY 781 CTACCTCATCTAGAGAGAGCAATTTAGTGAACAAGAAATTCAGATGAATATCTG 840
DB 781 CTACCTCATCTAGAGAGAGCAATTTAGTGAACAAGAAATTCAGATGAATATCTG 840
QY 841 GTGAACGACAAAGAAACGCCCAAAATCTGATGATTTCCCTTCTTATGTAAGACC 900
DB 841 GTGAACGACAAAGAAACGCCCAAAATCTGATGATTTCCCTTCTTATGTAAGACC 900
QY 901 TGGCTGTGTGTATTAAGAGATGTTGTGAAGAGAGTACAGTGAATCTACAG 960
DB 901 TGGCTGTGTGTATTAAGAGATGTTGTGAAGAGAGTACAGTGAATCTACAG 960
QY 961 GGAGGCCATGCAATCCGATCTTGATGCTGTGTGAAGCAATTCAGATGATGTTGG 1020
DB 961 GGAGGCCATGCAATCCGATCTTGATGCTGTGTGAAGCAATTCAGATGATGTTGG 1020
QY 1021 ATCAGATTCAGTTTCAATCAGTTTATGATGATTTGAAGTGAATCTCTGACCTCAG 1080
DB 1021 ATCAGATTCAGTTTCAATCAGTTTATGATGATTTGAAGTGAATCTCTGACCTCAG 1080
QY 1081 AAGATTATAGCTTATGTAAGAGACAAAGACTCTCAGATGAAGATGATGATATTC 1140
DB 1081 AAGATTATAGCTTATGTAAGAGACAAAGACTCTCAGATGAAGATGATGATATTC 1140
QY 1141 AAGTTATCTGTATCAGAGGAGAGATGATACAGATTCATTGTAAGAGATCTGAAA 1200
DB 1141 AAGTTATCTGTATCAGAGGAGAGATGATACAGATTCATTGTAAGAGATCTGAAA 1200
QY 1201 TTTCTTGAAGTATGTAAGATGCACTTCATGCAATGAATGAATGATCCCGCTTCAT 1260
DB 1201 TTTCTTGAAGTATGTAAGATGCACTTCATGCAATGAATGAATGATCCCGCTTCAT 1260
QY 1261 CACATTGCAACAGATGTTGGCCCTTCGTGAGATTTGGCTTCTGAAATGAAGGGAAG 1320
DB 1261 CACATTGCAACAGATGTTGGCCCTTCGTGAGATTTGGCTTCTGAAATGAAGGGAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCAATGGAATCTCAACACAGCTGAAGGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCAATGGAATCTCAACACAGCTGAAGGGCT 1380
QY 1381 TTGATGTTCTGATGTAAGAAATCTATAGGAATGATTTCCAGAGAGTCAATGTTGAG 1440
DB 1381 TTGATGTTCTGATGTAAGAAATCTATAGGAATGATTTCCAGAGAGTCAATGTTGAG 1440
QY 1441 AAAATGATGATTAATTAACAAGGCTTCAATCAACAAGAGTGAAGCTATTTCTAGC 1500
DB 1441 AAAATGATGATTAATTAACAAGGCTTCAATCAACAAGAGTGAAGCTATTTCTAGC 1500
QY 1501 CATCAACTTCTAGTGAATTTATTAAGCAAGCAAGAGATGTAAGAGTTGAAAGG 1560

Db 1501 CATCACTTCTAGTACATTATTTATAGCAGCCAGAGATGTGAAGATTGAAAGG 1560
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US-10-843-641A-450
; Sequence 450, Application US/10843641A
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531

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Db 121 CAGCAGAGACGCTGCTCCCGGATTTAGTCGATGACAGGCGCCAGTGCCTGCGCCG 180
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US-11-069-642-136
; Sequence 136, Application US/11069642
; Publication No. US20050260626a1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELA, TODD M.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 136
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

US-11-069-642-136

Query Match 100.0%; Score 2372; DB 15; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: August 4, 2006, 13:38:17
Job time : 2943 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 20:42:58 ; Search time 322 Seconds

(without alignments)
11667.258 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters: 4386554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	984.4	41.5	34088	US-11-266-748A-23848	Sequence 23848, A
3	962.4	40.6	1000	US-11-266-748A-114799	Sequence 114799, A
4	962.4	40.6	1000	US-11-266-748A-119930	Sequence 119930, A
5	962.4	40.6	1000	US-11-266-748A-281679	Sequence 281679, A
6	962.4	40.6	1000	US-11-266-748A-308319	Sequence 308319, A
7	962.4	40.6	1000	US-11-266-748A-390721	Sequence 390721, A
8	962.4	40.6	1000	US-11-266-748A-481439	Sequence 481439, A
9	777.6	32.8	1000	US-11-266-748A-221947	Sequence 221947, A
10	777.6	32.8	1000	US-11-266-748A-287544	Sequence 287544, A
11	777.6	32.8	1000	US-11-266-748A-338973	Sequence 338973, A
12	777.6	32.8	1000	US-11-266-748A-398267	Sequence 398267, A
13	777.6	32.8	1000	US-11-266-748A-469313	Sequence 469313, A
14	773.4	32.6	1000	US-11-266-748A-29783	Sequence 29783, A
15	594.8	25.1	631	US-11-266-748A-17558	Sequence 17558, A
16	481.8	20.3	674	US-11-266-748A-219905	Sequence 219905, A
17	418.6	17.6	75976	US-10-539-228-239	Sequence 228, App
18	226.2	9.5	68689	US-11-266-748A-23956	Sequence 23956, A
19	226.2	9.5	28454	US-10-540-898-951	Sequence 951, App
20	226.2	9.5	180227	US-10-539-228-308	Sequence 308, App
21	226	9.5	267156	US-11-266-748A-32012	Sequence 32012, A
22	226	9.5	684973	US-11-266-748A-32013	Sequence 32013, A
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24	225.2	9.5	30328	US-11-266-748A-25024	Sequence 25024, A

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26	222.2	9.4	126755	8	US-11-266-748A-58550	Sequence 58550, A
27	221.4	9.3	100445	6	US-10-539-228-170	Sequence 170, App
28	221.4	9.3	254396	6	US-10-540-898-534	Sequence 534, App
29	221	9.3	118456	8	US-11-266-748A-58957	Sequence 58957, A
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31	220.6	9.3	155379	8	US-11-266-748A-59410	Sequence 59410, A
32	220.6	9.3	155379	8	US-11-266-748A-59410	Sequence 59410, A
33	220.4	9.3	242825	8	US-11-266-748A-32745	Sequence 32745, A
34	220.4	9.3	355211	6	US-10-540-898-242	Sequence 242, App
35	220.4	9.3	390183	6	US-10-540-898-937	Sequence 937, App
36	220.2	9.3	148828	8	US-11-266-748A-24893	Sequence 24893, A
37	219.8	9.3	109681	6	US-10-540-898-795	Sequence 795, App
38	219.8	9.3	113456	8	US-11-266-748A-58942	Sequence 58942, A
39	219.8	9.3	201239	8	US-11-266-748A-22854	Sequence 22854, A
40	219.8	9.3	394191	6	US-10-506-549-3	Sequence 3, App1
41	219.6	9.3	9730	6	US-10-501-834-219	Sequence 219, App
42	219.6	9.3	11102	8	US-11-266-748A-33590	Sequence 33590, A
43	219.6	9.3	11283	8	US-11-266-748A-30885	Sequence 30885, A
44	219.6	9.3	99291	6	US-10-539-228-744	Sequence 744, App
45	219.6	9.3	150000	8	US-11-266-748A-23591	Sequence 23591, A

ALIGNMENTS

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RESULT 1
US-10-511-937-615
; Sequence 615, Application US/10511937
; Publication No. US20060088361
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511, 937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/131, 831
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 10/325, 899
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 615
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-615
Query Match      100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GCACCGCGCGAGCTTGCTTGCGGGGCTGTGTGCGCCCTGTGTGCGAAAGATGGA 60
      1 GCACCGCGCGAGCTTGCTTGCGGGGCTGTGTGCGCCCTGTGTGCGAAAGATGGA 60
Db      1 GCACCGCGCGAGCTTGCTTGCGGGGCTGTGTGCGCCCTGTGTGCGAAAGATGGA 60
QY      61 GCAAGAGCCGAGCCGAGGGGGCGCGCCGACCCCTTGACCGAGATCTGCTGCTTTCG 120
      61 GCAAGAGCCGAGCCGAGGGGGCGCGCCGACCCCTTGACCGAGATCTGCTGCTTTCG 120
Db      61 GCAAGAGCCGAGCCGAGGGGGCGCGCCGACCCCTTGACCGAGATCTGCTGCTTTCG 120
QY      121 CAGCAGGAGGACGCTCCCTCCCGGATTAGTGGTACGAGCGCCAGTGGCCGCGCGCG 180
      121 CAGCAGGAGGACGCTCCCTCCCGGATTAGTGGTACGAGCGCCAGTGGCCGCGCGCG 180
Db      121 CAGCAGGAGGACGCTCCCTCCCGGATTAGTGGTACGAGCGCCAGTGGCCGCGCGCG 180
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QY	1261	CAKATTCGACACAGATGTTGGGCCCTTGTGTGAATATGGCTTCTCTGAAGATTAAGGGAAAG	1320
Db	1261	CACATTCACACAGATGTTGGGCCCTTGTGTGAATATGGCTTCTCTGAAGATTAAGGGAAAG	1320
QY	1321	ATTAAGGGGAAAATCTCTGAGAAAGCCAAACTGGAATACTCAACAAGCTGAAGAGGCT	1380
Db	1321	ATTAAGGGGAAAATCTCTGAGAAAGCCAAACTGGAATACTCAACAAGCTGAAGAGGCT	1380
QY	1381	TTGATGTTCTCGATTGTGTAATAAAACCTATATGTGAATGATTCACAGAGCTCATGTGTGAGG	1440
Db	1381	TTGATGTTCTCGATTGTGTAATAAAACCTATATGTGAATGATTCACAGAGCTCATGTGTGAGG	1440
QY	1441	AAATATGATGATTAATTAATACACAGCTTCACAAATCACAGAAAGTGAAGACTATATTCACG	1500
Db	1441	AAATATGATGATTAATTAATACACAGCTTCACAAATCACAGAAAGTGAAGACTATATTCACG	1500
QY	1501	CATCAACTCTTAGTAGCATTAATTAATAGCAGCCAAAGATGTGAAGAATTGTAAGAGG	1560
Db	1501	CATCAACTCTTAGTAGCATTAATTAATAGCAGCCAAAGATGTGAAGAATTGTAAGAGG	1560
QY	1561	AAGAAACCCAGACAAAGAAAGAGTGTGAATCTAGTTTGCCCTTAATGCAATGAAAC	1620
Db	1561	AAGAAACCCAGACAAAGAAAGAGTGTGAATCTAGTTTGCCCTTAATGCAATGAAAC	1620
QY	1621	CTTGTTGATTTGTTCAGAGCTGCACCTTAATAATGTTGCATTTGTCCATGCGCAAAACAGAC	1680
Db	1621	CTTGTTGATTTGTTCAGAGCTGCACCTTAATAATGTTGCATTTGTCCATGCGCAAAACAGAC	1680
QY	1681	ATCTTATGAGCTGCTTTAATCATGTCCAAAGAAAGCTTAAGAAAGAAATPAGCCCTGCCAG	1740
Db	1681	ATCTTATGAGCTGCTTTAATCATGTCCAAAGAAAGCTTAAGAAAGAAATPAGCCCTGCCAG	1740
QY	1741	TATGTAGACAAACAATTCAAATGATGTGTAACTTAATTTCCCTAGTTGACCTGTCTAT	1800
Db	1741	TATGTAGACAAACAATTCAAATGATGTGTAACTTAATTTCCCTAGTTGACCTGTCTAT	1800
QY	1801	AAGAGAAATTAATATTTCTTAACCTATATPAAACCTTAGAATTTAGCAACCTGAATTTAT	1860
Db	1801	AAGAGAAATTAATATTTCTTAACCTATATPAAACCTTAGAATTTAGCAACCTGAATTTAT	1860
QY	1861	CACATATATCAAAGTGAAGAAAATGCTCAATTCACATAGATTTCTTCTCTTAGTATAT	1920
Db	1861	CACATATATCAAAGTGAAGAAAATGCTCAATTCACATAGATTTCTTCTCTTAGTATAT	1920
QY	1921	TGACCTACTTTGTGTAGTGAATAGTGAATCTTAATTAATTTGACTTGAATATGAGCT	1980
Db	1921	TGACCTACTTTGTGTAGTGAATAGTGAATCTTAATTAATTTGACTTGAATATGAGCT	1980
QY	1981	CATCCTTTACACCACTCTTAATTTTAATTAATTTCTATCTGTCTTAATAGAGATGAC	2040
Db	1981	CATCCTTTACACCACTCTTAATTTTAATTAATTTCTATCTGTCTTAATAGAGATGAC	2040
QY	2041	TTGGTTTTTTTTTCTTAATATGATATATGATATGATTAATGATCTTAATATTTTTTTTG	2100
Db	2041	TTGGTTTTTTTTTCTTAATATGATATATGATATGATTAATGATCTTAATATTTTTTTTG	2100
QY	2101	AGACCGAGTCTTGCTCTGTGTACCAAGCTGAGTGCAGTGTGATCTTGGCTCACTGCA	2160
Db	2101	AGACCGAGTCTTGCTCTGTGTACCAAGCTGAGTGCAGTGTGATCTTGGCTCACTGCA	2160
QY	2161	AGCTCTGCCCCCGGGGTGCAACATTTCTGTGCTCAACCTCCCAATTAGCTTGGCC	2220
Db	2161	AGCTCTGCCCCCGGGGTGCAACATTTCTGTGCTCAACCTCCCAATTAGCTTGGCC	2220
QY	2221	TACATGATCTTGCCCAACAACCTGGCTAATTTTTTGTACTTTTATGTAGAGCAAGGTTTC	2280
Db	2221	TACATGATCTTGCCCAACAACCTGGCTAATTTTTTGTACTTTTATGTAGAGCAAGGTTTC	2280
QY	2281	ACCGTGTAGCCAGAGATGATCTGCATCTCTGACCTCGTGTATGCGCCCACTCGGCTCC	2340
Db	2281	ACCGTGTAGCCAGAGATGATCTGCATCTCTGACCTCGTGTATGCGCCCACTCGGCTCC	2340
QY	2341	CAAACTGCTGGATTTACAGGATGAGCCACCG	2372

Db 2341 CAAAGTGGGATTACAGGCATGAGCCACCG 2372

RESULT 2
US-11-266-748A-23848

Sequence 23848, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptional Microarray Technology and

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR FILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: PatentIn version 3.3

SEQ ID NO 23848

LENGTH: 34088

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (787)..(787)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (820)..(832)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (834)..(840)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (851)..(851)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (861)..(877)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (921)..(928)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (921)..(928)

LOCATION: (937)..(960)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (967)..(970)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (981)..(981)

OTHER INFORMATION: n is a, c, g, or t

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NAME/KEY: misc_feature

LOCATION: (1027)..(1028)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1052)..(1077)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1075)..(1087)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1085)..(1093)

OTHER INFORMATION: n is a, c, g, or t

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1190)..(1198)

OTHER INFORMATION: n is a, c, g, or t

US-11-266-748A-23848

Query Match 41.5%; Score 984.4; DB 8; Length 34088;

Best Local Similarity 99.0%; Pred. No. 1.4e-165;

Matches 1022; Conservative 0; Mismatches 6; Indels 4; Gaps 3;

QY 1200 ATTTCCTAGCTGATGATTTGGAATGCACTTCAGCAATGAAATGAAATCCCTCCCTTCCA 1259

Db 33059 ATTTCATGAAAGACTATTTGGAATGCACTTCAGCAATGAAATGAAATCCCTCCCTTCCA 33118

QY 1260 TCACATTCGCAAGAGTGTGGCCCTTCGTGGAATTTGGCTTCCTGAAGATTAAGGANA 1319

Db 33119 TCACATTCGCAAGAGTGTGGCCCTTCGTGGAATTTGGCTTCCTGAAGATTAAGGANA 33178

QY 1320 GATAAAGGGGAAATCTGAGAAAGCCAACTGAAAACTCAACAAGCTGAGAGGCG 1379

Db 33179 GATAAAGGGGAAATCTGAGAAAGCCAACTGAAAACTCAACAAGCTGAGAGGCG 33238

QY 1380 TTTGATGTTCTGATTTGTAATAAACTATAGTAATGATTCAGAGATCATGTGTTGAG 1439

Db 33239 TTTGATGTTCTGATTTGTAATAAACTATAGTAATGATTCAGAGATCATGTGTTGAG 33298

QY 1440 GAAATGATGATTAATAATTAACAAGCTTCACATGACAGAAAGTGAAGACTATTTCTGAG 1499

Db 33299 GAAATGATGATTAATAATTAACAAGCTTCACATGACAGAAAGTGAAGACTATTTCTGAG 33358

QY 1500 CCATCACTTCTAGTAGCATTATTTATAGACGCCAAGAGATGTAAGAGTTTGAAGG 1559

Db 33359 CCATCACTTCTAGTAGCATTATTTATAGACGCCAAGAGATGTAAGAGTTTGAAGG 33418

QY 1560 GAAAGAAACCAAGACAAAGAAAGAGGTGGAATTTAGTTGCCCTTTATGCTTGA 1619

Db 33419 GAAAGAAACCAAGACAAAGAAAGAGGTGGAATTTAGTTGCCCTTTATGCTTGA 33478

QY 1620 CTTGTGTGATTTGTCAGAGTGCACCTTAATAATGTTGATTCATGTCAGCAAAACAGGA 1679

Db 33479 CTTGTGTGATTTGTCAGAGTGCACCTTAATAATGTTGATTCATGTCAGCAAAACAGGA 33538

QY 1680 CATCTTATGCGCTGCTTTACATGTGCAAAAGAGCTAAAGAAAGAAATTAAGCCCTGCCA 1739

Db 33539 CATCTTATGCGCTGCTTTACATGTGCAAAAGAGCTAAAGAAAGAAATTAAGCCCTGCCA 33598

QY 1740 GTATGTAGCAACAACCAATTAATGATTTGTGTAATTTTCCCTAGTGAACCTGTCTA 1799

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Db 33599 GTATGTAGACACCAATTCATTAATGATGTGCTAACTTAATTTCCCTAGTGAACCTGTCTA 33658
Qy 1800 TAAAGAAATTAATATTTCTTACATATATTAACCTAGGAATTTAGAACACGGAATTTAT 1859
Db 33659 TAAAGAAATTAATATTTCTTACATATATTAACCTAGGAATTTAGAACACGGAATTTAT 33718
Qy 1860 TCACATATATCAAAAGTGAAGAAAATGCTCAATTCACATAGATTTCTCTTTAGTATTA 1919
Db 33719 TCACATATATCAAAAGTGAAGAAAATGCTCAATTCACATAGATTTCTCTTTAGTATTA 33778
Qy 1920 TTGACCTTACTTTGGTAGTGAATAGTGAATCTTATCTAATTTGACTTGAATATGTAAC 1979
Db 33779 TTGACCTTACTTTGGTAGTGAATAGTGAATCTTATCTAATTTGACTTGAATATGTAAC 33838
Qy 1980 TCATCTCTTACACCAACCTCCATTTTAAATTTTCACTCTGCTTAAATGAGAACTA 2039
Db 33839 TCATCTCTTACACCAACCTCCATTTTAAATTTTCACTCTGCTTAAATGAGAACTA 33898
Qy 2040 CTTGG-TTTTTTTTTTCTTAATATATGATATGACATTTAAATGTAATTTATTTT 2098
Db 33899 CTTGGTTTTTTTTTTCTTAATATATGATATGACATTTAAATGTAATTTATTTT 33958
Qy 2099 TGAACCGAGTCTTGCTCTGTTTACCAGGCTGGAAGTGAAGTGG-GTGATCTTGCTCACT 2157
Db 33959 TGAACCGAGTCTTGCTCTGTTTACCAGGCTGGAAGTGAAGTGGCGTGAATCTTGCTCACT 34018
Qy 2158 GCAAGCTTGCTCCCTCCCGGCTTGCCACCATTCCTCCCTCAAGCTCCCAATTAAGCTTG 2217
Db 34019 GCAAGCTTGCTCC-TCGCCGGGTTGCAACCATTTCTCTGCTCAAGCTCCCAATTAAGCTTG 34076
Qy 2218 GCTTACAGTCAT 2229
Db 34077 GCTTACAGTCAT 34088

RESULT 3
US-11-266-748A-114799
; Sequence 114799, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; APPLICANT: Johnston, Patrick
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 114799
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-114799

Query Match 40.6%; Score 962.4; DB 8; Length 1000;
Best Local Similarity 99.5%; Pred. No. 9.1e-162;
Matches 997; Conservative 0; Mismatches 1; Indels 4; Gaps 3;
Qy 1230 TCATGCAATGAATGATCCGCCCTTCATCACTTGAACAAGATGTTGGGCGCTTCTGT 1289
Db 1 TCATGCAATGAATGATCCGCCCTTCATCACTTGAACAAGATGTTGGGCGCTTCTGT 60
Qy 1290 GAGAAATGGCTTCTGGAAGATTAAGGAAAGATTAAGGGGAAATCTGTGAAAGCCAAA 1349
Db 61 GAGAAATGGCTTCTGGAAGATTAAGGAAAGATTAAGGGGAAATCTGTGAAAGCCAAA 120
Qy 1350 CTGAAAATCTACACAAGCTGAAAGAGCGCTTGAATGTTCTGTGATTTGTAATAAACTATA 1409
Db 121 CTGAAAATCTACACAAGCTGAAAGAGCGCTTGAATGTTCTGTGATTTGTAATAAACTATA 180
Qy 1410 GTGAATGATTCAGAGGTACATGCTTGAAGGAAATGATGTAATAATTAACAAGCTTCA 1469
Db 181 GTGAATGATTCAGAGGTACATGCTTGAAGGAAATGATGTAATAATTAACAAGCTTCA 240
Qy 1470 CAATCACAAGAAAGTGAAGACTATTTCTCAGCATCACTTCTAGTACATTTATTAAGC 1529
Db 241 CAATCACAAGAAAGTGAAGACTATTTCTCAGCATCACTTCTAGTACATTTATTAAGC 300
Qy 1530 AGCCAAGAGATGTAAGAGTTGAAAGGGAAGAAACCCAGACAAAGAAAGAGATGTG 1589
Db 301 AGCCAAGAGATGTAAGAGTTGAAAGGGAAGAAACCCAGACAAAGAAAGAGATGTG 360
Qy 1590 GAATCTGTTGGCCCTTAATAGCAATGAACTGTGAGATTTGTCAAGGTGCACTTAA 1649
Db 361 GAATCTGTTGGCCCTTAATAGCAATGAACTGTGAGATTTGTCAAGGTGCACTTAA 420
Qy 1650 AATGTTGCTATTTGTCATAGGCAAAACAGACATCTTAATGCGCTCTTACATGTGCAAG 1709
Db 421 AATGTTGCTATTTGTCATAGGCAAAACAGACATCTTAATGCGCTCTTACATGTGCAAG 480
Qy 1710 AAGCTAAAGAAAGAAATTAAGCCCTGCCAGATATGAGACAACTTAATGATGTTG 1769
Db 481 AAGCTAAAGAAAGAAATTAAGCCCTGCCAGATATGAGACAACTTAATGATGTTG 540
Qy 1770 CTAATTAATTTCCCTAGTTGACCTGCTATTAAGAAATTAATTAATTTCTAATATATA 1829
Db 541 CTAATTAATTTCCCTAGTTGACCTGCTATTAAGAAATTAATTAATTTCTAATATATA 600
Qy 1830 CCTTAGAATTTAGACAACTGAAATTTATTCATATATCAATATCAAAAGTGAAGAAATGCC 1889
Db 601 CCTTAGAATTTAGACAACTGAAATTTATTCATATATCAATATCAAAAGTGAAGAAATGCC 660
Qy 1890 ATTCAATAGATTTCTCTTTAGATATTAATGACTTAATGCTTGGTAGTGAATGTGAAT 1949
Db 661 ATTCAATAGATTTCTCTTTAGATATTAATGACTTAATGCTTGGTAGTGAATGTGAAT 720
Qy 1950 ACTTACTATTAATTTGACTTGAATATGTCATCCCTTTACACCAACCTTAATTTTAA 2009
Db 721 ACTTACTATTAATTTGACTTGAATATGTCATCCCTTTACACCAACCTTAATTTTAA 780
Qy 2010 TAATTTACTCTGCTTAAATGAGAACTACTGG-TTTTTTTTTTCTTAATATATATA 2068
Db 781 TAATTTACTCTGCTTAAATGAGAACTACTGGTTTTTTTTTTCTTAATATATATA 840
Qy 2069 TGACATTTAAATGTAATTAATTTTGTGAGACGAGTCTGCTGTATCCAGGC 2128
Db 841 TGACATTTAAATGTAATTAATTTTGTGAGACGAGTCTGCTGTATCCAGGC 900
Qy 2129 TGAAGTGAAGTGG-GTGATCTTGGCTGACTGAACTTGCCTCCCGGGTTGCAACA 2187
Db 901 TGAAGTGAAGTGGCTGATCTTGGCTGACTGAACTTGCCTCCCGGGTTGCAACA 958
Qy 2188 TTCTCCTGCTCAGGCTCCCAATTTAGCTTGCGCTACAGTCAT 2229
Db 959 TTCTCCTGCTCAGGCTCCCAATTTAGCTTGCGCTACAGTCAT 1000

	RESULT 4	
US-11-266-748A-119930/C		
/ Sequence 119930, Application US/11266748A		
/ Publication No. US2006013463A1		
/ GENERAL INFORMATION:		
/ APPLICANT: Harkin, Paul		
/ APPLICANT: Johnston, Patrick		
/ APPLICANT: Mulligan, Karl		
/ TITLE OF INVENTION: Transcription Microarray Technology and		
/ TITLE OF INVENTION: Methods of Using the Same		
/ FILE REFERENCE: 55815-0102 (319189)		
/ CURRENT APPLICATION NUMBER: US/11/266,748A		
/ CURRENT FILING DATE: 2005-11-03		
/ PRIOR APPLICATION NUMBER: EP 04105479.2		
/ PRIOR FILING DATE: 2004-11-03		
/ PRIOR APPLICATION NUMBER: EP 04105482.6		
/ PRIOR FILING DATE: 2004-11-03		
/ PRIOR APPLICATION NUMBER: EP 04105483.4		
/ PRIOR FILING DATE: 2004-11-03		
/ PRIOR APPLICATION NUMBER: EP 04105507.0		
/ PRIOR FILING DATE: 2004-11-03		
/ PRIOR APPLICATION NUMBER: EP 04105485.9		
/ PRIOR FILING DATE: 2004-11-03		
/ PRIOR APPLICATION NUMBER: EP 04105484.2		
/ PRIOR FILING DATE: 2004-11-03		
/ PRIOR APPLICATION NUMBER: US 60/662,276		
/ PRIOR FILING DATE: 2005-03-14		
/ PRIOR APPLICATION NUMBER: US 60/700,293		
/ PRIOR FILING DATE: 2005-07-18		
/ NUMBER OF SEQ ID NOS: 483996		
/ SOFTWARE: PatentIn version 3.3		
/ SEQ ID NO 119930		
/ LENGTH: 1000		
/ TYPE: DNA		
/ ORGANISM: Homo Sapiens		
US-11-266-748A-119930		
Query Match	40.6%; Score 962.4; DB 8; Length 1000;	
Best Local Similarity	99.5%; Pred. No. 9.1e-162;	
Matches	997; Conservative	0; Mismatches
		1; Indels
		4; Gaps
		3
OY	1230 TCATGCAATGAATGAATCCCTTCCTCATCATTGCCACAGATGTGGCCCTTGGT	1288
Db	1000 TCATGCATGAATGAATATCCCCCTTCATCATCTTGAAAGATGTGGCCCTTGGT	941
OY	1290 GAGAAATGGCTTCTCGAAGATTAAGGAAAAGATAAGGGAATCTTCGAGAAGCCAAA	1344
Db	940 GAGAAATGGCTTCTCGAAGATTAAGGAAAAGATAAGGGAATCTTCGAGAAGCCAAA	881
OY	1350 CTGAAAACTCAACAAGCTGGAAGAAGGGCTTTGATGTTCCGATGTGTAATAAACTATA	1405
Db	880 CTGAAAACTCAACAAGCTGGAAGAAGGGCTTTGATGTTCCGATGTGTAATAAACTATA	821
OY	1410 GTGAATGATTCAGAGAGTCATGTGTGTAAGAAAATGATGATTAATTAACAACAACCTCA	1465
Db	820 GTGAATGATTCAGAGAGTCATGTGTGTAAGAAAATGATGATTAATTAACAACAACCTCA	761
OY	1470 CAATCACAGAAGAGGAAGACTATTTCTCAGCCATCACTTCTTAGTAGCATTTATTAAGC	1522
Db	760 CAATCACAGAAGAGGAAGACTATTTCTCAGCCATCACTTCTTAGTAGCATTTATTAAGC	701
OY	1530 AGCCAAGAAGATGTGAAGAAGTTTGAAGAAGGAAGAACCCCAAGACAAAGAAGAGAGTGTG	1589
Db	700 AGCCAAGAAGATGTGAAGAAGTTTGAAGAAGGAAGAACCCCAAGACAAAGAAGAGAGTGTG	641
OY	1590 GAATCTAGTTGGCCCTTAATGCCATTGAACCTTGTGTGATTTGTCAAAGTGCACCTAAA	1644
Db	640 GAATCTAGTTGGCCCTTAATGCCATTGAACCTTGTGTGATTTGTCAAAGTGCACCTAAA	581
OY	1650 AATGGTTCATTTGTCATGAGCAAAACAGACACTTATAGGCTGCTTATCATATGTCGAAG	1705
Db	580 AATGGTTCATTTGTCATGAGCAAAACAGACACTTATAGGCTGCTTATCATATGTCGAAG	521

QY	1710	AAGCTAAAGAAAGAGATTAAGCCCTGCCAGTAGTGTGCAACAATTCAATGATGTG	1768
Db	520	AAGCTAAAGAAAGAAATTAAGCCCTGCCAGTAGTGTGCAACAACAATTCAATGATGTG	461
QY	1770	CTAAGCTAATTTCCCTAGTGAACCTGCTATTAAGATATTAATATTCTTAATATTA	1829
Db	460	CTAAGCTAATTTCCCTAGTGAACCTGCTATTAAGATATTAATATTCTTAAGTATTA	401
QY	1830	CCCTAGGAATTTAGACAACCTGAATTTATTCATATATCAATTAAGTGAAGAAATGCCCTCA	1889
Db	400	CCCTAGGAATTTAGACAACCTGAATTTATTCATATATCAATTAAGTGAAGAAATGCCCTCA	341
QY	1890	ATTGACATGATTTCTTCTCTTTAGTATTAATGACCTAATTGGTAGTGAATGTGAT	1949
Db	340	ATTGACATGATTTCTTCTCTTTAGTATTAATGACCTAATTGGTAGTGAATGTGAT	281
QY	1950	ACTTACATATAATTGACTGGAATATGTAAGTCATCCCTTACACAACCTCCCAATTTTAA	2009
Db	280	ACTTACATATAATTGACTGGAATATGTAAGTCATCCCTTACACAACCTCCCAATTTTAA	221
QY	2010	TAATTTCTACCTGTCTTAATAATGAGAAGTCTGG--TTTTTTTTCTTAATAATGATA	2068
Db	220	TAATTTCTACCTGTCTTAATAATGAGAAGTCTGGTTTTTTTTCTTAATAATGATA	161
QY	2069	TGACATTTAAATGTACTTATTTATTTTTTTGAGACCGAGTCTGTCTCTGTTAACCGAGC	2128
Db	160	TGACATTTAAATGTACTTATTTATTTTTTTGAGACCGAGTCTGTCTCTGTTAACCGAGC	101
QY	2129	TGAGTGTGAGTGG--GTGATCTTGGCTCATCTGCANAGCTCTGCCCTCCCGGAGTTGCACCA	2187
Db	100	TGAGTGTGAGTGGGCGTATCTTGGCTCATCTGCACAGCTCTGCC--TCCCGGAGTTGCACCA	43
QY	2188	TTTCCTCGCTCAGAGCTCCCAATTAGAGCTGGCCCAAGTAT	2229
Db	42	TTTCCTCGCTCAGAGCTCCCAATTAGAGCTGGCCCAAGTAT	1

RESULT 5
US-11-266-748A-281679
Sequence 281679, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Hartson, Paul
APPLICANT: Jackson, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266, 748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,216
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 281679
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-281679

Query Match 40.6%; Score 962.4; DB 8; Length 1000;
Best Local Similarity 99.5%; Pred. No. 9.1e-162;
Matches 997; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

QY 1230 TCATGCAATGAATGAATCCCTTCATCATCTGCAAGATGTTGGCCCTTCGT 1289
DB 1 TCATGCAATGAATGAATCCCTTCATCATCTGCAAGATGTTGGCCCTTCGT 60

QY 1290 GAGAAATGGCTTCTGAAAGATTAAGGGAATTAAGGGGAATCTCTGAGAAAGCCCAA 1349
DB 61 GAGAAATGGCTTCTGAAAGATTAAGGGAATTAAGGGGAATCTCTGAGAAAGCCCAA 120

QY 1350 CTGGAATACTCAACAAGCTGGAAGAGGCTTTGATGTTCTGATTTGAAAAAACTATA 1409
DB 121 CTGGAATACTCAACAAGCTGGAAGAGGCTTTGATGTTCTGATTTGAAAAAACTATA 180

QY 1410 GTGAATGATTCAGAGATCATGTGTTGAGAAAAATGATTAATAATCAACAAGCTTCA 1469
DB 181 GTGAATGATTCAGAGATCATGTGTTGAGAAAAATGATTAATAATCAACAAGCTTCA 240

QY 1470 CAATCAACAAGAAAGTGAAGACTATTTCTGAGCATCACTTCTGATGATTAATTAATGC 1529
DB 241 CAATCAACAAGAAAGTGAAGACTATTTCTGAGCATCACTTCTGATGATTAATTAATGC 300

QY 1530 AGCCAAGAAAGTGAAGAGTGTGAAAGGGAAGAAACCAAGCAAGAAAGAGAGTGTG 1589
DB 301 AGCCAAGAAAGTGAAGAGTGTGAAAGGGAAGAAACCAAGCAAGAAAGAGAGTGTG 360

QY 1590 GAATCTAGTTGGCCCTTAATGCCATGAACTTGTGATTTGTCAAGGTGCACTTAA 1649
DB 361 GAATCTAGTTGGCCCTTAATGCCATGAACTTGTGATTTGTCAAGGTGCACTTAA 420

QY 1650 AATGTTGCATTTGTCCATGAGCAAAACAGACATCTTAATGAGCTGCTTACATGTCGAAG 1709
DB 421 AATGTTGCATTTGTCCATGAGCAAAACAGACATCTTAATGAGCTGCTGCTTACATGTCGAAG 480

QY 1710 AAGCTTAAGAAAGAAATGAAGCCCTGCCAGATGTAGACAACCAATCAATGATTTGTG 1769
DB 481 AAGCTTAAGAAAGAAATGAAGCCCTGCCAGATGTAGACAACCAATCAATGATTTGTG 540

QY 1770 CTAACTTAATTTCCCTAGTGAAGCTGTCTATTAAGAAATTAATTAATTTCTAATATTA 1829
DB 541 CTAACTTAATTTCCCTAGTGAAGCTGTCTATTAAGAAATTAATTAATTTCTAATATTA 600

QY 1830 CCTTAGGAATTTAGCAACCTGGAATTTATTCATATATCAAAAGTGAAGAAATGCCCA 1889
DB 601 CCTTAGGAATTTAGCAACCTGGAATTTATTCATATATCAAAAGTGAAGAAATGCCCA 660

QY 1890 ATTCAATAGATTTCTCTCTTAATTAATGAAGCTGCTGATGATGATGATGAT 1949
DB 661 ATTCAATAGATTTCTCTCTTAATTAATGAAGCTGCTGATGATGATGATGATGAT 720

QY 1950 ACTTACTAATTTGACTGGAATATGAGCTCATCTTTACACCAACTCTAATTTTAA 2009
DB 721 ACTTACTAATTTGACTGGAATATGAGCTCATCTTTACACCAACTCTAATTTTAA 780

QY 2010 TAATTTCTACTGCTTCTTAATGAGAAGTCTTG- TTTTCTTTTCTTAATATATGATA 2068
DB 781 TAATTTCTACTGCTTCTTAATGAGAAGTCTTG- TTTTCTTTTCTTAATATATGATA 840

QY 2069 TGACATTAATTAATTAATTAATTTTGTGAGACCGAGCTGCTGCTGATACCAAGGC 2128
DB 841 TGACATTAATTAATTAATTAATTTTGTGAGACCGAGCTGCTGCTGATACCAAGGC 900

QY 2129 TGAAGTGAAGTGG- GTGATCTTGAGCTCACTGCAAGCTGCTCCCTCCGGGTGCAACA 2187
DB 901 TGAAGTGAAGTGGCGGTGATCTTGAGCTCACTGCAAGCTGCTCC- TCCGGGTGCAACA 958

QY 2188 TTCTCTGCTGAGCTTCCCAATTAAGCTTGGCTTACAGTCAT 2229
DB 959 TTCTCTGCTGAGCTTCCCAATTAAGCTTGGCTTACAGTCAT 1000

RESULT 6
US-11-266-748A-308319/c
; Sequence 308319, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: US/11/266, 748A
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 308319
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-308319

Query Match 40.6%; Score 962.4; DB 8; Length 1000;
Best Local Similarity 99.5%; Pred. No. 9.1e-162;
Matches 997; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

QY 1230 TCATGCAATGAATGAATCCCTTCATCATCTGCAAGATGTTGGCCCTTCGT 1289
DB 1000 TCATGCAATGAATGAATCCCTTCATCATCTGCAAGATGTTGGCCCTTCGT 941

QY 1290 GAGAAATGGCTTCTGAAAGATTAAGGGAATTAAGGGGAATCTCTGAGAAAGCCCAA 1349
DB 940 GAGAAATGGCTTCTGAAAGATTAAGGGAATTAAGGGGAATCTCTGAGAAAGCCCAA 881

QY 1350 CTGGAATACTCAACAAGCTGGAAGAGGCTTTGATGTTCTGATTTGAAAAAACTATA 1409
DB 880 CTGGAATACTCAACAAGCTGGAAGAGGCTTTGATGTTCTGATTTGAAAAAACTATA 821

QY 1410 GTGAATGATTCAGAGATCATGTGTTGAGAAAAATGATTAATAATCAACAAGCTTCA 1469
DB 820 GTGAATGATTCAGAGATCATGTGTTGAGAAAAATGATTAATAATCAACAAGCTTCA 761

QY 1470 CAATCAACAAGAAAGTGAAGACTATTTCTGAGCATCACTTCTGATGATTAATTAATGC 1529
DB 760 CAATCAACAAGAAAGTGAAGACTATTTCTGAGCATCACTTCTGATGATTAATTAATGC 701

QY 1530 AGCCAAGAAAGTGAAGAGTGTGAAAGGGAAGAAACCAAGCAAGAAAGAGAGTGTG 1589
DB 700 AGCCAAGAAAGTGAAGAGTGTGAAAGGGAAGAAACCAAGCAAGAAAGAGAGTGTG 641

QY 1590 GAATCTAGTTGGCCCTTAATGCCATGAACTTGTGATTTGTCAAGGTGCACTTAA 1649
DB 640 GAATCTAGTTGGCCCTTAATGCCATGAACTTGTGATTTGTCAAGGTGCACTTAA 581

QY 1650 AATGTTGCATTTGTCCATGAGCAAAACAGACATCTTAATGAGCTGCTTACATGTCGAAG 1709
DB 580 AATGTTGCATTTGTCCATGAGCAAAACAGACATCTTAATGAGCTGCTTACATGTCGAAG 521

QY 1710 AAGCTAAAGAAAGAAATAGCCCTGCGCAGATATGAGCAACCAATTCAAATGATTG 1769
DB 520 AAGCTAAAGAAAGAAATAGCCCTGCGCAGATATGAGCAACCAATTCAAATGATTG 461
QY 1770 CTAACTTATTTCCCTAGTTGACCTGTCTATTAAGAAATTAATTTCTAACTATATA 1829
DB 460 CTAACTTATTTCCCTAGTTGACCTGTCTATTAAGAAATTAATTTCTAACTATATA 401
QY 1830 CCTAGGAATTTAGAACACCTGAATTTATTCATATATCAAAAGGAGAAATGCTCA 1889
DB 400 CCTAGGAATTTAGAACACCTGAATTTATTCATATATCAAAAGGAGAAATGCTCA 341
QY 1890 ATTCAATGATTTCTCTTATGATATGAGCACTTGTGTGTAAGTAAGTAAT 1949
DB 340 ATTCAATGATTTCTCTTATGATATGAGCACTTGTGTGTAAGTAAGTAAT 281
QY 1950 ACTTACTATTAATTTGACTTGAATATGATGATCTCATCTTTTACCAACTCTTAATTTAA 2009
DB 280 ACTTACTATTAATTTGACTTGAATATGATGATCTCATCTTTTACCAACTCTTAATTTAA 221
QY 2010 TAAATTTCTACTCTGTCTTAAATGAGAGTACTTG- TTTTCTTTTCTTAAATATGATA 2068
DB 220 TAAATTTCTACTCTGTCTTAAATGAGAGTACTTG- TTTTCTTTTCTTAAATATGATA 161
QY 2069 TGACATTTAAATGTACTTATTTTGTGAGACCGAGTCTGCTTAAACCAAGC 2128
DB 160 TGACATTTAAATGTACTTATTTTGTGAGACCGAGTCTGCTTAAACCAAGC 101
QY 2129 TGGAGTGCAGTG- GTGATCTTGCTCACTGCAAGCTGCGCTCCCGGTTGCAACA 2187
DB 100 TGGAGTGCAGTGCGGTGATCTTGCTCACTGCAAGCTGCGC- TCCCGGTTGCAACA 43
QY 2188 TTCTCTGCTCAGCTCCCAATTAGCTTGCGCTTACAT 2229
DB 42 TTCTCTGCTCAGCTCCCAATTAGCTTGCGCTTACAT 1

RESULT 7

US-11-266-748A-390721
Sequence 390721, Application US/11266748A
Publication No. US2006013463A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patent version 3.3
SEQ ID NO 390721
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens

US-11-266-748A-390721

Query Match	40.6%;	Score 962.4;	DB 8;	Length 1000;
Best Local Similarity	99.5%;	Pred. No. 9.1e-162;		
Matches 997;	Conservative 0;	Mismatches 1;	Indels 4;	Gaps 3;
QY 1230 TCATGCAATGAATGAATATCCCCCTTCATCATATTCGACAGATGTTGGCCCTTCGT 1289				
DB 1 TCATGCAATGAATGAATATCCCCCTTCATCATATTCGACAGATGTTGGCCCTTCGT 60				
QY 1290 GAGAAATGGCTTCTGAGATTAAGGAAAGTAAAGGGAAATCTCTGAGAAAGCCAA 1349				
DB 61 GAGAAATGGCTTCTGAGATTAAGGAAAGTAAAGGGAAATCTCTGAGAAAGCCAA 120				
QY 1350 CTGGAATACTCAACAGCTGAAGAGGCTTGTATGTTCTGATTTGTAATAAACTATA 1409				
DB 121 CTGGAATACTCAACAGCTGAAGAGGCTTGTATGTTCTGATTTGTAATAAACTATA 180				
QY 1410 GTGAATGATTCAGAGAGTCATGTTGAGAAATGATTAATAACAGAGCTCA 1469				
DB 181 GTGAATGATTCAGAGAGTCATGTTGAGAAATGATTAATAACAGAGCTCA 240				
QY 1470 CAATCAAGAAAGTGAAGATCTATTCAGCATCACTTCTAGTATTAATTAATG 1529				
DB 241 CAATCAAGAAAGTGAAGATCTATTCAGCATCACTTCTAGTATTAATTAATG 300				
QY 1530 AGCCAAAGATGTGAAGATTTGAAGGAAAGCCAAAGCAAGAGAGAGTGTG 1589				
DB 301 AGCCAAAGATGTGAAGATTTGAAGGAAAGCCAAAGCAAGAGAGAGTGTG 360				
QY 1590 GAATGATGTTGGCCCTTAAATGCAATGAACTTGTGATTTGCAAGTGTGACTAA 1649				
DB 361 GAATGATGTTGGCCCTTAAATGCAATGAACTTGTGATTTGCAAGTGTGACTAA 420				
QY 1650 AATGTTGATTTGTCATAGGCAAGACATCTTAATGAGCTGCTTACATGTCGAAG 1709				
DB 421 AATGTTGATTTGTCATAGGCAAGACATCTTAATGAGCTGCTTACATGTCGAAG 480				
QY 1710 AAGCTAAAGAAAGAAATAGCCCTGCGCAGATATGAGCAACCAATTCAAATGATTG 1769				
DB 481 AAGCTAAAGAAAGAAATAGCCCTGCGCAGATATGAGCAACCAATTCAAATGATTG 540				
QY 1770 CTAACTTATTTCCCTAGTTGACCTGTCTATTAAGAAATTAATTTCTAACTATATA 1829				
DB 541 CTAACTTATTTCCCTAGTTGACCTGTCTATTAAGAAATTAATTTCTAACTATATA 600				
QY 1830 CCTAGGAATTTAGAACACCTGAATTTATTCATATATCAAAAGGAGAAATGCTCA 1889				
DB 601 CCTAGGAATTTAGAACACCTGAATTTATTCATATATCAAAAGGAGAAATGCTCA 660				
QY 1890 ATTCAATGATTTCTCTTATGATATGAGCACTTGTGTGTAAGTAAGTAAT 1949				
DB 661 ATTCAATGATTTCTCTTATGATATGAGCACTTGTGTGTAAGTAAGTAAT 720				
QY 1950 ACTTACTATTAATTTGACTTGAATATGATGATCTTTTACCAACTCTTAATTTAA 2009				
DB 721 ACTTACTATTAATTTGACTTGAATATGATGATCTTTTACCAACTCTTAATTTAA 780				
QY 2010 TAAATTTCTACTCTGTCTTAAATGAGAGTACTTG- TTTTCTTTTCTTAAATATGATA 2068				
DB 781 TAAATTTCTACTCTGTCTTAAATGAGAGTACTTG- TTTTCTTTTCTTAAATATGATA 840				
QY 2069 TGACATTTAAATGTAACTTATTTTGTGAGACCAAGCTTGTCTGTAACCAAGC 2128				
DB 841 TGACATTTAAATGTAACTTATTTTGTGAGACCAAGCTTGTCTGTAACCAAGC 900				
QY 2129 TGGAGTGCAGTG- GTGATCTTGCTCACTGCAAGCTTGCCTCCCGGTTGCAACA 2187				
DB 901 TGGAGTGCAGTGCGGTGATCTTGCTCACTGCAAGCTTGCCTCCCGGTTGCAACA 958				
QY 2188 TTCTCTGCTCAGCTCCCAATTAGCTTGCGCTTACAT 2229				
DB 959 TTCTCTGCTCAGCTCCCAATTAGCTTGCGCTTACAT 1000				

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RESULT 8
US-11-266-748A-481439/c
; Sequence 481439, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 481439
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-481439

Query Match      40.6%; Score 962.4; DB 8; Length 1000;
Best Local Similarity 99.5%; Pred. No. 9,1e-162;
Matches 997; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

QY 1230 TCATGCAATGAAGTAATCCCTTCATCATGATGGAACAGATGTTGGCCCTTGGT 1289
DB 1000 TCATGCAATGAAGTAATCCCTTCATCATGATGGAACAGATGTTGGCCCTTGGT 941

QY 1290 GAGAAATGGCTTCTGAAAGATTAAGGAAAGTAAGGGAAATCTCTGAGAAACCAA 1349
DB 940 GAGAAATGGCTTCTGAAAGATTAAGGAAAGTAAGGGAAATCTCTGAGAAACCAA 881

QY 1350 CTGGAAGAACTCAACCAAGCTGAGAGGGCTTGAATGTTCCATGATTTAAAAAACTATA 1409
DB 880 CTGGAAGAACTCAACCAAGCTGAGAGGGCTTGAATGTTCCATGATTTAAAAAACTATA 821

QY 1410 GTGAATGATTCAGAGAGTCATGTGTGAGAAAAATGATTAATAACACAGCTTCA 1469
DB 820 GTGAATGATTCAGAGAGTCATGTGTGAGAAAAATGATTAATAACACAGCTTCA 761

QY 1470 CAATCAAGAAGAGTGAAGACTATTCTAGCCATCACTTCTAGTAGCATTTATTAAGC 1529
DB 760 CAATCAAGAAGAGTGAAGACTATTCTAGCCATCACTTCTAGTAGCATTTATTAAGC 701

QY 1530 AGCCAAAGAGATGTGAAGAGTTTGAAGGGAGAAACCAAGACAAAGAGAGTGTG 1589
DB 700 AGCCAAAGAGATGTGAAGAGTTTGAAGGGAGAAACCAAGACAAAGAGAGTGTG 641

QY 1590 GAATTAATGTTGCCCTTAATGCCATTTGAACCTTGATGATTTGTCAGAGGTGACCTTAA 1649
DB 640 GAATTAATGTTGCCCTTAATGCCATTTGAACCTTGATGATTTGTCAGAGGTGACCTTAA 581

QY 1650 AATGTTGCAATGTCATGAGCAAAACAGACATCTTATGCGCTTTCATGTCAGAAAG 1709
DB 1650 AATGTTGCAATGTCATGAGCAAAACAGACATCTTATGCGCTTTCATGTCAGAAAG 1709
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DB 580 AATGTTGCAATGTCATGAGCAAAACAGACATCTTATGCGCTTTCATGTCAGAAAG 521
QY 1710 AAGCTTAAGAAAAGAAATTAAGCCCTGCCAGTATGAGACAAACCAATTCAAATGATGTG 1769
DB 520 AAGCTTAAGAAAAGAAATTAAGCCCTGCCAGTATGAGACAAACCAATTCAAATGATGTG 461
QY 1770 CTAACTAATTTCCCTTAATGAGACCTGTCTATPAAGAGATTAATATTTCTAACTATATA 1829
DB 460 CTAACTAATTTCCCTTAATGAGACCTGTCTATPAAGAGATTAATATTTCTAACTATATA 401
QY 1830 CCTTAGAATTTAACAACCTGAAATTTATTCATATATCAATAGTAGAAAAAGCCCTCA 1889
DB 400 CCTTAGAATTTAACAACCTGAAATTTATTCATATATCAATAGTAGAAAAAGCCCTCA 341
QY 1890 ATTGACATGATTTCTTCTCTTATGTAATTAATGACCTACTTGTGTAAGTAATGTAAT 1949
DB 340 ATTGACATGATTTCTTCTCTTATGTAATTAATGACCTACTTGTGTAAGTAATGTAAT 281
QY 1950 ACTTACTATATTTGACTTGAATATGAGCTCATCTTTACACCAACTCTTAATTTTAAA 2009
DB 280 ACTTACTATATTTGACTTGAATATGAGCTCATCTTTACACCAACTCTTAATTTTAAA 221
QY 2010 TAAATTTCTACTCTGTCTTAAATGAGAGTACTTGG-TTTTTTTTTCTTAAATATGATA 2068
DB 220 TAAATTTCTACTCTGTCTTAAATGAGAGTACTTGGTTTTTTTTTTTTCTTAAATATGATA 161
QY 2069 TGACATTTAAATGTAATGTAATTTATTTTTTTGAGACGAGCTTGCTGTATACCAAGGC 2128
DB 160 TGACATTTAAATGTAATGTAATTTATTTTTTTGAGACGAGCTTGCTGTATACCAAGGC 101
QY 2129 TGGAGTGCAGTGG-GTGATCTTGGCTCACTGCAAGCTTGCCTCCCGGGTTGACACA 2187
DB 100 TGGAGTGCAGTGGGTATCTTGGCTCACTGCAAGCTTGCCT--TCCGGGGTTGACACA 43
QY 2188 TTCTCTGCTCTCAGCCTTCCCAATTAAGCTTGCCCTCAAGTCAT 2229
DB 42 TTCTCTGCTCTCAGCCTTCCCAATTAAGCTTGCCCTCAAGTCAT 1

RESULT 9
US-11-266-748A-221947
; Sequence 221947, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 221947
; LENGTH: 1000
; TYPE: DNA
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Db      781  GCTCACTCAAGCTCTGCC--TCCCGGGTCCGACCACTTCCTCCAGCCTCCCAAT 838
Qy      2211 TAGCTTGCCCTACAGTCACTGTCGCCACCACTGGCTAATTTTGTACTTTAGTAG 2270
Db      839  TAGCTTGCCCTACAGTCACTGTCGCCACCACTGGCTAATTTTGTACTTTAGTAG 898
Qy      2271 ACAGGTTTCAACCGTGTAGCCAGAGATGTCGTCTGATCTCTGACCTCGTATCCGCCAC 2330
Db      899  ACAGGTTTCAACCGTGTAGCCAGAGATGTCGTCTGATCTCTGACCTCGTATCCGCCAC 958
Qy      2331 CTCGGCTTCCCAAGTGTGGGATTCACAGCATGAGCCACCG 2372
Db      959  CTCGGCTTCCCAAGTGTGGGATTCACAGCATGAGCCACCG 1000
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RESULT 11
US-11-266-748A-338973/c

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/ Sequence 338973, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcription Microarray Technology and
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ CURRENT FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 338973
/ LENGTH: 1000
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
US-11-266-748A-338973
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Query Match 32.8%; Score 777.6; DB 8; Length 1000;
Best Local Similarity 99.0%; Pred. No. 4.9e-129;
Matches 814; Conservative 0; Mismatches 4; Indels 4; Gaps 3;

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Qy      1553 TGAAGGGAAGAAACCAAGAAAGAGAGTGTGATCTAGTTGCCCTTAATTC 1612
Db      820  TGAGACAGAGAAACCAAGAAAGAGAGTGTGATCTAGTTGCCCTTAATTC 761
Qy      1613 CATTAACCTTGTGATTTGTCAAGGTGACCTTAATAATGTGATTCATGGCA 1672
Db      760  CATTAACCTTGTGATTTGTCAAGGTGACCTTAATAATGTGATTCATGGCA 701
Qy      1673 AACAGACATCTTATGCGCTGTTTACATGTGCAGAAAGAGCTAAAGAAAGATTAAGCC 1732
Db      700  AACAGACATCTTATGCGCTGTTTACATGTGCAGAAAGAGCTAAAGAAAGATTAAGCC 641
Qy      1733 CTGCCAGATGTAGCAACCAATTCATATGTGCTAATTTTCCCTAGTTGAC 1792
Db      640  CTGCCAGATGTAGCAACCAATTCATATGTGCTAATTTTCCCTAGTTGAC 581
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Qy      1793 CTGCTATAGAGAAATATATATTTCTACTATATTAACCTTAGAATTTAGACAACCTGA 1852
Db      580  CTGCTATAGAGAAATATATATTTCTACTATATTAACCTTAGAATTTAGACAACCTGA 521
Qy      1853 AATTATTCATATATATTAAGTGAAGAAAGCCGCAATTCACATAGATTTCTCTCTT 1912
Db      520  AATTATTCATATATATTAAGTGAAGAAAGCCGCAATTCACATAGATTTCTCTCTT 461
Qy      1913 AGTATTAATTCACCTATTGTTAGTGAATATAGTAATCTTACTATATTTGACTGTGAAT 1972
Db      460  AGTATTAATTCACCTATTGTTAGTGAATATAGTAATCTTACTATATTTGACTGTGAAT 401
Qy      1973 ATGTAGCTATCTTTACACCAACTCTTAATTTTAATATTTCTCTGTTAATG 2032
Db      400  ATGTAGCTATCTTTACACCAACTCTTAATTTTAATATTTCTCTGTTAATG 341
Qy      2033 AGAAGTACTTGG--TTTTTTTTTCTTAATATATATATATATATTAATTAATTAATTA 2091
Db      340  AGAAGTACTTGGTTTTTTTTTCTTAATATATATATATATATTAATTAATTAATTA 281
Qy      2092 TTTTTTTGAGACGAGCTTGTCTGTGTACCCAGGCTGAGTGCAGTGG--GTGATCTTG 2150
Db      280  TTTTTTTGAGACGAGCTTGTCTGTGTACCCAGGCTGAGTGCAGTGGGTATCTTG 221
Qy      2151 GCTCACTCAAGCTCTGCTCCCGGGTTGCAACCAATTTCTGCTCAGCTCCCAAT 2210
Db      220  GCTCACTCAAGCTCTGCC--TCCGGGTTGCAACCAATTTCTGCTCAGCTCCCAAT 163
Qy      2211 TAGCTTGCCCTACAGTCACTGTCGCCACCACTGGCTAATTTTGTACTTTAGTAG 2270
Db      162  TAGCTTGCCCTACAGTCACTGTCGCCACCACTGGCTAATTTTGTACTTTAGTAG 103
Qy      2271 ACAGGTTTCAACCGTGTAGCCAGAGATGTCGTCTGATCTCTGACCTCGTATCCGCCAC 2330
Db      102  ACAGGTTTCAACCGTGTAGCCAGAGATGTCGTCTGATCTCTGACCTCGTATCCGCCAC 43
Qy      2331 CTCGGCTTCCCAAGTGTGGGATTCACAGCATGAGCCACCG 2372
Db      42  CTCGGCTTCCCAAGTGTGGGATTCACAGCATGAGCCACCG 1
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RESULT 12

US-11-266-748A-398267
/ Sequence 398267, Application US/11266748A

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/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcription Microarray Technology and
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ CURRENT FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/700,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 398267
```

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; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-398267

Query Match      32.8%; Score 777.6; DB 8; Length 1000;
Best Local Similarity 99.0%; Pred. No. 4.9e-129;
Matches 814; Conservative 0; Mismatches 4; Indels 4; Gaps 3;

QY 1553 TGAAGGGAAGAAACCCAGACAAAGAGATGTGGAATCTAGATTGGCCCTTAATGC 1612
DB 181 TGAAGACAGAAAGAACCCAGACAAAGAGAGATGTGGAATCTAGATTGGCCCTTAATGC 240
QY 1613 CATTGAACCTTGTGATTTGTCAAGTTCGACCTTAATAAATGTTGATGTCCATGGCAA 1672
DB 241 CATTGAACCTTGTGATTTGTCAAGTTCGACCTTAATAAATGTTGATGTCCATGGCAA 300
QY 1673 AACAGACACTTTATGAGCCCTGCTTTACATGTGCAAAAGCTAAAGAAAGAAATAGGC 1732
DB 301 AACAGACACTTTATGAGCCCTGCTTTACATGTGCAAAAGCTAAAGAAAGAAATAGGC 360
QY 1733 CTGCCAGATGTAGCAACCAATTCGAATGATTGCTACTTAATTTCCCTAGTTGAC 1792
DB 361 CTGCCAGATGTAGCAACCAATTCGAATGATTGCTACTTAATTTCCCTAGTTGAC 420
QY 1793 CTGCTATAAGAAATATATATTTCTAATCTATATAACCTAGAAATTTAGAACCTGA 1852
DB 421 CTGCTATAAGAAATATATATTTCTAATCTATATAACCTAGAAATTTAGAACCTGA 480
QY 1853 AATTTATTCATATATATCAAGAGTGAAGAAATGCTCAATTCATAGATTTCTCTCTT 1912
DB 481 AATTTATTCATATATCAAGAGTGAAGAAATGCTCAATTCATAGATTTCTCTCTT 540
QY 1913 AGTATATTTGACCTACTTTGTAAGTGAATAGTGAATCTACTATATATTTGACTGAAT 1972
DB 541 AGTATATTTGACCTACTTTGTAAGTGAATAGTGAATCTACTATATATTTGACTGAAT 600
QY 1973 ATGTAGCTATCTTTTACACCAACTCTTAATTTTAATATTTCTACTCTCTTAAAG 2032
DB 601 ATGTAGCTATCTTTTACACCAACTCTTAATTTTAATATTTCTACTCTCTTAAAG 660
QY 2033 AGAAGTACTTGG-TTTTTTTTTTCTTAATATATATATATATATATTAATATTA 2091
DB 661 AGAAGTACTTGGTTTTTTTTTTTTTTCTTAATATATATATATATATTAATATTA 720
QY 2092 TTTTTTTTGAAGCCGAGTCTTGCTGTTAACCCAGGCTGAGTGCAGTGG-GTGATCTTG 2150
DB 721 TTTTTTTTGAAGCCGAGTCTTGCTGTTAACCCAGGCTGAGTGCAGTGGGTGATCTTG 780
QY 2151 GCTCACTGACAGCTCTGCCCTCCCGGGTTTGGACCAATTTCTGCTCAAGCTCCCAAT 2210
DB 781 GCTCACTGACAGCTCTGCCCTCCCGGGTTTGGACCAATTTCTGCTCAAGCTCCCAAT 838
QY 2211 TAGCTTGGCTCAAGTCACTGTCGACACACACCTGGCTAATTTTTGTACTTTAGTAGAG 2270
DB 839 TAGCTTGGCTCAAGTCACTGTCGACACACACCTGGCTAATTTTTGTACTTTAGTAGAG 898
QY 2271 ACAGGGTTTCAACGTTGTAGCCAGAGATGCTCGATCTCTGACCTCGTGAATCCGCCAC 2330
DB 899 ACAGGGTTTCAACGTTGTAGCCAGAGATGCTCGATCTCTGACCTCGTGAATCCGCCAC 958
QY 2331 CTGGGCTTCCCAAGTGTGGATTTACAGGCAATGACCAACCG 2372
DB 959 CTGGGCTTCCCAAGTGTGGATTTACAGGCAATGACCAACCG 1000

RESULT 13
US-11-266-748A-469313/C
; Sequence 469313, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
```

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; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 469313
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-469313

Query Match      32.8%; Score 777.6; DB 8; Length 1000;
Best Local Similarity 99.0%; Pred. No. 4.9e-129;
Matches 814; Conservative 0; Mismatches 4; Indels 4; Gaps 3;

QY 1553 TGAAGGGAAGAAACCCAGACAAAGAGAGTGTGATCTAGTTGCCCTTAATGC 1612
DB 820 TGAAGACAGAAAGAACCCAGACAAAGAGAGTGTGATCTAGTTGCCCTTAATGC 761
QY 1613 CATTGAACCTTGTGATTTGTCAAGTTCGACCTTAATAAATGTTGATGTCCATGGCAA 1672
DB 760 CATTGAACCTTGTGATTTGTCAAGTTCGACCTTAATAAATGTTGATGTCCATGGCAA 701
QY 1673 AACAGACACTTTATGAGCCCTGCTTTACATGTGCAAAAGCTAAAGAAAGAAATAGGC 1732
DB 700 AACAGACACTTTATGAGCCCTGCTTTACATGTGCAAAAGCTAAAGAAAGAAATAGGC 641
QY 1733 CTGCCAGATGTAGCAACCAATTCGAATGATTGCTACTTAATTTCCCTAGTTGAC 1792
DB 640 CTGCCAGATGTAGCAACCAATTCGAATGATTGCTACTTAATTTCCCTAGTTGAC 581
QY 1793 CTGCTATAAGAAATATATATTTCTAATCTATATAACCTAGAAATTTAGAACCTGA 1852
DB 580 CTGCTATAAGAAATATATATTTCTAATCTATATAACCTAGAAATTTAGAACCTGA 521
QY 1853 AATTTATTCATATATCAAGTGAAGAAATGCTCAATTCATAGATTTCTCTCTT 1912
DB 520 AATTTATTCATATATCAAGTGAAGAAATGCTCAATTCATAGATTTCTCTCTT 461
QY 1913 AGTATATTTGACCTCTTTGTAAGTGAATAGTGAATCTACTAATTTTGACTGAAT 1972
DB 460 AGTATATTTGACCTCTTTGTAAGTGAATAGTGAATCTACTAATTTTGACTGAAT 401
QY 1973 ATGTAGCTCATCTTTTACACCAACTCTAATTTTAAATATTTCTACTCTTAAAG 2032
DB 400 ATGTAGCTCATCTTTTACACCAACTCTAATTTTAAATATTTCTACTCTTAAAG 341
QY 2033 AGAAGTACTTGG-TTTTTTTTTTCTTAATATATATATATATATTAATATTA 2091
DB 340 AGAAGTACTTGGTTTTTTTTTTTTTTCTTAATATATATATATATTAATATTA 281
QY 2092 TTTTTTTTGAAGCCGAGTCTTGCTGTTAACCCAGGCTGAGTGCAGTGG-GTGATCTTG 2150
DB 280 TTTTTTTTGAAGCCGAGTCTTGCTGTTAACCCAGGCTGAGTGCAGTGGGTGATCTTG 221
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QY 2151 GCTGACTGCAAGCTCTGCGCTCCCGGGGTGGCAACATTCTCCGGCTCAGGCTCCCAAT 2210
Db 220 GCTGACTGCAAGCTCTGCGCTCCCGGGGTGGCAACATTCTCCGGCTCAGGCTCCCAAT 163
QY 2211 TAGCTTGCGCTCAAGTCACTGTCGACCAACACTGGCTAATTTTGTATCTTTAGTAGAG 2270
Db 162 TAGCTTGCGCTCAAGTCACTGTCGACCAACACTGGCTAATTTTGTATCTTTAGTAGAG 103
QY 2271 ACAGGGTTTCAACCGTTTATGACCAAGATGCTCGATCTCTGACCTCGTATCGGCCAC 2330
Db 102 ACAGGGTTTCAACCGTTTATGACCAAGATGCTCGATCTCTGACCTCGTATCGGCCAC 43
QY 2331 CTGGGCTCCCAAGGTGCTGGGATTAACAGCATGAGCCACG 2372
Db 42 CTGGGCTCCCAAGGTGCTGGGATTAACAGCATGAGCCACG 1

RESULT 14
US-11-266-748A-29783
; Sequence 29783, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 29783
; LENGTH: 1540
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-29783

Query Match 32.6%; Score 773.4; DB 8; Length 1540;
Best Local Similarity 99.4%; Pred. No. 2.8e-128;
Matches 808; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

QY 1562 AGAAACCCAGCAAGAGAGAGAGAGATCTAGTTGGCCCTTAATGCAATTGAACC 1621
Db 730 AGAAACCCAGCAAGAGAGAGAGAGATCTAGTTGGCCCTTAATGCAATTGAACC 789
QY 1622 TTGTGATTTGTCAAGTGCAGCTTAAATGTTGCTGATTCATGCGAAACAGGACA 1681
Db 790 TTGTGATTTGTCAAGTGCAGCTTAAATGTTGCTGATTCATGCGAAACAGGACA 849
QY 1682 TCTTATGCGCTCTTACATGTCGAAAGAGCTAAAGAAAGAAAGAAAGAAAGAAAG 1741
Db 850 TCTTATGCGCTCTTACATGTCGAAAGAGCTAAAGAAAGAAAGAAAGAAAGAAAG 909
QY 1742 ATGTGACAAACCAATCAATGATGTTGCTAATTTTCCCTAGTGAACCTGTCTATA 1801
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Db 910 ATGTGACAAACCAATCAATGATGTTGCTAATTTTCCCTAGTGAACCTGTCTATA 969
QY 1802 AGAAATTTATTTATTTCTAATATATATTAACCTAGAAATTTAGACAACTGAATTTATTC 1861
Db 970 AGAAATTTATTTATTTCTAATATATATTAACCTAGAAATTTAGACAACTGAATTTATTC 1029
QY 1862 ACATATATCAAAAGTGAAGAAATGCTCAATTCACATGATTTCTTCTTTAGATATAT 1921
Db 1030 ACATATATCAAAAGTGAAGAAATGCTCAATTCACATGATTTCTTCTTTAGATATAT 1089
QY 1922 GACCTACTTTGTGTGTAATGTAATGTAATCTTACTATATTTGACTGGAATATGATGTC 1981
Db 1090 GACCTACTTTGTGTGTAATGTAATGTAATCTTACTATATTTGACTGGAATATGATGTC 1149
QY 1982 ATCCCTTACCAACCTCCTAATTTTAAATATTTCTACTGCTGTCTAAATAGAGATGACT 2041
Db 1150 ATCCCTTACCAACCTCCTAATTTTAAATATTTCTACTGCTGTCTAAATAGAGATGACT 1209
QY 2042 TGG-TTTTTTTTTTTCTTAATATGTAATGACATTTAAATGTAATTTTATTTTGG 2100
Db 1210 TGGTTTTTTTTTTCTTAATATGTAATGACATTTAAATGTAATTTTATTTTGG 1269
QY 2101 AGACCGAGTCTTGTCTGTGTACCCAGAGCTGAGTGCAGTGG-TGTATCTTGGCTCACCTGC 2159
Db 1270 AGACCGAGTCTTGTCTGTGTACCCAGAGCTGAGTGCAGTGGATCTTGGCTCACCTGC 1329
QY 2160 AAGCTGCGCTCCCGGGGTGGACCATTCCTCGCTCAGGCTCCCAATTAAGCTTGGC 2219
Db 1330 AAGCTGCGCTCCCGGGGTGGACCATTCCTCGCTCAGGCTCCCAATTAAGCTTGGC 1387
QY 2220 CTACAGTCACTGCGACACACACCTGCGTAAATTTTGTACTTTTATGAGACAGGGTTT 2279
Db 1388 CTACAGTCACTGCGACACACACCTGCGTAAATTTTGTACTTTTATGAGACAGGGTTT 1447
QY 2280 CACCGTGTAGCAGAGATGTCGTGATCTCTGACCTGTGATCGGCCACCTGCGCTC 2339
Db 1448 CACCGTGTAGCAGAGATGTCGTGATCTCTGACCTGTGATCGGCCACCTGCGCTC 1507
QY 2340 CCAAGTCTGGGATTAACGAGATGAGCCACG 2372
Db 1508 CCAAGTCTGGGATTAACGAGATGAGCCACG 1540

RESULT 15
US-11-266-748A-17558
; Sequence 17558, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
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; SOFTWARE: Patentin version 3.3
; SEQ ID NO 17558
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-17558

Query Match 25.1%; Score 594.8; DB 8; Length 631;
Best Local Similarity 99.5%; Pred. No. 1.2e-96;
Matches 607; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY	1435	TTGAGAAAATGATGATAAATAATTAACAACAGCTTCAACATCACAGAAAGTGAAGACTATT	1494
DB	23	TTGAGAAAATGATGATAAATAATTAACAACAGCTTCAACATCACAGAAAGTGAAGACTATT	82
QY	1495	CTCAGCCATCAACTCTAGTACATTATTATAGCAGCCAGAGAGATGTGAAGAGTTTG	1554
DB	83	CTCAGCCATCAACTCTAGTACATTATTATAGCAGCCAGAGAGATGTGAAGAGTTTG	142
QY	1555	AAAGGAGAAACCCAGACAAAGAGAGAGTGGAAATCTAGTTGGCCCTTAATGCCA	1614
DB	143	AAAGGAGAAACCCAGATCAAGAGAGAGAGTGGAAATCTAGTTGGCCCTTAATGCCA	202
QY	1615	TTGAACTTGTGTGATTTGTCAAGGTGCACTTAAATGTTGCAATGTCATGCGCAAAA	1674
DB	203	TTGAACTTGTGTGATTTGTCAAGGTGCACTTAAATGTTGCAATGTCATGCGCAAAA	262
QY	1675	CAGACATCTTATGCGCTGCTTTACATGTGCAAGAGCTAAAGAAAGAAATTAAGCCCT	1734
DB	263	CTGACATCTTATGCGCTGCTTTACATGTGCAAGAGCTAAAGAAAGAAATTAAGCCCT	322
QY	1735	GCCGAGTATGTAGAACCAATTCAAATGTTGTGCTAATTTCCCTAGTTGACCT	1794
DB	323	GCCGAGTATGTAGAACCAATTCAAATGTTGTGCTAATTTCCCTAGTTGACCT	382
QY	1795	GTCATAAGAGATTAATATTTCTAATAATAACCTAGGAATTTAGACAACCTGAAA	1854
DB	383	GTCATAAGAGATTAATATTTCTAATAATAACCTAGGAATTTAGACAACCTGAAA	442
QY	1855	TTTATTCACATATATCAAAAGTAGAAAAATGCCCTCAATTCACATGATTTCTCTTTAG	1914
DB	443	TTTATTCACATATATCAAAAGTAGAAAAATGCCCTCAATTCACATGATTTCTCTTTAG	502
QY	1915	TATATTTGACCTACTTTGGTAGTGAATAGTAATCTTACTATAATTGACTTGATAT	1974
DB	503	TATATTTGACCTACTTTGGTAGTGAATAGTAATCTTACTATAATTGACTTGATAT	562
QY	1975	GTAGCTCATCCCTTTACACCAACTCCTAATTTAAATAATTTCTACTGCTTAATAG	2034
DB	563	GTAGCTCATCCCTTTACACCAACTCCTAATTTAAATAATTTCTACTGCTT-AATGAG	621
QY	2035	AAGTACTTGG 2044	
DB	622	AAGTACTTGG 631	

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Job time : 327 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 12:26:04 ; Search time 11262 Seconds
(without alignments)
11777.717 Million cell updates/sec

Title: US-09-966-724B-2

Perfect score: 2372

Sequence: 1 GCACCGCGGAGCTTGGCTG.....ATTACAGCATGAGCACCG 2372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_g881:*
12: gb_g882:*
13: gb_g883:*
14: gb_g884:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1001	42.2	3028	6	AK004719 Mus muscu
4	997.8	42.1	2870	6	AK160069 Mus muscu
5	904.2	38.1	3062	6	AK168690 Mus muscu
6	846.6	35.7	2770	6	AK150530 Mus muscu
7	824.2	34.7	2770	6	AK150530 Mus muscu
8	824.2	34.7	2772	6	AK152685 Mus muscu
9	758.6	32.0	892	3	BU150642 AGENCOURT
10	733.4	30.3	743	8	CR789372 DKFZP459J
11	718.4	30.3	759	8	DR006283 TC118660
12	712.2	28.6	743	1	CF407361 CH3H048.A
13	701.2	28.6	743	1	AI927905 WP03C08.X
14	679.4	28.6	709	7	BF057574 7K46C07.X
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16	656	27.7	670	4	CB162955 K-EST0223
17	654.6	27.6	831	4	CO734475 SILH03C08
18	638	26.9	739	8	CR629819 DKFZP469A
19	633.4	26.7	3007	6	AK004881 Mus muscu

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22	612	25.8	778	7	BE900427	BE900427 601673652
23	606.4	25.6	612	7	AM500514	AM500514 UT-HR-BNO
24	603	25.4	773	2	BI335419	BI335419 602998303
25	586.6	24.7	779	8	CO737650	CO737650 SILH03C18
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27	569	24.0	581	9	DA723121	DA723121 DA723121
28	565.4	23.8	571	7	AM500516	AM500516 UT-HR-BNO
29	564.6	23.8	573	7	AM176629	AM176629 IL4-CT007
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31	552.8	23.3	695	4	CB166600	CB166600 IBE603020
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33	535.2	22.6	964	7	BE300019	BE300019 600944138
34	530.6	22.6	847	3	BQ672178	BQ672178 AGENCOURT
35	526.4	22.2	537	11	AQ077720	AQ077720 CIT-HSP-2
36	519	21.9	555	7	BE296905	BE296905 601176992
37	513.6	21.7	792	8	CO572036	CO572036 AGENCOURT
38	512.8	21.6	616	8	CR750239	CR750239 DKFZP469B
39	485.2	20.5	578	10	DY160684	DY160684 001030BKU
40	481.8	20.3	674	7	AM755448	AM755448 EST387557
41	481	20.3	826	14	AY407997	AY407997 Homo sapi
42	478.2	20.2	773	4	CA316218	CA316218 UT-M-FW0-
43	477	20.1	849	8	CV116656	CV116656 AGENCOURT
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45	469	19.8	826	14	AY407998	AY407998 Pan trogl

ALIGNMENTS

RESULT 1
LOCUS CR857268 3147 bp mRNA linear HTC 12-NOV-2004
DEFINITION Pongo pygmaeus mRNA, cDNA DKFZp469A1622 (from clone DKFZp469A1622).
ACCESSION CR857268
VERSION CR857268.1 GI:55725399
KEYWORDS HTC.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Pongo pygmaeus (orangutan)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pongo.
1 (bases 1 to 3147)
Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fodor, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp469A1622) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp469A1622
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
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/gene="DKFZp469A1622"

REFERENCE AUTHORS CONSRM TITLE JOURNAL COMMENT

FEATURES source

gene

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Query Match 91.9%; Score 2179.6; DB 6; Length 3147;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2291; Conservative 0; Mismatches 59; Indels 16; Gaps 6;

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QY 1868 ATCAAG 1927

JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carinci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichannel sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6
AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.
TITLE Antisense Transcription in the Mammalian Transcriptome
JOURNAL Science 309, 1564-1566 (2005)
REFERENCE 7
AUTHORS The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
TITLE The transcriptional landscape of the Mammalian Genome
JOURNAL Science 309, 1559-1563 (2005)
REFERENCE 8
AUTHORS Aichi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carinci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Teijima, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers
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AKI60069
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VERSION
AKI60069.1
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REFERENCE
AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
PUBMED
10349636
REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
PUBMED
11042159
REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitanaka, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
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Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
PUBMED
11076861
REFERENCE
AUTHORS
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, K., Hara, A., Fukunishi, Y., Kono, H., Adachi, D., Fukuda, S.,
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Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gastonich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Momberechts, P., Nordone, P.,
Ring, B., Rindwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Sessa, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Toyo-oka, K., Wang, K. H., Weitz, C., Whiteaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Haegawa, Y., Kawaji, H., Kortsch, S.,
and Hayashizaki, Y.
TITLE
RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium
JOURNAL
Nature 409 (6821), 685-690 (2001)
PUBMED
11217851
REFERENCE
AUTHORS
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Ose, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
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 Malais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
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 12466851

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 Banal, M., Baxter, L., Beisel, K.W., Bersano, T., Bonin, H., Chalk, A.M.,
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 Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T.,
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 Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L.,
 Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S.,
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8 (bases 1 to 2870)

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 Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A.,
 Muramatsu, M. and Hayashizaki, Y.

Direct Submision
 Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa, 230-0045, Japan (E-mail: genome-ree@sc.riken.jp).
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

COMMENT

CDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Takashi Ishikawa (Department of Surgery
 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama
 236-0004 Japan) whose assistance we gratefully acknowledge.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 location/Qualifiers

FEATURES

source

1..2870

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CDS

Query Match 42.1%; Score 997.8; DB 6; Length 2870;
 Best Local Similarity 79.3%; Pred. No. 1.6e-169;
 Matches 1301; Conservative 0; Mismatches 292; Indels 48; Gaps 8;

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425 AAAGCTGTGTGTCACAAAAGACACTTATACATGAAAGAGGTTCTTTTATTCCTGG 484

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199 AAAATCCGTTGAGCGGCAAAAAGCACTTACATATGAAAGATTAATTTATATG 258
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485 CCAGTATATATGACTAAAGATTAATATGAGAGAGACAACATATTTATTTGTC 544
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658 TCTGTGTATGAGTGAAGAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 717
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1198 ATGTGTT---GAGAGAGAGAGATTAAGGAGAGAGAGAGAGAGAGAGAG 1257
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1487 AGACTATTTCTGAGCATCAATCTTCTAGTATTAATTTATGAGAGAGAGAG 1546
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Db 1375 GAATGCAATGAACTTGTGTATGATTTGTCAAGGTGACCTTAAATGTTGAT 1434
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Oy 1667 TGGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1726
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Db 1435 CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1494
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Oy 1727 TAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1786
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Db 1495 CAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1554
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Oy 1787 GTTGAAGCTG---TGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1843
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Db 1555 GGTGAGCTGCTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1612
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Oy 1844 ACAAGCTGAAATTTATTCATATATCAAGAGAGAGAGAGAGAGAGAGAG 1902
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Db 1613 ACAAGCTGAGATTTATTTATATCAATTAAGAGAGAGAGAGAGAGAG 1672
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Oy 1903 TCTTCTCTTGTATGATTAATGGA 1923
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Db 1673 TCACCTATATTAATTTATCTGGA 1693
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RESULT 5
AKI68690
LOCUS
DEFINITION
Mus musculus 13 days embryo liver cDNA, RIKEN full-length enriched
library, clone:1920045106 product:transformed mouse 3T3 cell double
minute 2, full insert sequence.
ACCESSION
AKI68690
VERSION
AKI68690.1 GI:74219907
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency, full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2
3
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
JOURNAL
PUBMED
REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, U., Nishi, K., Katsunuma, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, N., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Iwama, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL
PUBMED
REFERENCE
AUTHORS
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, D., Fukuda, S.,
Aizawa, K., Iwama, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I.,

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CONSRMT	Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kado, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Pleischmann, W., Gaasterland, T., Giesi, C., Kling, B., Kochiwa, H., Kuell, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staudt, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carinci, P., de Bonaldo, M.F., Brownstein, M.T., Bult, C., Flecher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D., Hofman, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Momberte, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wymshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.
TITLE	Riken Genome Exploration Research Group Phase II Team and the PANTOM Consortium
JOURNAL	Functional annotation of a full-length mouse cDNA collection
PUBMED	Nature 409 (6821), 685-690 (2001)
REFERENCE	11217851
AUTHORS	5 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapi, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bratt, D., Brusic, V., Chochia, C., Cordani, L.E., Cousins, S., Dalla, E., Dargatz, T.A., Flecher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Giesi, C., Godzik, A., Gough, J., Grimmond, S., Gustinich, S., Hirokawa, N., Jackson, J.J., Jarvis, E.D., Kana, A., Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konaga, A., Kurochkin, I.V., Lee, Y., Lemaire, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Petosa, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sadelin, A., Schneider, C., Semp, C.A., Setou, M., Shimada, K., Sultana, R., Takemura, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Veierdo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wymshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Aitawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
TITLE	PANTOM Consortium
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
PUBMED	Nature 420 (6915), 563-573 (2002)
REFERENCE	12466851
AUTHORS	6 Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Fith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Bremner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Altman, V., Allen, J.E., Ambesi-Imbondato, A., Adeweller, R., Aturaliya, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crome, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernarido, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Flecher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemmen, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustinich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishtikawa, T., Jaki, M., Kanapi, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, M., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S.,
CONSRMT	Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Noji, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavoni, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sadelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semp, C.A., Sano, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugura, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Zhao, S., Zimmer, A., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zierdor, R., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, B.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Matick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori, Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Niimura, Y., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watabiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
TITLE	PANTOM Consortium
JOURNAL	The transcriptional landscape of the mammalian genome
PUBMED	Science 309 (5740), 1559-1563 (2005)
REFERENCE	16141072
AUTHORS	7 Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Fith, M., Ravasi, T., Pang, K.C., Hallinan, J., Matick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sadelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.
CONSRMT	Riken Genome Exploration Research Group
TITLE	Antisense transcription in the mammalian transcriptome
JOURNAL	Science 309 (5740), 1564-1566 (2005)
PUBMED	16141073
REFERENCE	8 (bases 1 to 3062)
AUTHORS	Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, N., Kojima, M., Kono, H., Murata, M., Nakamura, M., Niimura, Y., Nishigori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ location/Qualifiers
SOURCE	1.3062 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM DB:1920045106" /db_xref="taxon:10090" /clone="1920045106" /tissue_type="liver" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="13 days embryo" 1.3062 /note="putative transformed mouse 373 cell double minute 2 (MGD MG1:96952 GB BC050902, evidence: BLASTN, 100%, match=2392)"
misc_feature	

ORIGIN

Query Match 38.1%; Score 904.2; DB 6; Length 3062;
 Best Local Similarity 76.3%; Pred. No. 1.2e-153;
 Matches 1288; Conservative 0; Mismatches 288; Indels 111; Gaps 10;

QY 305 CAGGCAAAATGCAATACCAACATGCTGTACCTAATGATGATGCTGTACACCTCACA 364
 DB 242 CAGGCAATGCAATACCAACATGCTGTCTACCGAGGATGCTGCAGACACTCACA 301
 QY 365 GATTCGAGCTTCGGAACAGAGACCT----- 391
 DB 302 GATTCGAGCTTCGGAACAGAGACTGTGTTGATTTCTCCCTCGAGTGTGAATATA 361
 QY 392 -----GTTAGACCAAAAGCCATGCTTTTGAATTAATTAAGTCTGTGTTG 438
 DB 362 GCTGTTTACAGGTTAGACCAAAACATGCTTTTGAAGTTTAAAGTCCGTGAG 421
 QY 439 CACAAAAGACACTTATATCTATGAAAGAGTTCTTTTATCTTGGCCAGTATATTATGA 498
 DB 422 CGCAAAACGACACTTACACTATGAAAGAGATTATTTATATTGGCCAGTATATTATGA 481
 QY 499 CTAAGACATTATATGAGAGAGAGACCAACATTTGATATTTGTTCAATAGATCTTCAG 558
 DB 482 CTAAGAGGTTATATGACAGAGAGACGACATTTGATTTGTTCAATATATCTCCAG 541
 QY 559 GAGATTTGTTGGCGTCCAGCTTCTCTGTAAGAGACAGAGAAATATATACATGA 618
 DB 542 GAGATGCTTTGAGATCCCGAGTTTCTCTGTAAGAGACAGAGAAATATATGCAATGA 601
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 DB 602 TCTACAGAAATTTAGTGGCTGTAAAGTACGA-----AGACTCTGGACATGCTGA 652
 QY 679 GTGAGAACAGGTGTACCTTGAAGGTGGAGTGTCAAAAAGACCTTGTACAAAGCTTC 738
 DB 653 GTGAGAGAGAGCTGCAGCTTAAG-----ATCTTTGCAAGGGCTAC 695
 QY 739 AGGAAGAGAAACCTTCATCTTCACATTTGTTTCTAGACCATCTACCTCATCTAGAGGA 798
 DB 696 CAGAGAGAAACCTTCATCTTCATCTGTATTTATTTCTAGACTGTCTACCTCATCTAGAGGA 755
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 DB 816 GCC-----GCAAGTCCCTGTCTTGTGATCCAGGCTGGGCTGTGTGAGCTGA 863
 QY 919 GGGAGATATGTTGNG-----AAAGAAAGAGTATGAGTATCTACAGGGA 963
 DB 864 GGGAGATATGACCGCGCGGCGGACAGACAGATGACAGACAGACAGCGACGACGATCCACAGGA 923
 QY 964 CGCCATCGAATCCGAGTCTTGAATGCTGTGTAAGTGAACATTCAGGTGATGGTTGATC 1023
 DB 924 CGCCCTGCGATCAGGATCTTGAATGCTGTGTAAGTGAACATTCAGGTGATGGTTGATC 983
 QY 1024 AGGATTCAGTTCTGATCAGTTTACGTTGAATTTGAAGTTGAAGTCTCTGAGCTGGAG 1043
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QY 1264 ATTGCAACAGATGTTGGGCCCTTCTGTGAGATTTGGCTTCTGAAGATTAAGGAGAGATA 1323
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 QY 1324 AAGGGGAAATCTCTGAG 1383
 DB 1284 AAGTGAAGATCTCTGAG 1343
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 DB 1404 ACAGCAG 1463
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 DB 1464 CATCACTTCTAGTATGATATTTATATGACAGCCCAAGAGAGAGAGAGAGAGAGAGAGAG 1520
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 DB 1521 AAGAAACCAAG 1580
 QY 1621 CTTGTGATTTGTTCAAGGTTGACCTTAATAATGAGTGTGATGATGATGATGATGATGAT 1680
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 DB 1641 ACCTCATGTCATGTTTCAAGGTTGACCTTAATAATGAGTGTGATGATGATGATGATGATGAT 1700
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 DB 1701 TGTGACAGACCAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1760
 QY 1798 TATTAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1857
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 QY 1858 ATTCATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1916
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 QY 1917 TAATGA 1923
 DB 1879 TCTGGA 1885

RESULT 6
 DV775435 1180 bp mRNA linear EST 23-NOV-2005
 LOCUS DV775435
 DEFINITION Hw_Fat_23_050802 All Bos taurus CF-24-HW fat cDNA library Bos
 taurus cDNA, mRNA sequence.
 ACCESSION DV775435
 VERSION DV775435.1 GI:82628295
 KEYWORDS EST.
 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 REFERENCE Yoon,D.H., Lee,S.H., Park,E.W., Cho,Y.M., Lee,J.H., Kim,H.,
 Kim,H.Y., Park,J.H. and Oh,S.J.
 Gene Expression Profiling of the Bovine Liver, adipose, and
 skeletal muscle
 TITLE JOURNAL
 COMMENT Unpublished (2005)
 Contact: Dr. Du-Hak Yoon
 National Livestock Research Institute, RDA
 564 Omeokhun-dong, Suwon, 441-350, Korea
 Tel: 82 31 290 1593

Fax: 82 31 290 1792
Email: dhyoon@da.go.kr.
Location/Qualifiers
FEATURES
source

1. 1180
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/sex="Four males mixed"
/cell_type="adipocyte"
/dev_stage="24 months old"
/lab_host="XLI-BlueMR" strain"
/clone_lib="Bos taurus CF-24-HW fat cDNA library"
/note="Organ: adipose tissue; Vector: Uni-ZAPXR; Site_1:
EcoRI; Site_2: Xho I"

ORIGIN

Query Match 35.7%; Score 846.6; DB 10; Length 1180;
Best Local Similarity 87.3%; Pred. No. 3.2e-142;
Matches 987; Conservative 0; Mismatches 134; Indels 10; Gaps 5;
461 GAAAGAGGTTCTTTTATCTGGCCAGTATTTATGATAAAGATTATGATGAGA 520
25 GTAAAGGTTATATTTATCTGGCCAGTATTCAGTACACGATTATATGATGAAAA 84
521 GCACACATATTTATATTTGTTCAATGATCTTCTAGAGATTGTTGGCGGCAAG 580
85 ACAACACATATTTGTTGATTTGTTCAATGATCTTCTAGGGGATTGTTGGAGTCCCAAG 144
581 CTTCTCTGTGAAGAGCACAGAAAAATATATCCATGATCTACAGAACCTTGTAGTAGT 640
145 CTTCTCTGTGAAGAGCACAGAAAAATATATCAATGATCTACAGAAATTTGTAGTAGT 204
641 CAATGACAGGAATATGCGACTCAGTATCTCTGTGAGTGAAGACAGGTGACCTTGA 700
205 CAGTACAGCAAGACATCATGATTTGAGGACATCTGTGATGAAAAAGGTGTCACCTTGA 264
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761 ACATTTGTTCTAGACCATCTACTCTCATCTGAAAGAGAGCAATTTAGTACAGAGA 820
325 AGATATGTTCTTACACCATCTACCTCATCTGAAAGAGAGAGAGTATGAGACAGAGA 384
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385 AAATTCAGATGATATATCTGTGAAAGACAGAGAAAGCCCAAAATCTGATGATTTTC 444
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445 CTTTCTCTTGTGAAGAGCTGTGCTGTGTATTAAGGGAGATATGTTGAAAGAG 504
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1121 TGAAGATGATGATGATATCAAGTACTGTATTCAGAGGAGGAGAGATGATACAGATTC 1180
685 TGAAGATGATGATGATATCGAGTACTGTATTCAGAGGAGGAGAGATGATACAGATTC 744
1181 ATTGAAGAAGATCTCTGAATTTCTTCTGAGTACATTTATGAAATGCACTTCATGCAATGA 1240
745 ATTGAAGAAGATCTCTGAATTTCTTCTGAGTACATTTATGAAAGTGTACTTCTGCAATGA 804
1241 AATGAATCCCCCTTCATCATGATTCAGAAAGATGTTGGCCCTTCGTGAATTTGGCT 1300

Db 805 AATGAATCTCCCTTCACCTCAGCAAGATGTTGGCCCTTCGTGAATTTGGCT 864
Qy 1301 TCTTGAAGTAAAGGAAAGATTAAGGGGAAATCTCTGAGAAAGCCAACTGGAACCTC 1360
Db 865 TCTTGAAGTAAAGGAAAGATTAAGGGGAAATGTTCTGAGAAAGCC-NACTGAGGAGACTC 923
Qy 1361 AACACAGCTGAAGAGGCTTGTGATGTTCTGATTTGTAAGAAAGCTATGATGATGATTC 1420
Db 924 GATGACAGAAAGACGAGGCTTGTGATGTTCTGATGTTCTGATGTTCTGATGTTCTGATG 982
Qy 1421 CAGAGAGTATGTTGTTGAGAAATGATGATTAATTAATTAATTAATTAATTAATTAATTAAT 1480
983 C-GAAGATCATGTTGTTGAGAAATGATGATTAATTAATTAATTAATTAATTAATTAATTAAT 1041
Qy 1481 AAGTGAAG--ACTATTTCTGAGCATCACTT-----CTATGTCATTTATTTATGAGCC 1533
Db 1042 AAGTGAAGAACTTCTGAGCATCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1101
Qy 1534 AAGAGATGTTGAAGATTTGAAAGGAAAGAAAGCCAGACAAAGAGGA 1584
Db 1102 AAAAAAATTCAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 1152
RESULT 7
AK150530
LOCUS
DEFINITION
AK150530
Mus musculus bone marrow macrophage cDNA, RIKEN full-length
enriched library, clone:1830011G16 product:transformed mouse 313
cell double minute 2, full insert sequence.
AK150530
AK150530.1 GI:74151685
VERSION
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
REFERENCE
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitanaka, T., Tashiro, H., Itoh, M.,
Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, S.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
JOURNAL
PUBMED
REFERENCE
AUTHORS
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, K., Irawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, K. I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Koehwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nakai, F., Pesole, G.,
Quackenbush, J., Schriml, L. M., Steubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,

CONSRMT	Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
JOURNAL	Takeuchi, C., Fujita, M., Gariboldi, M., Guerinich, S., Hill, D.,
PUBMED	Hofmann, K., Hume, D.A., Kamliya, M., Lee, N.H., Lyons, P.,
REFERENCE	Marchionni, L., Mashima, J., Mazzarelli, J., Momberts, P., Nordone, P.,
AUTHORS	Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Saeki, H.,
	Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
	Toyo-Oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L.,
	Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohzuki, S.
	and Hayashizaki, Y.
CONSRMT	RIKEN Genome Exploration Research Group Phase II Team and the
JOURNAL	PANTOM Consortium
PUBMED	Functional annotation of a full-length mouse cDNA collection
REFERENCE	Nature 409 (6821), 685-690 (2001)
AUTHORS	11217851
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	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
	Mikado, I., Osato, N., Saito, R., Suzuki, H., Yamashita, T.,
	Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
	Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
	Hume, D.A., Quackenbush, J., Schiraldi, L.M., Kanapin, A., Matsuda, H.,
	Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
	Chothia, C., Corbani, L.E., Cousins, S., Della, E., Dragani, T.A.,
	Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
	Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
	Guinichich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kengawa, A.,
	Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongsava, A.,
	Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
	Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
	Nunata, K., Okido, T., Pavan, W.J., Petter, G., Pesole, G.,
	Petrovsky, N., Pillai, R., Pontius, J.V., Qi, D., Ramachandran, S.,
	Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
	Sandelin, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K.,
	Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
	Verardo, R., Wagner, J., Wahlestedt, C., Wang, Y., Watanabe, Y.,
	Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
	Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
	Hayatsu, N., Hirozane-Kishikawa, T., Komori, H., Nakamura, M.,
	Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
	Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imochi, K.,
	Itch, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
	Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
	Rogers, J., Birney, E. and Hayashizaki, Y.
CONSRMT	PANTOM Consortium
JOURNAL	Analysis of the mouse transcriptome based on functional annotation
PUBMED	of 60,770 full-length cDNAs
REFERENCE	Nature 420 (6915), 563-573 (2002)
AUTHORS	12466851
	6
	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C.,
	Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodius, R.,
	Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R.,
	Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E.,
	Ambesi-Impombato, A., Apweiler, R., Auraliya, R.N., Bailey, T.L.,
	Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M.,
	Chiu, K.P., Choudhary, V., Christoffel, A., Clutterbuck, D.R.,
	Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G.,
	di Bernardo, D., Down, T., Engstrom, P., Fagioli, M., Faulner, G.,
	Fletcher, C.F., Fukushima, T., Furuno, M., Fukui, S., Gariboldi, M.,
	Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E.,
	Guinichich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N.,
	Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T.,
	Jaffe, M., Kanapin, A., Katoh, M., Kawasawa, Y., Keisel, J., Kitamura, H.,
	Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K.,
	Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J.,
	Liu, S., McWilliam, S., Madan, B., Mader, M., Marchionni, L.,
	Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S.,
	Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H.,
	Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, P., Ohara, O.,
	Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavese, G.,
	Pesole, G., Petrovsky, N., Piazza, S., Reed, J.C., Reid, J.F., Ring, B.Z.,
	Ringwald, M., Ros, B., Ruan, Y., Salzberg, S.L., Sandelin, A.,
	Schneider, C., Schonbach, C., Sekiguchi, K., Sempke, C.A., Seno, S.,
	Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D.,
	Sinclair, B., Sperling, S., Stupka, E., Sugawara, K., Sultana, R.,
	Takeuchi, Y., Taki, K., Tamada, K., Tan, S.L., Tang, S., Taylor, M.S.,
	Tegener, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R.,
	Wei, C.L., Yagi, K., Yamashita, H., Zabarovsky, E., Zhu, S., Zimmer, A.,
	Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T.,
	Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A.,
	Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M.,
	Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itch, M.,
	Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M.,
	Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M.,
	Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K.,
	Watanabe, A., Okumura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
CONSRMT	PANTOM Consortium
JOURNAL	The transcriptional landscape of the mammalian genome
PUBMED	Science 309 (5740), 1559-1563 (2005)
REFERENCE	16141072
AUTHORS	7
	Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M.,
	Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H.,
	Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T.,
	Pang, K.C., Hallinan, J., Mattick, J.S., Hume, D.A., Lipovich, L.,
	Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A.,
	Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and
	Wahlestedt, C.
CONSRMT	RIKEN Genome Exploration Research Group
JOURNAL	Antisense transcription in the mammalian transcriptome
PUBMED	Science 309 (5740), 1564-1566 (2005)
REFERENCE	16141073
AUTHORS	8 (bases 1 to 2770)
	Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K.,
	Hori, F., Iida, J., Imamura, K., Imotani, K., Itch, M., Kanagawa, S.,
	Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N.,
	Nishiyori, K., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D.,
	Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A.,
	Muramatsu, M. and Hayashizaki, Y.
JOURNAL	Direct Submission
PUBMED	Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
REFERENCE	Physical and Chemical Research (RIKEN), Laboratory for Genome
AUTHORS	Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
	RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
	Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
	URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
	Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome
	Encyclopedia Project of Genome Exploration Research Group in RIKEN
	Genomic Sciences Center and Genome Science Laboratory in RIKEN
	Division of Experimental Animal Research in Riken contributed to
	prepare mouse tissues.
	Tissues were provided by David A. Hume (Dept. of Biochemistry and
	Microbiology/Parasitology Institute for Molecular Bioscience
	University of Queensland Brisbane, Q 4072 Australia) whose
	assistance we gratefully acknowledge.
	Please visit our web site for further details.
	URL: http://genome.gsc.riken.jp/
	URL: http://fantom.gsc.riken.jp/.
FEATURES	location/Qualifiers
SOURCE	1..2770
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	/strain="C57BL/6J"
	/db_xref="PANTOM DB:I830011G16"
	/db_xref="taxon:10090"
	/clone="I830011G16"
	/cell_type="macrophage"
	/tissue_type="bone marrow"
	/clone_lib="RIKEN full-length enriched mouse cDNA library"
	1..2770
	/note="putative
	transformed mouse 3T3 cell double minute 2 (MGD MG1:96952
	GB RC050902, evidence: BLASTN, 100%, match=2291)"
ORIGIN	Query Match
	34.7%; Score 824.2; DB 6; Length 2770;

Best Local Similarity 74.5%; Pred. No. 3.1e-138;
Matches 1223; Conservative 0; Mismatches 273; Indels 145; Gaps 9;

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Oy 305 CAGGGAATGTCATACCAACATGCTCTACTACTGATGCTGCTGTAACCACTCACA 364
Db 76 CAGGCAATGTCATACCAACATGCTCTACTACTGATGCTGCTGTAACCACTCACA 135
Oy 365 GATTCAGCTTCGCAACAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
Db 136 GATTCAGCTTCGCAACAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 195
Oy 425 AAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
Db 196 AAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255
Oy 485 CCAAGTATATATATATATATATATATATATATATATATATATATATATATATAT 544
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Oy 605 AATATATACCATGATCTACAGGAACTTGTAGTATGCTACAGCAATCATCCGAGCTC 664
Db 376 AATATATACCATGATCTACAGGAACTTGTAGTATGCTACAGCAATCATCCGAGCTC 426
Oy 665 AGTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 724
Db 427 TGGCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
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Db 480 ----- 479
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Db 1038 AGAAGAGGCTTGTGATGTTCTGATTTGTAAGAAATCTATAGTAATGATTCAGAGAGTC 1097
Oy 1430 ATGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1486
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Db 1335 CGGCAAGAGCTGAGACCTCATGTCATGTTTCACTGTCAGCAAGAGAGAGAGAGAGAGAG 1394
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Db 1395 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1454
Oy 1787 GTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1843
Db 1455 GCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1512
Oy 1844 ACAACCTGAAATTTTATCAATATATATATATATATATATATATATATATATATATATAT 1902
Db 1513 ACAACCTGAAATTTTATCAATATATATATATATATATATATATATATATATATATATAT 1572
Oy 1903 TCTTCTCTTATGATATATATGA 1923
Db 1573 TCACCTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1593

RESULT 8
AK152685
LOCUS
DEFINITION
Mus musculus bone marrow macrophage cDNA, RIKEN full-length
enriched library, clone:1830082J21 product:transformed mouse 3T3
cell double minute 2, full insert sequence.
ACCESSION
AK152685
VERSION
AK152685.1 GI:74220382
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
2
10349636
REFERENCE
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
3
11042159
REFERENCE
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

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Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwaka, S., Inoue, K., Ozawa, Y., Izawa, M., Ohara, E., Matsuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

Riken integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

11076861

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kado, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochi, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, T., Pease, G., Quackenbush, J., Schriml, L.M., Staudt, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzei, J., Mombauer, P., Nordone, P., Rung, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyszewski, B., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S., and Hayashizaki, Y.

Riken Genome Exploration Research Group Phase II Team and the FANTOM Consortium

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

11217851

5

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brasic, V., Chotha, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kana, A., Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Munata, K., Okido, T., Pavan, W.J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sadelin, A., Schneider, C., Semp, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wyszewski, B., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayashizaki, Y., Hironaka, K., Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imochi, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E., and Hayashizaki, Y.

FANTOM Consortium

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420 (6915), 563-573 (2002)

12466851

6

Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodaira, R., Shimokawa, K., Bajic, V.B., Bremner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Aurreal, R.N., Bailey, T.L., Bansal, M., Baxter, L., Belsel, K.W., Bersano, T., Bono, H., Chalk, A.M.,

Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemant, P., Gengler, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashizaki, Y., Hensch, T.K., Hirokawa, N., Hill, D., Huh, J., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kels, J., Kitamura, H., Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Lunni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morita, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavoni, G., Pease, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sadelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semp, C.A., Sero, S., Sees, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugita, K., Sultana, R., Takenaka, Y., Taki, K., Tammo, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamashita, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hume, D.A., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawai, H., Kawasawa, Y., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plesey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, A., Okamura-Oho, Y., Suzuki, H., Kawai, J., and Hayashizaki, Y.

Riken Genome Exploration Research Group

Antisense transcription in the mammalian transcriptome

Science 309 (5740), 1559-1563 (2005)

16141072

7

Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakamichi, M., Nakamura, M., Nishida, H., Yagi, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J.S., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghini, M.A., Sadelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Y., Lenhard, B., and Wahlestedt, C.

Riken Genome Exploration Research Group

Antisense transcription in the mammalian transcriptome

Science 309 (5740), 1564-1566 (2005)

16141073

8 (bases 1 to 2772)

Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imochi, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume (Dep't. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: <http://fantom.gsc.riken.jp/>.
Location/Qualifiers

FEATURES
source

1..2772
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="1830082J21"
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/issue_type="bone marrow"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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misc_feature

ORIGIN

/note="putative
transformed mouse 3T3 cell double minute 2 (MGD|MG1:96952
GB|BC050902, evidence: BLASTN, 99%, match=2293)"

Query Match 34.7%; Score 824.2; DB 6; Length 2772;
Best Local Similarity 74.5%; Pred. No. 3.1e-138;
Matches 1223; Conservative 0; Mismatches 273; Indels 145; Gaps 9;

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76 CAGGCCAATGTGCATATCCCAATGCTCTGTACCTACTGATGGTCTGTAAACCACTCACA 135
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365 GATTCAGCTTGGAGAACAGAGACCCCTGGTTAGACCAAGCCATGCTTTGAAGTTAT 424
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136 GATTCAGCTTGGAGAACAGAGACCCCTGGTTAGACCAAGCCATGCTTTGAAGTTAT 195
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196 AAAGTCGTGTGGTGCACAAAAGACACTATATCTATGAAAGAGTTATTTTATATTTGG 255
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605 AAATATATACATGATCTACAGAGACCTGGTATGATGATGATGATGATGATGATGATGAT 664
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376 AAATATATGATGATCTACAGAGACCTGGTATGATGATGATGATGATGATGATGATGAT 426
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665 AGGTACATCTGTGATGATGAGAACAGGTGTCACTTGAAGGTGGAGTGTCAAAAGAGACT 724
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427 TGGCACATCTGTGATGATGAGAACAGGTGTCACTTGAAGGTGGAGTGTCAAAAGAGACT 479
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725 TGTACAGAGCTTCAGAGAGAACCTTCACTTCTCACTTGTGTTTCTAGACCACTTAC 784
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480 ----- 479
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785 CTATCTAGAGAGAGACCAATTAATGAGACAGAGAAATTCAGATGAATTAATCTGTGTA 844
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845 AGCAGAAAGAAACCCCAAAATCTGATAGTATTTCCCTTCTCTTGAATGAAGCTGGC 904
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510 GCGGACCGGAAAGCGCC-----GCAAGTCCCTGTCTTGAATCCAGGCTGGG 557
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905 TCTGTGTGAATTAAGGAGATATGTTGTG-----AAAGAGCAGTACGAG 949
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558 TCTGTGTGAATTAAGGAGATATGTTGTG-----AAAGAGCAGTACGAG 617
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618 CGAGTCCACAGAGAGCCCATCGATCCGATCTTGAATGCTGTGTAAGTGAACATTCAGG 677
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678 TGATTTGCTGTGATCAGATTCAGTTTCAATGATCAGTTTGAATGATTTGAAGTTGAATC 737
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1070 TCTGCATCAGAGAGATTAATGAGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1129
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738 TCTGCATCAGAGAGATTAATGAGCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 797
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1130 TGAGGTATATCAAGTATCTGTGTATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1189
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798 TGAGGTATATCAG 857
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918 TCCCTTCATCAG 977
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978 TAAAGGAAAG 1037
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1844 ACAACCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1902
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1513 ACAACATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1572
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1903 TCTTCTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1923
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1573 TCACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1573
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RESULT 9
BU150642 892 bp mRNA linear EST 03-SEP-2002
LOCUS AGENCOURT 8058664 NIH_MGC_102 Homo sapiens cDNA IMAGE:6213293
DEFINITION 5' mRNA sequence.
ACCESSION BU150642
VERSION BU150642.1 GI:22664174
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 892)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 DNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Plate: L10M2378 row: m column: 06
 High quality sequence stop: 648.
 Location/Qualifiers

FEATURES

1. .892
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 /clone="IMAGE:6213293"
 /issue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 102"
 /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

ORIGIN

Query Match 32.0%; Score 758.6; DB 3; Length 892;
 Best Local Similarity 95.3%; Pred. No. 2,4e-126;
 Matches 847; Conservative 0; Mismatches 34; Indels 8; Gaps 6;
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 61 CATCATTCGCAACAGATGTTGGCCCTTCGCGAAGATTTGCTTCTGGAAGTAAAGGA 120
 1318 AAGATTAAGGGGAATCTCTGGAAGCAAACTGSAAACTCAACACAGCTGAAGAG 1377
 121 AAGATTAAGGGGAATCTCTGGAAGCAAACTGSAAACTCAACACAGCTGAAGAG 180
 1378 GCTTTGATGTTCTGATTTGTAACAACTATAGTAATGATTCAGAGAGTCATGTGTTG 1437
 181 GCTTTGATGTTCTGATTTGTAACAACTATAGTAATGATTCAGAGAGTCATGTGTTG 240
 1438 AGAAAAATGATGATTAATTAACAAGCTTCACATCAACAAGATGAAGCTATTCTC 1497
 241 AGAAAAATGATGATTAATTAACAAGCTTCACATCAACAAGATGAAGCTATTCTC 300
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 301 AGCCATCAACTCTAGTAGCATTTATTATAGAGCAAGAAATGGAAGAGTTGAAA 360
 1558 GGGAAAGAAACCCAGACAAAGAGAGAGTGTGAAATCTAGTTGGCCCTTAATGCAATG 1617
 361 GGGAAAGAAACCCAGACAAAGAGAGAGTGTGAAATCTAGTTGGCCCTTAATGCAATG 420
 1618 AACCTTGTTGATTTTGTCAAGGTCGACCTTAATAAATGTTGCTTCCATGCAAAACG 1677
 421 AACCTTGTTGATTTTGTCAAGGTCGACCTTAATAAATGTTGCTTCCATGCAAAACG 480
 1678 GACATCTTATGGCCGTCTTATCATGTGCAAGAGCTAAAGAAAGATTAAGCCCTGCC 1737

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 Db 481 GACATCTTATGGCCGTCTTATCATGTGCAAGAGCTAAAGAAAGAAATGAAGCCCTGCC 540
 1738 CAGATGATAGCAACCAATCAATATGATTTGGCTAACTTTTCCCTAGTGAAGCTGTC 1797
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 661 TATTCACATATATCAAAAGTGAAGAAATGCTCAATTTACATAGATTTCTCTTTAGTA 720
 1917 TAAATGACCTAC-TTTGTGATGGAATAGTAATGTAATCTACTATATA-TTTGACTGAATAT 1974
 721 TAAATGACCTACCTTTTGGAGTGAATAGTAATGTAATCTACTATATAATTTTGACTGAATAT 780
 1975 GTAGC--TCATCCTTTACACCAACTCC--TAATTTTAATATTTCTACT-CTGTCTTAA 2029
 781 GGAGCCCTCATTTCTTTACCCCACTCCCTAATTTTAATTAATTTCTACTCGGCTTAA 840
 2030 ATGAGAGTACTGTTTCTTTTCTTTTCTTAAATATGTAATGACATTTAA 2078
 841 AGAGAAAGAACTGGGGTCTTTTCTTTTCTTAAATAAGAAATATGGA 889

RESULT 10
 CR789372 743 bp mRNA linear EST 01-OCT-2004
 LOCUS DKFZp4590965 r1.459 (synonym: pcor1) Pongo pygmaeus cDNA clone
 DEFINITION DKFZp4590965-5', mRNA sequence.
 CR789372
 ACCESSION CR789372.1 GI:53708254
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Pongo pygmaeus (orangutan)
 Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Pongo.
 1 (bases 1 to 743)
 Bahr, A., Lauber, J., Mewes, H.W., Well, B., Amid, C., Osanger, A.,
 Fobo, G., Han, M. and Wiemann, S.
 Pongo pygmaeus mRNA (Bahr, A., Lauber, J., Mewes, H.W., et al.)
 Unpublished (2004)
 COMMENT
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen
 (Hilden/Germany) within the cDNA sequencing consortium of the
 German Genome Project. This clone (DKFZp4590965) is available at
 the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
 Berlin, Germany. Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp4590965>
 Further information about the clone and the sequencing project is
 available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

1. .743
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
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 /note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN

Query Match 30.9%; Score 733.4; DB 8; Length 743;

Best Local Similarity 99.2%; Pred. No. 8,5e-122;	
Matches 737; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
Qy	870 GATGATATTCCTTCCTTCTGATGAAAGCCGCTCTGCTGTAATAGGAGATATCT 929
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Qy	930 TGTGAAGAAGCAGTAGCAGTGAATCTACAGGAGCCGATCCGATCTTGATGCT 989
Db	61 TGTGAAGAAGCAGTAGCAGTGAATCTACAGGAGCCGATCCGATCTTGATGCT 120
Qy	990 GGTGTAAGTGAACATTCAGGTGATGTTGATCAGAGTTCAGTTTCAATCAGTTTACT 1049
Db	121 GGTGTAAGTGAACATTCAGGTGATGTTGATCAGAGTTCAGTTTCAATCAGTTTACT 180
Qy	1050 GTAGAAATTTGAGTTGAATCTCTCCAGCTACAGAAATTAAGCTTATGTAAGAGACAA 1109
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Qy	1110 GAACCTCAGATGAGATGATGATGATATCAAGTTACTGTGATCAGGAGGAGAGT 1169
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Qy	1170 GATACAGATTCATTTGAGAAAGATCCTGAAATTTCTTAGCTAGCTATTGAAATGCACT 1229
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Db	541 GTGAATGATTCAGAGAGTCATGTGTTGAGAAAAATGATGATTAATTAACAGACCTTCA 600
Qy	1470 CAATCAAGAAAGAGAGAGATCTATCTAGCCATCACTTCTAGTAGCATTTATTAATAC 1529
Db	601 CAATCAAGAAAGAGAGAGATCTATCTAGCCATCACTTCTAGTAGCATTTATTAATAC 660
Qy	1530 AGCCAAAGAGATGTGAAGAAGTTTGAAGGAAAGAAACCAAGACAAAGAGAGAGTGTG 1589
Db	661 AGCCAAAGAGATGTGAAGAAGTTTGAAGGAAAGAAACCAAGACAAAGAGAGAGTGTG 720
Qy	1590 GAATCTAGTTGGCCCTTAATGC 1612
Db	721 GAATCTAGTTGGCCCTTAATGC 743

RESULT 11
LOCUS DR006283 759 bp mRNA linear EST 17-MAY-2005
DEFINITION TC118660 Human prostate, large insert, PCMV expression library Homo sapiens cDNA clone TC118660 5' similar to Homo sapiens Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) (MDM2), transcript variant MDM2, mRNA sequence.
ACCESSION DR006283
VERSION DR006283.1 GI:66266156
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 759)
Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,

Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W. High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts Unpublished (2005) Contact: Kovacs, KF High Throughput cDNA Cloning Origene Technologies, Inc. (www.origene.com) 6 Taft Court, Suite 100, Rockville, MD 20850, USA Tel: 301 340 3188 Fax: 301 340 8606 Email: CDNA@origene.com This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc. Please contact Origene for access. Origene Technologies, Inc. 6 Taft Ct. Suite 100 Rockville, MD 20850 Tel: (301) 340-3188 http://www.origene.com Seq primer: PCMV 5prime forward vector primer, Origene Technologies Inc.	
FEATURES	
source	Location/Qualifiers 1..759 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="TC118660" /issue_type="prostate" /clone_lib="Human prostate, large insert, PCMV expression library" /note="Organ: Prostate; Vector: pCMV6-XL4, Site 1: Bcor1; Site 2: Xho1/SalI compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"
ORIGIN	
Query Match 30.3%; Score 718.4; DB 9; Length 759; Best Local Similarity 97.2%; Pred. No. 4,3e-119; Matches 742; Conservative 0; Mismatches 14; Indels 7; Gaps 1;	
Qy	134 CFTCCCTCCCGGATTAAGTCGTACAGCGCCAGTGCCTCGCCCGAGAGTGAATGA 193
Db	4 CGAGCCTCCCGGATTAAGTCGTACAGCGCCAGTGCCTCGCCCGAGAGTGAATGA 63
Qy	194 TCCCGAGGCCGAGGCGTCTGCTTCCGCACTAGTCCCGTGAAGAACTGGGG 253
Db	64 TCCCGAGGCCGAGGCGTCTGCTTCCGCACTAGTCCCGTGAAGAACTGGGG 116
Qy	254 AGTCTTGAGGGACCCCGAGCTCCAGCGGAAACCCCGGATGTGAGAGAGCAAT 313
Db	117 AGTCTTGAGGGACCCCGAGCTCCAGCGGAAACCCCGGATGTGAGAGAGCAAT 176
Qy	314 GTGCAATACCAACATGTGTGTAACCTAGTGTGTGTAAACCACTCAGATTCAGC 373
Db	177 GTGCAATACCAACATGTGTGTAACCTAGTGTGTGTAAACCACTCAGATTCAGC 236
Qy	374 TTCCGAACCAAGACCTCTGTTAGCCAAAGCATTTGTTGAAGTTATTAAGTCTGT 433
Db	237 TTCCGAACCAAGACCTCTGTTAGCCAAAGCATTTGTTGAAGTTATTAAGTCTGT 296
Qy	434 TGTGTCACAAAAGACACTTATACATGAAAGAGTTCTTTTATCTTGGCAGATAT 493
Db	297 TGTGTCACAAAAGACACTTATACATGAAAGAGTTCTTTTATCTTGGCAGATAT 356
Qy	494 TATGATTAACGATTATATGATGAGAGCAACAATATTTGATTTGTTCAATGATCT 553
Db	357 TATGATTAACGATTATATGATGAGAGCAACAATATTTGATTTGTTCAATGATCT 416
Qy	554 TCTAGAGATTTGTTGGCGTGCCAGCTTCTGTGAAAGAGCAGAGAAATATATAC 613

Db	417	TCATGAGATTGTTTGGCGTCCAGCTTCTCTGTGAAAGCAGGAAAATTTATAC	476
Qy	614	CATGATCTACAGGAACCTTGTAAGTCAATCAGCAGGAATCATGACTCAGGTATC	673
Db	477	CATGATCTACAGGAACCTTGTAAGTCAATCAGCAGGAATCATGACTCAGGTATC	536
Qy	674	TGTGAGTGAACAAGCTGTCACTTTGAAGTGGAGTATCAAAAAGACCTTTGTAACA	733
Db	537	TGTGAGTGAACAAGCTGTCACTTTGAAGTGGAGTATCAAAAAGACCTTTGTAACA	596
Qy	734	GCTTCAGGAAGAAACCTTCATCTTCAATTTGGTTTCTAGACCATCTCATCTAG	793
Db	597	GCTTCAGGAAGAAACCTTCATCTTCAATTTGGTTTCTAGACCATCTCATCTAG	656
Qy	794	AAGGAGCAATTACTGACAGGAAGAAATTCAATGATTAATTTGGTGAACGACAA	853
Db	657	AAGGAGAGCATTTAGTGAAGACAGGAAGAAATTCAGATCAATTCCTGGTGAACGACAA	716
Qy	854	AAAAGCCACAATCTGATAGATTATTCCTTTCCCTTTGATGA	896
Db	717	AAAAGCCACAATCTGATAGATTATTCCTTTCCCTTTGATGA	759

RESULT 12	
CF407361	
LOCUS	940 bp mRNA
DEFINITION	CH3#048_A05T7 Canine heart normalized cDNA library in pBluescript
ACCESSION	CF407361
VERSION	CF407361.1 GI:34408184
KEYWORDS	EST.
SOURCE	Canis familiaris (dog)
ORGANISM	Canis familiaris

REFERENCE	1 (bases 1 to 940)
AUTHORS	Yi, Y., Desai, R., Olarte, M., Henthorn, P. and George A.L.
TITLE	Expressed sequence tags from Canine heart.
JOURNAL	Unpublished (2003)
COMMENT	Other_ESTS: CH3#048_A0573

FEATURES	Location/Qualifiers
SOURCE	1. .940

shepherd, pointer, Irish setter). Library construction:
oligo-dT primed"

Query Match	30.0%;	Score 712.2;	DB 5;	Length 940;
Best Local Similarity	89.0%;	Pred. No. 5.4e-118;		
Matches 804; Conservative	0;	Mismatches 84;	Indels 15;	Gaps 3;

QY	940	UCACATACAGATGATCTCAACAGGACGGCCATCCGATCCGATCTTGAAGCTGGATAGTG	999
Db	38	GCAGATGACAGTGAATCAACAGGGACGGCCATCAAAATCCGAGCTTGAAGCTGGATAGTG	97
QY	1000	AACATTCAGGAGATTTGGTTGGATCAGGATTCAGTTTCAGATTCAGTTTAGTAGTAATTTG	1059
Db	98	AACATTCAGGAGATTTGGTTGGATTCAGGATTCAGTTTCAGATTCAGTTTAGTAGTAATTTG	157
QY	1060	AAGTTGAATCTCTCGACTCAGAGATTAATAGCTTTAGTGAAGAGCAAGAACTCTCAG	1119
Db	158	AAGTTGAGTCTCTGATTCAGAGATTAATAGCTTTAGTGAAGAGCAAGAACTCTCAG	217
QY	1120	ATGAAGATGATAGAGTATATCAAGTTACGTGTATCGAGCAGGGAGAGATACAGATT	1179
Db	218	ATGAAGATGATAGAGTATATCAAGTTACGTGTATCGAGCAGGGAGAGATACAGATT	277
QY	1180	CATTGGAAGAAGATCTCGAAATTTCTTAGCTGACTATTGGAATGCACTTCATGCATG	1239
Db	278	CATTGGAAGAAGATCTCGAAATTTCTTAGCTGACTATTGGAATGCACTTCATGCATG	337
QY	1240	AAATGAATCCCCCTTCATCAGATTGCAACAGATGTTGGGCTTCGTGAGAAATTGGC	1289
Db	338	AAATGAATCCCTCTTCCACTCATTGCAATAGATGTTGGGCTTCGTGAGAAATTGGC	397
QY	1300	TTCTCGAAGATTAAGGGAAGATTAAGGGGAATCTGTGGAAGGCCAACTGTGAAACT	1359
Db	398	TTCTCGAAGATTAAGGGAAGATTAAGGGGAATCTGTGGAAGGCCAACTGTGAAACT	445
QY	1360	CAACAAGAGCTGAAGAGGGCTTTGATGTCCTGTGTTGAAAAAACTATAGTGATGATT	1419
Db	446	CAACAAGAGTGAAGAGGGCTTTGATGTCCTGTGTTGAAAAAAAGCTGCAGCGATGTT	505
QY	1420	CCAGAGACTCAATGTGTGAGGAAAAATGATGATAAAATTTACAAAGCTTCACATACAG	1479
Db	506	CCAGAGATCAATGTGTGAGGAAAAATGATGATAAAATTTACAAAGCTTCACATCCAG	565
QY	1480	AAAGTGAAGACTATTTCCAGCCATCAACTCTCTAGTATTAATTTATAGAGCCAGAG	1539
Db	566	AAAGTGAAGACTATTTCCAGCCATCAACTCTCTAGTATTAATTTATAGAGCCAGAG	625
QY	1540	ATGTGAAGAAGTTTGAAGGGAAGAAACCAAGACAAGAAAGAGAGTGTGAATCTGATT	1599
Db	626	ATGTGAAGAAGTTTGAAGGGAAGAAACCAAGACAAGAAAGAGAGTGTGAATCTGATT	685
QY	1600	TGCCCCCTTAATGCAATTGAACCTTGTGTGATTTGTCAAGTCGACTTAATAATGTTGCA	1659
Db	686	TTCCCCCTTAATGCAATTGAACCTTGTGTGATTTGCCAAGTCGACTTAATAACGTTGCA	745
QY	1660	TTGTTCATGCGAAAAACAGAGACATCTTATAGGCTGCTTTACATGACGAAGAAGCTAAGA	1719
Db	746	TTGTTCATGCGAAAAACAGAGACATCTTATAGGATCTTCACTGTGCAAGAAGCTAAGA	805
QY	1720	AAAGGAATAGCCCTGCCAGATGTAGACAAACAATTCAGATGATTTGCTAACTTATT	1779
Db	806	GAGGGGAT-AGCCCTGTACGATATGTAGACCAACCATTCAGATGATTTGCTAACTTATT	864
QY	1780	TCCTCCATGTTGACCTGTCTATPAAG- AATATATATTTCTAATCTATATAACCTTAGA	1837
Db	865	TCCTCCATGTTGACCTGTCTATPAAGTATATATATTTCTAATCTATATAACCTTAAG	924
QY	1838	ATT 1840	
Db	925	ATT 927	

RESULT 13					
A1927905/c					
LOCUS	A1927905	743 bp	mRNA	linear	EST 08-MAR-2000
DEFINITION	wp03c08.x1 NCL_COAP Kid1 Homo sapiens cdna clone IMAGE:2465758 3'				

similar to gb:M92424 MDW2 PROTEIN (HUMAN);, mRNA sequence.
 AI927905 GI:5663869
 VERSION AI927905.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 743)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 458 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 459.
 Location/Qualifiers
 1..743
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:2463758"
 /lab_host="DH10B"
 /clone_1lb="NCI CGAP Kid11"
 /note="Organ: kidney; Vector: pT73D-Pac1; Site 1: Not I;
 Site 2: Eco RI; Plasmid DNA from the normalized library
 NCI CGAP Kid3 was prepared, and 88 circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from a pool of 5,000 clones made
 from the same library (clones 132376-132391).
 145607-145675, and 150055-150285). Subtraction by
 Bento Soares and M. Patricia Bonaldi."

ORIGIN
 Query Match 29.6%; Score 701.2; DB 1; Length 743;
 Best Local Similarity 97.3%; Pred. No. 5.4e-116;
 Matches 723; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1288 GTGAGATTGGCTTCTGAGTAAGGAAAGATPAAGGGGAAATCTCTGAGAAAGCA 1347
 |||||
 DB 743 GTGACATTGGCTTCTGAGTAAGGCAAGATPAAGGGGTAATCTCTGAGAAAGCA 684
 |||||
 QY 1348 AACTGGAAGAACTCAACAAGCTGAAGGGCTTGTGATTTCTGATTTAAAAAAGTA 1407
 |||||
 DB 663 AACTGGAAGAACTCAACAAGCTGAAGGGCTTGTGATTTCTGATTTAAAAAAGTA 624
 |||||
 QY 1408 TAGTAATGATTCAGAGAGTATGTTGAGGAAATGATGATTAATTAACAAGCTT 1467
 |||||
 DB 623 TAGTAATGATTCAGAGAGTATGTTGAGGAAATGATGATTAATTAACAAGCTT 564
 |||||
 QY 1468 CACATCAACAAGAAAGTGAAGCTATTCTCAGCCATCACTTCTAGTACATTAATTATA 1527
 |||||
 DB 563 CACATCAACAAGAAAGTGAAGCTATTCTCAGCCATCACTTCTAGTACATTAATTATA 504
 |||||
 QY 1528 GCAGCAGAAGATGTAAGGTTGAAGGGAAGAAACCAAGAACAAGAGAGAGCT 1587
 |||||
 DB 503 GCAGCAGAAGATGTAAGGTTGAAGGGAAGAAACCAAGAACAAGAGAGAGCT 444
 |||||
 QY 1588 TGGAACTAGTTGGCCCTTAATGCAATGAACCTTGTGTGATTTGTCAAGGTGACCTTA 1647
 |||||
 DB 443 TGGAACTAGTTGGCCCTTAATGCAATGAACCTTGTGTGATTTGTCAAGGTGACCTTA 384
 |||||

QY 1648 AAAATGGTTGATGTCATGCGCAAAAGACATCTTATGGCCGTCTTACATGCGAA 1707
 |||||
 DB 383 AAAATGGTTGATGTCATGCGCAAAAGACATCTTATGGCCGTCTTACATGCGAA 324
 |||||
 QY 1708 AGAAGCTAAAGAAAGAAATAGAGCCCTGCGCAGTATGTAGACAAATTCAGATG 1767
 |||||
 DB 323 AGAAGCTAAAGAAAGAAATAGAGCCCTGCGCAGTATGTAGACAAATTCAGATG 264
 |||||
 QY 1768 TGTCTACTTATTTCCCTTGTGAGTGGACCTGTCTATTAAGAGATTAATTTCTACTATAT 1827
 |||||
 DB 263 TGTCTACTTATTTCCCTTGTGAGTGGACCTGTCTATTAAGAGATTAATTTCTACTATAT 205
 |||||
 QY 1828 AACCTAGAAATTTAGACAACTGAAATTTATTCATATCAAGTAAGTAAGTCCCT 1887
 |||||
 DB 204 AACCTAGAAATTTAGACAACTGAAATTTATTCATATCAAGTAAGTAAGTCCCT 145
 |||||
 QY 1888 CAATTCACATGATTTCTCTCTTGTAGTAAATTAATGACCTAGTGTAGTGAATAGTA 1947
 |||||
 DB 144 CAATTCACATGATTTCTCTCTTGTAGTAAATTAATGACCTAGTGTAGTGAATAGTA 85
 |||||
 QY 1948 ATACTTACTATTAATTTGACCTGAATATGAGCTCATCTTTACACCAACTCTTAATTTTA 2007
 |||||
 DB 84 ATACTTACTATTAATTTGACCTGAATATGAGCTCATCTTTACACCAACTCTTAATTTTA 25
 |||||
 QY 2008 AATAATTTCTACTCTGTCTTAA 2030
 |||||
 DB 24 AATAATTTCTACTCTGTCTTAA 2

RESULT 14
 BP057574 709 bp mRNA linear EST 16-OCT-2000
 LOCUS 7k46c07.x1 NCI CGAP Ovi8 Homo sapiens cDNA clone IMAGE:3478285 3'
 DEFINITION similar to SW:MDW2_HUMAN Q00987 MDW2 PROTEIN ;, mRNA sequence.
 BP057574
 ACCESSION BP057574.1 GI:10811470
 VERSION
 KEYWORDS EST.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 709)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
 Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 481.
 Location/Qualifiers
 1..709
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 /mol_type="mRNA"
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 /clone="IMAGE:3478285"
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 /clone_1lb="NCI CGAP Ovi8"
 /note="Organ: Ovary; Vector: pT73D-Pac1; Site 1: Not I;
 Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
 TGTTACCAATGTGAAGTGGAGCGCGCGGACATTTTCTTTTCTTTT 3'];

ORIGIN
 Query Match 29.6%; Score 701.2; DB 1; Length 743;
 Best Local Similarity 97.3%; Pred. No. 5.4e-116;
 Matches 723; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 1288 GTGAGATTGGCTTCTGAGTAAGGAAAGATPAAGGGGAAATCTCTGAGAAAGCA 1347
 |||||
 DB 743 GTGACATTGGCTTCTGAGTAAGGCAAGATPAAGGGGTAATCTCTGAGAAAGCA 684
 |||||
 QY 1348 AACTGGAAGAACTCAACAAGCTGAAGGGCTTGTGATTTCTGATTTAAAAAAGTA 1407
 |||||
 DB 663 AACTGGAAGAACTCAACAAGCTGAAGGGCTTGTGATTTCTGATTTAAAAAAGTA 624
 |||||
 QY 1408 TAGTAATGATTCAGAGAGTATGTTGAGGAAATGATGATTAATTAACAAGCTT 1467
 |||||
 DB 623 TAGTAATGATTCAGAGAGTATGTTGAGGAAATGATGATTAATTAACAAGCTT 564
 |||||
 QY 1468 CACATCAACAAGAAAGTGAAGCTATTCTCAGCCATCACTTCTAGTACATTAATTATA 1527
 |||||
 DB 563 CACATCAACAAGAAAGTGAAGCTATTCTCAGCCATCACTTCTAGTACATTAATTATA 504
 |||||
 QY 1528 GCAGCAGAAGATGTAAGGTTGAAGGGAAGAAACCAAGAACAAGAGAGAGCT 1587
 |||||
 DB 503 GCAGCAGAAGATGTAAGGTTGAAGGGAAGAAACCAAGAACAAGAGAGAGCT 444
 |||||
 QY 1588 TGGAACTAGTTGGCCCTTAATGCAATGAACCTTGTGTGATTTGTCAAGGTGACCTTA 1647
 |||||
 DB 443 TGGAACTAGTTGGCCCTTAATGCAATGAACCTTGTGTGATTTGTCAAGGTGACCTTA 384
 |||||

Qy	905	TCTGTGTGTAATAGGGAGATATGTTGTGAAGAAGCAGTAGCAGTGAATCTTACAGGAC	964
Db	668	TCTGTGTGTAATAGGGAGATATGTTGTGAAGAAGCAGTAGCAGTGAATCTTACAGGAC	727
Qy	965	GCATCGAATCCGGAT-CTTGATGCTGGT-GTAACTGAACATTCAAGTGAATGTTGG	1020
Db	728	GCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAAGGAGTTGTTG	785

Search completed: August 4, 2006, 19:19:34
Job time : 11274 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 13:41:36 / Search time 13538 Seconds
(without alignments)
11204.261 Million cell updates/sec

Title: US-09-966-724B-2
Perfect score: 2372
Sequence: 1 GCACCGCGCGAGCTTGCTG.....ATTACAGCATGAGCCACCG 2372

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 636136 seqs, 31973710525 residues

Word size : 1

Total number of hits satisfying chosen parameters: 6531138

Minimum DB seq length: 5
Maximum DB seq length: 500

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pac:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_hcg:*
13: gb_in:*
14: gb_on:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401	16.9	456	5	HSN278976 Homo sapi
2	359	15.1	388	5	AF092843 Homo sapi
3	313	13.2	399	2	BD005478 Cellular
4	313	13.2	399	2	AR202601 Sequence
5	313	13.2	399	5	HSJ33202
6	250	10.5	480	5	AF385327
7	245	10.3	393	5	HSN278977
8	240	10.1	318	5	HSN491700
9	225	9.5	309	2	BD005479
10	225	9.5	309	2	AR202602
11	225	9.4	297	5	HSJ33203
12	222	9.4	297	5	HSN278978
13	222	9.4	297	5	HSN50516
14	209	8.8	209	7	G66929
15	183	7.7	210	5	HSN50518
16	175	7.4	213	5	HSN50519
17	172	7.3	224	5	AF385324
18	168	7.1	288	5	AF385326

19	167	7.0	319	2	AX587650	AX587650 Sequence
20	157	6.6	364	5	HSN278976	AJ278976 Homo sapi
21	153	6.5	198	5	HSN50517	AJ50517 Homo sapi
22	148	6.2	199	2	AR229721	AR229721 Sequence
23	144	6.1	153	5	HSN491701	AJ491701 Homo sapi
24	142	6.0	201	7	BV206635	BV206635 sqm12145
25	138	5.8	199	2	AR229722	AR229722 Sequence
26	120	5.1	165	5	HSN50520	AJ50520 Homo sapi
27	88	3.7	401	7	BV193037	BV193037 sqm17651
28	78	3.3	397	2	AX981948	AX981948 Sequence
29	78	3.3	397	2	BD116807	BD116807 EST and e
30	78	3.3	397	2	AR421254	AR421254 Sequence
31	77	3.2	427	7	AB140799	AB140799 Homo sapi
32	77	3.2	291	5	AB152167	AB152167 Homo sapi
33	76	3.2	291	5	HSN278978	HSN278978
34	73	3.1	73	2	BD074010	BD074010 Antisense
35	73	3.1	73	2	AR721415	AR721415 Sequence
36	73	3.1	401	7	BV195288	BV195288 sqm18401
37	71	3.0	315	5	AY270309	AY270309 Homo sapi
38	69	2.9	353	2	AX245117	AX245117 Sequence
39	69	2.9	426	2	CQ469958	CQ469958 Sequence
40	69	2.9	426	2	CQ479126	CQ479126 Sequence
41	69	2.9	446	2	CQ503928	CQ503928 Sequence
42	69	2.9	449	2	CQ473654	CQ473654 Sequence
43	69	2.9	469	2	CQ482823	CQ482823 Sequence
44	69	2.9	475	2	CQ500302	CQ500302 Sequence
45	69	2.9	475	2	CQ509237	CQ509237 Sequence
46	69	2.9	475	2	CQ509244	CQ509244 Sequence
47	69	2.9	475	2	CQ512729	CQ512729 Sequence
48	69	2.9	499	7	BV012530	BV012530 HSC226 (n
49	68	2.9	68	2	CQ876224	CQ876224 Sequence
50	68	2.9	68	2	CQ975386	CQ975386 Sequence
51	68	2.9	281	5	S70707	S70707 (repetitive
52	68	2.9	297	8	AF458110	AF458110 Synthetic
53	68	2.9	309	8	AY341576	AY341576 Synthetic
54	68	2.9	325	8	AY341577	AY341577 Synthetic
55	68	2.9	355	8	AF458109	AF458109 Synthetic
56	68	2.9	386	8	AF458108	AF458108 Synthetic
57	68	2.9	412	8	AF458114	AF458114 Synthetic
58	68	2.9	422	8	AY341575	AY341575 Synthetic
59	68	2.9	433	8	AF458107	AF458107 Synthetic
60	68	2.9	437	8	AF458113	AF458113 Synthetic
61	68	2.9	440	8	AF458112	AF458112 Synthetic
62	68	2.9	450	8	AY341573	AY341573 Synthetic
63	68	2.9	453	8	AF458115	AF458115 Synthetic
64	68	2.9	463	2	CQ407177	CQ407177 Sequence
65	68	2.9	480	5	AF015155	AF015155 Homo sapi
66	67	2.8	241	2	CQ699533	CQ699533 Sequence
67	67	2.8	480	2	AX977481	AX977481 Sequence
68	67	2.8	480	2	BD112340	BD112340 EST and e
69	67	2.8	480	2	AR416787	AR416787 Sequence
70	66	2.8	412	7	AB131382	AB131382 Homo sapi
71	65	2.7	365	7	AB147854	AB147854 Homo sapi
72	65	2.7	399	7	AB137509	AB137509 Homo sapi
73	64	2.7	157	5	DQ193118	DQ193118 Homo sapi
74	64	2.7	212	2	CQ408208	CQ408208 Sequence
75	64	2.7	448	7	AF192029	AF192029 Homo sapi
76	64	2.7	482	7	BV198158	BV198158 sqm19671
77	60	2.5	60	2	CQ542955	CQ542955 Sequence
78	60	2.5	362	2	AX984612	AX984612 Sequence
79	60	2.5	362	2	BD119471	BD119471 EST and e
80	60	2.5	362	2	AR423918	AR423918 Sequence
81	60	2.5	416	2	CQ464560	CQ464560 Sequence
82	60	2.5	441	2	AX986356	AX986356 Sequence
83	60	2.5	441	2	BD121215	BD121215 EST and e
84	60	2.5	441	2	AR425662	AR425662 Sequence
85	59	2.5	121	2	CQ686451	CQ686451 Sequence
86	59	2.5	343	2	CQ432690	CQ432690 Sequence
87	59	2.5	348	2	CQ423842	CQ423842 Sequence
88	59	2.5	374	2	CQ407892	CQ407892 Sequence
89	59	2.5	421	2	CQ407826	CQ407826 Sequence
90	59	2.5	453	2	CQ395168	CQ395168 Sequence
91	59	2.5	453	2	CQ401508	CQ401508 Sequence

C 92	59	2.5	469	5	AY190793	C 165	55	2.3	288	8	HSU14568	U14568 **ALU WARM
C 93	58	2.4	170	2	CQ706690	C 166	55	2.3	299	5	HSALUCOL	X75335 H.sapiens A
C 94	58	2.4	185	2	CQ499343	C 167	55	2.3	317	5	HSU67827	U67827 Human prima
C 95	58	2.4	185	2	CQ508313	C 168	55	2.3	322	2	AX978974	AX978974 Sequence
C 96	58	2.4	191	2	BD038032	C 169	55	2.3	322	2	BD113833	BD113833 EST and e
C 97	58	2.4	191	2	AR738293	C 170	55	2.3	322	2	AR418280	AR418280 Sequence
C 98	58	2.4	191	2	AX902499	C 171	55	2.3	328	2	AX918265	AX918265 Sequence
C 99	58	2.4	251	7	BV187788	C 172	55	2.3	328	2	BD053798	BD053798 Sequence
C 100	58	2.4	281	2	CQ472768	C 173	55	2.3	328	2	AR754059	AR754059 Sequence
C 101	58	2.4	305	5	AY680020	C 174	55	2.3	343	5	AF344192	AF344192 Homo sapi
C 102	58	2.4	326	2	CQ518112	C 175	55	2.3	346	5	HSUDALU1	X13240 Human Tu-a1
C 103	58	2.4	354	2	CQ468351	C 176	55	2.3	347	5	AY270560	AY270560 Homo sapi
C 104	58	2.4	384	2	CQ487985	C 177	55	2.3	378	2	CQ481614	CQ481614 Sequence
C 105	58	2.4	388	2	CQ478711	C 178	55	2.3	382	2	AX983066	AX983066 Sequence
C 106	58	2.4	399	2	AX071526	C 179	55	2.3	382	2	BD117925	BD117925 EST and e
C 107	58	2.4	407	2	CQ478016	C 180	55	2.3	382	2	AR422372	AR422372 Sequence
C 108	58	2.4	407	2	CQ481729	C 181	55	2.3	385	2	CQ482993	CQ482993 Sequence
C 109	58	2.4	412	2	CQ394434	C 182	55	2.3	401	7	BV190239	BV190239 sqgm16652
C 110	58	2.4	412	2	CQ400793	C 183	55	2.3	401	7	BV198686	BV198686 sqgm19850
C 111	58	2.4	422	2	CQ486627	C 184	55	2.3	401	7	BV199101	BV199101 sqgm20000
C 112	58	2.4	425	2	CQ502870	C 185	55	2.3	404	2	AX335679	AX335679 Sequence
C 113	58	2.4	427	2	CQ499908	C 186	55	2.3	408	2	CQ502756	CQ502756 Sequence
C 114	58	2.4	430	2	CQ478745	C 187	55	2.3	408	7	AB152125	AB152125 Homo sapi
C 115	58	2.4	430	7	AB147097	C 188	55	2.3	413	2	CQ692899	CQ692899 Sequence
C 116	58	2.4	431	2	CQ469574	C 189	55	2.3	417	2	BD152511	BD152511 Primer fo
C 117	58	2.4	446	2	CQ499217	C 190	55	2.3	417	2	AX872449	AX872449 Sequence
C 118	58	2.4	450	2	CQ478143	C 191	55	2.3	423	5	AY318838	AY318838 Homo sapi
C 119	58	2.4	460	2	CQ469577	C 192	55	2.3	429	2	CQ395489	CQ395489 Sequence
C 120	58	2.4	460	2	CQ499942	C 193	55	2.3	429	2	CQ401824	CQ401824 Sequence
C 121	58	2.4	460	2	CQ508021	C 194	55	2.3	431	7	AB152216	AB152216 Homo sapi
C 122	58	2.4	463	2	AX983617	C 195	55	2.3	432	2	CQ692898	CQ692898 Sequence
C 123	58	2.4	463	2	BD118476	C 196	55	2.3	441	2	CQ473824	CQ473824 Sequence
C 124	58	2.4	463	2	AR422923	C 197	55	2.3	447	2	AX368896	AX368896 Sequence
C 125	58	2.4	467	2	CQ498722	C 198	55	2.3	449	2	CQ507108	CQ507108 Sequence
C 126	58	2.4	468	2	CQ516438	C 199	55	2.3	449	2	CQ521888	CQ521888 Sequence
C 127	57	2.4	481	2	CQ503076	C 200	55	2.3	451	2	CQ405886	CQ405886 Sequence
C 128	57	2.4	281	5	S70706	C 201	55	2.3	456	5	AY879679	AY879679 Pygathrix
C 129	57	2.4	405	7	G35449	C 202	55	2.3	459	7	AB145960	AB145960 Homo sapi
C 130	57	2.4	415	2	CQ396717	C 203	55	2.3	460	5	AY879664	AY879664 Pygathrix
C 131	57	2.4	415	2	CQ403026	C 204	55	2.3	460	5	AY879749	AY879749 Nasalis 1
C 132	57	2.4	424	7	AB142946	C 205	55	2.3	467	5	AY879740	AY879740 Macaca mu
C 133	57	2.4	429	2	CQ478526	C 206	55	2.3	475	2	CQ699315	CQ699315 Sequence
C 134	57	2.4	456	7	BV198615	C 207	55	2.3	478	5	AF077058	AF077058 Pan trogl
C 135	57	2.4	463	2	CQ409410	C 208	55	2.3	479	7	AB136012	AB136012 Homo sapi
C 136	57	2.4	466	2	CQ499724	C 209	55	2.3	480	2	CQ413810	CQ413810 Sequence
C 137	57	2.4	485	2	CQ481937	C 210	55	2.3	482	5	AY879739	AY879739 Papio cyn
C 138	57	2.4	489	2	CQ520554	C 211	55	2.3	486	2	CQ518143	CQ518143 Sequence
C 139	57	2.4	494	2	BD152315	C 212	55	2.3	490	5	AY190785	AY190785 Homo sapi
C 140	56	2.4	494	2	AX872253	C 213	55	2.3	500	5	AY520144	AY520144 Homo sapi
C 141	56	2.4	397	2	AX389181	C 214	54	2.3	201	7	BV203717	BV203717 sqgm21286
C 142	56	2.4	401	2	CQ463660	C 215	54	2.3	251	7	BV187974	BV187974 sqgm15621
C 143	56	2.4	490	5	AY620557	C 216	54	2.3	317	2	CQ676042	CQ676042 Sequence
C 144	55	2.3	149	2	AX916718	C 217	54	2.3	326	2	CQ477715	CQ477715 Sequence
C 145	55	2.3	149	2	BD052251	C 218	54	2.3	340	7	AB140916	AB140916 Homo sapi
C 146	55	2.3	149	2	AR752512	C 219	54	2.3	341	2	CQ686043	CQ686043 Sequence
C 147	55	2.3	170	2	AX911162	C 220	54	2.3	375	2	CQ498918	CQ498918 Sequence
C 148	55	2.3	170	2	BD046695	C 221	54	2.3	375	2	CQ507887	CQ507887 Sequence
C 149	55	2.3	170	2	AR746956	C 222	54	2.3	398	2	CQ673791	CQ673791 Sequence
C 150	55	2.3	191	2	AX906934	C 223	54	2.3	407	2	CQ480930	CQ480930 Sequence
C 151	55	2.3	191	2	BD042467	C 224	54	2.3	411	2	AX335968	AX335968 Sequence
C 152	55	2.3	191	2	AR742728	C 225	54	2.3	411	2	AX407798	AX407798 Sequence
C 153	55	2.3	192	2	AX906260	C 226	54	2.3	436	5	HSALURT	X74556 H. sapiens (
C 154	55	2.3	192	2	BD041793	C 227	54	2.3	447	2	CQ471762	CQ471762 Sequence
C 155	55	2.3	192	2	AR742054	C 228	54	2.3	458	2	CQ502086	CQ502086 Sequence
C 156	55	2.3	201	2	CQ930498	C 229	54	2.3	458	2	CQ510960	CQ510960 Sequence
C 157	55	2.3	222	2	AX396130	C 230	54	2.3	463	2	AX385336	AX385336 Sequence
C 158	55	2.3	238	5	HSU02066	C 231	54	2.3	487	5	AY879767	AY879767 Pygathrix
C 159	55	2.3	241	5	HOMALINE51	C 232	54	2.3	495	2	CQ663735	CQ663735 Sequence
C 160	55	2.3	251	7	BV193228	C 233	53	2.2	311	2	AX982288	AX982288 Sequence
C 161	55	2.3	261	5	HS063XCS	C 234	53	2.2	311	2	BD117147	BD117147 EST and e
C 162	55	2.3	266	5	AX982981	C 235	53	2.2	311	2	AR421594	AR421594 Sequence
C 163	55	2.3	266	2	BD117840	C 236	53	2.2	339	2	CQ506919	CQ506919 Sequence
C 164	55	2.3	266	2	AR422287	C 237	53	2.2	394	2	CQ516315	CQ516315 Sequence

C 238	53	2.2	412	5	AY288777	C 311	50	2.1	364	2	AX245180	AX245180 Sequence
C 239	53	2.2	415	5	AY246543	C 312	50	2.1	366	2	C0662742	C0662742 Sequence
C 240	53	2.2	416	5	C0486501	C 313	50	2.1	377	2	C0478505	C0478505 Sequence
C 241	53	2.2	439	7	C0477001	C 314	50	2.1	378	2	C0478006	C0478006 Sequence
C 242	53	2.2	446	7	AB146903	C 315	50	2.1	378	2	C0487353	C0487353 Sequence
C 243	53	2.2	494	5	AF533323	C 316	50	2.1	380	2	C0477851	C0477851 Sequence
C 244	53	2.2	500	2	AX389152	C 317	50	2.1	380	2	C0499052	C0499052 Sequence
C 245	52	2.2	395	2	AX070585	C 318	50	2.1	393	2	C0477856	C0477856 Sequence
C 246	52	2.2	407	2	C0464107	C 319	50	2.1	396	2	AX986523	AX986523 Sequence
C 247	52	2.2	451	7	AB141369	C 320	50	2.1	396	2	BD121382	BD121382 Sequence
C 248	52	2.2	461	2	C0526512	C 321	50	2.1	396	2	AR425829	AR425829 Sequence
C 249	52	2.2	471	7	AB146055	C 322	50	2.1	399	5	AY271002	AY271002 Sequence
C 250	52	2.2	474	7	AB136916	C 323	50	2.1	400	2	C0507164	C0507164 Sequence
C 251	52	2.2	486	7	HS934617A	C 324	50	2.1	401	5	HS8290442	HS8290442 Sequence
C 252	52	2.2	487	7	C0516425	C 325	50	2.1	416	2	CQ499057	CQ499057 Sequence
C 253	51	2.2	192	5	AY733782	C 326	50	2.1	416	2	CQ499207	CQ499207 Sequence
C 254	51	2.2	201	2	CQ928538	C 327	50	2.1	416	2	CQ499703	CQ499703 Sequence
C 255	51	2.2	231	2	AX916194	C 328	50	2.1	429	2	C0464658	C0464658 Sequence
C 256	51	2.2	231	2	BD051727	C 329	50	2.1	431	2	C0468683	C0468683 Sequence
C 257	51	2.2	231	2	AR751988	C 330	50	2.1	437	7	AB136990	AB136990 Sequence
C 258	51	2.2	300	2	BD213266	C 331	50	2.1	443	2	CQ473946	CQ473946 Sequence
C 259	51	2.2	300	2	AR766860	C 332	50	2.1	451	7	HS5728185	HS5728185 Sequence
C 260	51	2.2	301	5	AF505387	C 333	50	2.1	452	7	AB146744	AB146744 Sequence
C 261	51	2.2	310	2	C0684514	C 334	50	2.1	454	2	C0525406	C0525406 Sequence
C 262	51	2.2	315	2	AX983321	C 335	50	2.1	465	2	AX396073	AX396073 Sequence
C 263	51	2.2	315	2	BD118180	C 336	50	2.1	471	2	AX385774	AX385774 Sequence
C 264	51	2.2	315	2	AR422627	C 337	50	2.1	471	7	AB144548	AB144548 Sequence
C 265	51	2.2	319	5	HS164WD10	C 338	50	2.1	488	2	C0516143	C0516143 Sequence
C 266	51	2.2	342	2	CQ465499	C 339	49	2.1	449	2	C0694064	C0694064 Sequence
C 267	51	2.2	364	2	CS185923	C 340	49	2.1	119	2	BD036650	BD036650 Sequence
C 268	51	2.2	392	2	C0508809	C 341	49	2.1	249	2	AR736911	AR736911 Sequence
C 269	51	2.2	392	2	C0512217	C 342	49	2.1	249	2	AX901117	AX901117 Sequence
C 270	51	2.2	400	2	C0663878	C 343	49	2.1	275	2	CQ465871	CQ465871 Sequence
C 271	51	2.2	401	2	AX269790	C 344	49	2.1	275	2	CQ465992	CQ465992 Sequence
C 272	51	2.2	401	2	AX271321	C 345	49	2.1	275	2	CQ466119	CQ466119 Sequence
C 273	51	2.2	401	7	BV189547	C 346	49	2.1	301	2	CQ468975	CQ468975 Sequence
C 274	51	2.2	401	7	BV193556	C 347	49	2.1	317	2	BD229434	BD229434 Sequence
C 275	51	2.2	401	7	BV195408	C 348	49	2.1	334	2	CQ467158	CQ467158 Sequence
C 276	51	2.2	403	7	AY190767	C 349	49	2.1	364	2	CQ465504	CQ465504 Sequence
C 277	51	2.2	424	5	CQ527394	C 350	49	2.1	374	2	CQ468838	CQ468838 Sequence
C 278	51	2.2	432	2	AX977510	C 351	49	2.1	378	2	CQ468688	CQ468688 Sequence
C 279	51	2.2	432	2	BD112369	C 352	49	2.1	449	5	DO193418	DO193418 Sequence
C 280	51	2.2	432	2	AR416816	C 353	49	2.1	455	7	AB142480	AB142480 Sequence
C 281	51	2.2	461	2	CQ465724	C 354	49	2.1	474	5	AR879764	AR879764 Sequence
C 282	51	2.2	471	5	DO193060	C 355	49	2.1	477	5	AY879765	AY879765 Sequence
C 283	51	2.2	479	7	AB143860	C 356	49	2.1	497	5	HTMC3AB	HTMC3AB Sequence
C 284	51	2.2	484	7	CQ525825	C 357	48	2.0	111	2	BD037862	BD037862 Sequence
C 285	51	2.2	500	7	BV198295	C 358	48	2.0	111	2	AR738123	AR738123 Sequence
C 286	50	2.1	50	2	AR685320	C 359	48	2.0	111	2	AX902329	AX902329 Sequence
C 287	50	2.1	95	2	AX916923	C 360	48	2.0	137	2	AX911794	AX911794 Sequence
C 288	50	2.1	95	2	BD052456	C 361	48	2.0	137	2	BD047327	BD047327 Sequence
C 289	50	2.1	95	2	AR752717	C 362	48	2.0	137	2	AR747588	AR747588 Sequence
C 290	50	2.1	101	7	BV184442	C 363	48	2.0	201	2	CS242644	CS242644 Sequence
C 291	50	2.1	101	7	BV185611	C 364	48	2.0	206	2	CQ460699	CQ460699 Sequence
C 292	50	2.1	133	2	AX907387	C 365	48	2.0	251	7	BY188182	BY188182 Sequence
C 293	50	2.1	133	2	BD042920	C 366	48	2.0	289	5	HTMALND167	HTMALND167 Sequence
C 294	50	2.1	133	2	AR743181	C 367	48	2.0	333	2	CQ429251	CQ429251 Sequence
C 295	50	2.1	133	2	AX906290	C 368	48	2.0	376	7	AB146586	AB146586 Sequence
C 296	50	2.1	215	2	BD041823	C 369	48	2.0	389	7	AB141482	AB141482 Sequence
C 297	50	2.1	215	2	AR742084	C 370	48	2.0	401	7	BY198657	BY198657 Sequence
C 298	50	2.1	239	7	AB150286	C 371	48	2.0	405	2	CS011490	CS011490 Sequence
C 299	50	2.1	252	2	AX912210	C 372	48	2.0	494	7	BY188630	BY188630 Sequence
C 300	50	2.1	252	2	AX912231	C 373	48	2.0	496	2	AX390281	AX390281 Sequence
C 301	50	2.1	252	2	BD047743	C 374	47	2.0	90	5	HTMDLRF1	HTMDLRF1 Sequence
C 302	50	2.1	252	2	BD047764	C 375	47	2.0	164	2	AX981060	AX981060 Sequence
C 303	50	2.1	252	2	AR748004	C 376	47	2.0	164	2	BD115919	BD115919 Sequence
C 304	50	2.1	252	2	AR748004	C 377	47	2.0	164	2	AR420366	AR420366 Sequence
C 305	50	2.1	253	5	AY516812	C 378	47	2.0	204	2	AX915336	AX915336 Sequence
C 306	50	2.1	262	2	CQ486569	C 379	47	2.0	204	2	BD050869	BD050869 Sequence
C 307	50	2.1	273	2	CQ110831	C 380	47	2.0	204	2	AR751130	AR751130 Sequence
C 308	50	2.1	288	2	AR702541	C 381	47	2.0	281	2	AX971141	AX971141 Sequence
C 309	50	2.1	337	2	C0516381	C 382	47	2.0	281	2	BD109860	BD109860 Sequence
C 310	50	2.1	361	2	AX245185	C 383	47	2.0	281	2	AR414307	AR414307 Sequence

C 384	47	2.0	294	2	AX971136	457	46	1.9	420	2	CQ499871	CQ499871 Sequence
C 385	47	2.0	294	2	AX971137	458	46	1.9	426	2	CQ508673	CQ508673 Sequence
C 386	47	2.0	294	2	BD109855	459	46	1.9	426	2	AB137385	AB137385 Homo sapi
C 387	47	2.0	294	2	BD109856	460	46	1.9	437	2	CQ469543	CQ469543 Sequence
C 388	47	2.0	294	2	AR414302	461	46	1.9	438	5	AY270850	AY270850 Homo sapi
C 389	47	2.0	294	2	AR414303	462	46	1.9	438	7	AB138057	AB138057 Homo sapi
C 390	47	2.0	298	2	AX980723	463	46	1.9	440	2	CQ697425	CQ697425 Sequence
C 391	47	2.0	298	2	AX982524	464	46	1.9	440	7	AB142046	AB142046 Homo sapi
C 392	47	2.0	298	2	BD115582	465	46	1.9	441	5	AY271109	AY271109 Homo sapi
C 393	47	2.0	298	2	BD117383	466	46	1.9	471	7	AB130670	AB130670 Homo sapi
C 394	47	2.0	298	2	AR420029	467	46	1.9	481	5	AY620633	AY620633 Atelae ge
C 395	47	2.0	298	2	AR421830	468	46	1.9	493	2	CQ472923	CQ472923 Sequence
C 396	47	2.0	302	2	AX971134	469	46	1.9	155	2	CQ673077	CQ673077 Sequence
C 397	47	2.0	302	2	AX971139	470	45	1.9	191	2	AX962456	AX962456 Sequence
C 398	47	2.0	302	2	BD109853	471	45	1.9	201	2	CQ931438	CQ931438 Sequence
C 399	47	2.0	302	2	BD109858	472	45	1.9	237	2	AX911740	AX911740 Sequence
C 400	47	2.0	302	2	AR414300	473	45	1.9	237	2	BD047273	BD047273 Sequence
C 401	47	2.0	302	2	AR414305	474	45	1.9	237	2	AR747534	AR747534 Sequence
C 402	47	2.0	310	2	AX971140	475	45	1.9	250	2	CQ712391	CQ712391 Sequence
C 403	47	2.0	310	2	BD109859	476	45	1.9	251	7	BV198137	BV198137 sqm19663
C 404	47	2.0	312	2	AR414306	477	45	1.9	265	2	CQ431981	CQ431981 Sequence
C 405	47	2.0	312	2	AX981366	478	45	1.9	279	2	BD032164	BD032164 Sequence
C 406	47	2.0	312	2	BD116225	479	45	1.9	279	2	AR732425	AR732425 Sequence
C 407	47	2.0	312	2	AR420672	480	45	1.9	279	2	AX896631	AX896631 Sequence
C 408	47	2.0	314	2	AX981132	481	45	1.9	303	2	AX912649	AX912649 Sequence
C 409	47	2.0	314	2	AX981166	482	45	1.9	303	2	BD048182	BD048182 Sequence
C 410	47	2.0	314	2	BD115991	483	45	1.9	303	2	AR748443	AR748443 Sequence
C 411	47	2.0	314	2	BD116025	484	45	1.9	310	2	CQ673169	CQ673169 Sequence
C 412	47	2.0	314	2	AR420438	485	45	1.9	315	2	CQ464953	CQ464953 Sequence
C 413	47	2.0	314	2	AR420472	486	45	1.9	317	5	AY271182	AY271182 Homo sapi
C 414	47	2.0	316	2	CQ468848	487	45	1.9	336	2	CQ431109	CQ431109 Sequence
C 415	47	2.0	333	2	CQ423689	488	45	1.9	353	2	CQ422242	CQ422242 Sequence
C 416	47	2.0	347	2	CQ465180	489	45	1.9	353	2	CQ423132	CQ423132 Sequence
C 417	47	2.0	347	2	CQ472560	490	45	1.9	356	2	CQ469506	CQ469506 Sequence
C 418	47	2.0	386	2	CQ393568	491	45	1.9	371	2	CQ688497	CQ688497 Sequence
C 419	47	2.0	386	2	CQ399945	492	45	1.9	372	2	CQ481974	CQ481974 Sequence
C 420	47	2.0	391	2	AX247380	493	45	1.9	379	2	CQ503113	CQ503113 Sequence
C 421	47	2.0	400	7	G17369	494	45	1.9	379	2	AX972103	AX972103 Sequence
C 422	47	2.0	400	7	G31584	495	45	1.9	387	2	BD110822	BD110822 EST and e
C 423	47	2.0	400	7	G34163	496	45	1.9	387	2	AR415269	AR415269 Sequence
C 424	47	2.0	401	7	BV190474	497	45	1.9	387	5	AY270482	AY270482 Homo sapi
C 425	47	2.0	408	8	AY341574	498	45	1.9	393	2	AR412605	AR412605 Sequence
C 426	47	2.0	421	2	AX984327	499	45	1.9	401	7	CQ472805	CQ472805 Sequence
C 427	47	2.0	421	2	BD119186	500	45	1.9	401	2	BV194535	BV194535 sqm18138
C 428	47	2.0	421	2	AR423633	501	45	1.9	402	2	CQ480468	CQ480468 Sequence
C 429	47	2.0	422	2	CQ406330	502	45	1.9	402	2	AX071389	AX071389 Sequence
C 430	47	2.0	426	2	CQ479134	503	45	1.9	403	2	CQ431056	CQ431056 Sequence
C 431	47	2.0	430	2	CQ457455	504	45	1.9	417	2	CQ471300	CQ471300 Sequence
C 432	47	2.0	447	2	CQ489272	505	45	1.9	421	2	CQ427114	CQ427114 Sequence
C 433	47	2.0	447	2	CQ491621	506	45	1.9	429	2	AB147762	AB147762 Homo sapi
C 434	47	2.0	465	7	HSJ08H2	507	45	1.9	434	2	CQ518466	CQ518466 Sequence
C 435	47	2.0	473	2	CO500310	508	45	1.9	439	2	AX979747	AX979747 Sequence
C 436	47	2.0	473	2	HMMUT746	509	45	1.9	439	2	BD114606	BD114606 EST and e
C 437	47	2.0	480	7	AX386789	510	45	1.9	439	2	AR419053	AR419053 Sequence
C 438	47	2.0	498	7	BV198115	511	45	1.9	440	2	AX985809	AX985809 Sequence
C 439	47	2.0	500	2	CQ432616	512	45	1.9	440	2	BD120668	BD120668 EST and e
C 440	46	1.9	208	2	CQ701657	513	45	1.9	440	2	AR425115	AR425115 Sequence
C 441	46	1.9	226	5	HMMALNE652	514	45	1.9	440	2	AX390737	AX390737 Sequence
C 442	46	1.9	227	2	BD038133	515	45	1.9	443	2	CQ501639	CQ501639 Sequence
C 443	46	1.9	227	2	AR738394	516	45	1.9	443	2	CQ510563	CQ510563 Sequence
C 444	46	1.9	227	2	AX902600	517	45	1.9	446	7	AB146085	AB146085 Homo sapi
C 445	46	1.9	282	2	CQ682649	518	45	1.9	448	5	AY318849	AY318849 Pan trogl
C 446	46	1.9	282	5	AY270301	519	45	1.9	449	2	CQ463716	CQ463716 Sequence
C 447	46	1.9	324	7	AB142194	520	45	1.9	453	2	CQ394602	CQ394602 Sequence
C 448	46	1.9	349	7	HMMUT6929	521	45	1.9	453	2	CQ400957	CQ400957 Sequence
C 449	46	1.9	355	2	CQ469337	522	45	1.9	468	2	CQ417528	CQ417528 Sequence
C 450	46	1.9	364	2	CQ677114	523	45	1.9	474	5	AY879733	AY879733 Ttrachypit
C 451	46	1.9	394	2	CQ478674	524	45	1.9	479	5	AY879732	AY879732 Ttrachypit
C 452	46	1.9	396	2	CO503227	525	45	1.9	480	2	CO524506	CO524506 Sequence
C 453	46	1.9	396	2	CO512074	526	45	1.9	480	2	AX983277	AX983277 Sequence
C 454	46	1.9	401	7	BV193624	527	45	1.9	489	2	BD118136	BD118136 EST and e
C 455	46	1.9	410	2	CQ469358	528	45	1.9	489	2	AR422583	AR422583 Sequence
C 456	46	1.9	414	7	BV196092	529	44	1.9	76	2	BD037434	BD037434 Sequence

C 530	44	1.9	76	2	AR737695	Sequence	C 603	44	1.9	394	2	AX071538	AX071538 Sequence
C 531	44	1.9	76	2	AX901901	Sequence	604	44	1.9	401	2	AX270548	AX270548 Sequence
C 532	44	1.9	102	2	AR702610	Sequence	605	44	1.9	401	2	AX272079	AX272079 Sequence
C 533	44	1.9	108	5	HSU67803	U67803 Human small	606	44	1.9	401	7	BV192888	BV192888 sqmml7606
C 534	44	1.9	147	2	BD039919	Sequence	C 607	44	1.9	401	7	BV198666	BV198666 sqmml19844
C 535	44	1.9	147	2	AR740180	Sequence	608	44	1.9	405	2	CQ428889	CQ428889 Sequence
C 536	44	1.9	147	2	AX904386	Sequence	609	44	1.9	406	2	AX987239	AX987239 Sequence
C 537	44	1.9	148	2	BD039768	Sequence	610	44	1.9	406	2	BD122098	BD122098 EST and e
C 538	44	1.9	148	2	AR740029	Sequence	611	44	1.9	406	2	AR426545	AR426545 Sequence
C 539	44	1.9	148	2	AX904235	Sequence	612	44	1.9	406	7	HSC31E11	HSC31E11
C 540	44	1.9	158	5	AY516549	Homo sapi	613	44	1.9	409	2	AX871120	AX871120 Sequence
C 541	44	1.9	188	2	BD039971	Sequence	C 614	44	1.9	409	5	AY879647	AY879647
C 542	44	1.9	188	2	BD039973	Sequence	615	44	1.9	410	7	AB152232	AB152232 Homo sapi
C 543	44	1.9	188	2	AR740232	Sequence	C 616	44	1.9	430	2	CQ519628	CQ519628 Sequence
C 544	44	1.9	188	2	AR740234	Sequence	C 617	44	1.9	432	2	CQ521947	CQ521947 Sequence
C 545	44	1.9	188	2	AX904438	Sequence	C 618	44	1.9	432	7	BV196153	BV196153 sqmml18739
C 546	44	1.9	188	2	AX904440	Sequence	C 619	44	1.9	434	5	AY879645	AY879645 Mioplithec
C 547	44	1.9	197	2	AX322172	Sequence	C 620	44	1.9	441	7	AB147336	AB147336 Homo sapi
C 548	44	1.9	201	2	CS242640	Sequence	C 621	44	1.9	443	2	AX386927	AX386927 Sequence
C 549	44	1.9	201	2	CS242641	Sequence	C 622	44	1.9	445	2	CQ422656	CQ422656 Sequence
C 550	44	1.9	201	2	CS242645	Sequence	623	44	1.9	447	2	CQ422201	CQ422201 Sequence
C 551	44	1.9	234	2	CQ674644	Sequence	C 624	44	1.9	451	2	CQ473561	CQ473561 Sequence
C 552	44	1.9	237	2	BD039066	Sequence	C 625	44	1.9	451	5	AY879738	AY879738 Chlorocb
C 553	44	1.9	237	2	AR739327	Sequence	C 626	44	1.9	452	7	AB129621	AB129621 Homo sapi
C 554	44	1.9	237	2	AX903533	Sequence	C 627	44	1.9	456	2	CQ527763	CQ527763 Sequence
C 555	44	1.9	251	7	BV188018	Sequence	C 628	44	1.9	458	2	CQ520151	CQ520151 Sequence
C 556	44	1.9	257	5	GGU14689	Sequence	C 629	44	1.9	458	2	CQ520635	CQ520635 Sequence
C 557	44	1.9	258	2	BD029803	Sequence	C 630	44	1.9	462	2	AX987240	AX987240 Sequence
C 558	44	1.9	258	2	AR730064	Sequence	C 631	44	1.9	462	2	BD122099	BD122099 EST and e
C 559	44	1.9	258	2	AX894270	Sequence	C 632	44	1.9	462	2	CQ484519	CQ484519 Sequence
C 560	44	1.9	265	2	AX917347	Sequence	C 633	44	1.9	464	2	AR426546	AR426546 Sequence
C 561	44	1.9	265	2	BD052880	Sequence	C 634	44	1.9	464	7	AB130200	AB130200 Homo sapi
C 562	44	1.9	265	2	AR753141	Sequence	C 635	44	1.9	464	7	AB137289	AB137289 Homo sapi
C 563	44	1.9	272	2	BD038062	Sequence	C 636	44	1.9	465	7	HMUTR5324	HMUTR5324
C 564	44	1.9	272	2	AR738323	Sequence	C 637	44	1.9	471	2	CQ503835	CQ503835 Sequence
C 565	44	1.9	272	2	AX902529	Sequence	C 638	44	1.9	471	2	CQ512641	CQ512641 Sequence
C 566	44	1.9	274	2	CO689711	Sequence	C 639	44	1.9	479	2	CQ529911	CQ529911 Sequence
C 567	44	1.9	280	7	AB129787	Homo sapi	C 640	44	1.9	481	2	CQ513872	CQ513872 Sequence
C 568	44	1.9	284	5	HS35A12F	Sequence	641	44	1.9	490	2	BD125854	BD125854
C 569	44	1.9	292	2	CQ710934	Sequence	642	44	1.9	490	2	CQ781145	CQ781145 Sequence
C 570	44	1.9	298	2	BD039669	Sequence	C 643	44	1.9	490	2	AX389604	AX389604 Sequence
C 571	44	1.9	298	2	AR739930	Sequence	644	44	1.9	491	2	CQ477178	CQ477178 Sequence
C 572	44	1.9	298	2	AX904136	Sequence	645	44	1.9	492	2	CQ514631	CQ514631 Sequence
C 573	44	1.9	300	5	ORALUT	Sequence	646	44	1.9	500	7	G34608	G34608 human STS S
C 574	44	1.9	309	2	AX388368	Sequence	647	44	1.8	80	5	HOMBRFAC	HOMBRFAC
C 575	44	1.9	309	7	AB130846	Homo sapi	C 648	44	1.8	92	2	AX197472	AX197472 Sequence
C 576	44	1.9	309	7	AB136862	Sequence	649	44	1.8	165	2	AX906331	AX906331 Sequence
C 577	44	1.9	311	2	CO487790	Sequence	650	44	1.8	165	2	BD041864	BD041864 Sequence
C 578	44	1.9	316	2	AX980615	Sequence	651	44	1.8	165	2	AR742125	AR742125 Sequence
C 579	44	1.9	316	2	BD115474	Sequence	652	44	1.8	201	2	CQ926933	CQ926933 Sequence
C 580	44	1.9	316	2	AR419921	Sequence	C 653	44	1.8	201	2	CQ930352	CQ930352 Sequence
C 581	44	1.9	318	2	AX981896	Sequence	C 654	44	1.8	201	2	CQ930591	CQ930591 Sequence
C 582	44	1.9	318	2	BD116755	Sequence	C 655	44	1.8	204	7	BV200808	BV200808 sqmml20507
C 583	44	1.9	318	2	AR421202	Sequence	C 656	44	1.8	204	5	AR205207	AR205207 Homo sapi
C 584	44	1.9	326	5	HUMALURPTE	Sequence	657	44	1.8	215	2	AX916343	AX916343 Sequence
C 585	44	1.9	348	7	G49311	Sequence	658	44	1.8	215	2	BD051876	BD051876 Sequence
C 586	44	1.9	348	7	BV198786	Sequence	659	44	1.8	215	2	AR752137	AR752137 Sequence
C 587	44	1.9	350	2	CQ820053	Sequence	C 660	44	1.8	221	2	BD039504	BD039504 Sequence
C 588	44	1.9	351	2	AX246983	Sequence	C 661	44	1.8	221	2	AR739765	AR739765 Sequence
C 589	44	1.9	360	2	CO671170	Sequence	C 662	44	1.8	221	2	AX903971	AX903971 Sequence
C 590	44	1.9	361	2	CO691466	Sequence	663	44	1.8	226	2	AX911670	AX911670 Sequence
C 591	44	1.9	367	2	CQ420011	Sequence	664	44	1.8	226	2	BD047203	BD047203 Sequence
C 592	44	1.9	369	2	AX070634	Sequence	665	44	1.8	226	5	AR747464	AR747464 Sequence
C 593	44	1.9	371	2	CQ419353	Sequence	C 666	44	1.8	234	5	HSU02054	HSU02054 Human clone
C 594	44	1.9	371	2	CO514345	Sequence	667	44	1.8	241	2	BD040243	BD040243 Sequence
C 595	44	1.9	371	7	HSC32P9	Sequence	668	44	1.8	241	2	AR740504	AR740504 Sequence
C 596	44	1.9	375	5	H81SPOLYA	Sequence	669	44	1.8	241	2	AX904710	AX904710 Sequence
C 597	44	1.9	380	2	CO428246	Sequence	C 670	44	1.8	246	2	AX934995	AX934995 Sequence
C 598	44	1.9	383	2	CQ465681	Sequence	C 671	44	1.8	248	2	CQ672838	CQ672838 Sequence
C 599	44	1.9	387	7	CO669022	Sequence	C 672	44	1.8	250	2	CO696769	CO696769 Sequence
C 600	44	1.9	387	7	AB143387	Homo sapi	C 673	44	1.8	251	7	BV193156	BV193156 sqmml17690
C 601	44	1.9	392	2	CO466291	Sequence	C 674	44	1.8	251	7	BV196694	BV196694 sqmml19003
C 602	44	1.9	392	2	CS012297	Sequence	C 675	44	1.8	251	7	BV198601	BV198601 sqmml19824

C 676	43	1.8	251	7	BV199046	749	43	1.8	392	2	CQ469305	CQ469305 Sequence
C 677	43	1.8	255	7	AB129384	C 750	43	1.8	393	5	AY246451	AY246451 Pan trogl
C 678	43	1.8	267	7	CQ692636	C 751	43	1.8	396	2	CS147500	CS147500 Sequence
C 679	43	1.8	272	2	CQ464514	C 752	43	1.8	397	2	AX981812	AX981812 Sequence
C 680	43	1.8	274	2	AX907397	C 753	43	1.8	397	2	BD116671	BD116671 EST and e
C 681	43	1.8	274	2	BD042930	C 754	43	1.8	397	2	AR421118	AR421118 Sequence
C 682	43	1.8	274	2	AR743191	C 755	43	1.8	399	2	CQ459750	CQ459750 Sequence
C 683	43	1.8	291	2	AX980631	C 756	43	1.8	399	5	AY246453	AY246453 Pongo pyg
C 684	43	1.8	291	2	BD115490	C 757	43	1.8	400	2	G17084	G17084 human SRS S
C 685	43	1.8	291	2	AR419937	C 758	43	1.8	401	2	CQ499671	CQ499671 Sequence
C 686	43	1.8	292	2	AX980583	C 759	43	1.8	401	7	AX070077	AX070077 Sequence
C 687	43	1.8	292	2	AX981858	C 760	43	1.8	401	7	BV194455	BV194455 sqmml18112
C 688	43	1.8	292	2	BD115442	C 761	43	1.8	401	7	BV195759	BV195759 sqmml18576
C 689	43	1.8	292	2	BD116717	C 762	43	1.8	402	2	CQ393830	CQ393830 Sequence
C 690	43	1.8	292	2	AR419889	C 763	43	1.8	402	2	CQ400201	CQ400201 Sequence
C 691	43	1.8	292	2	AR421164	C 764	43	1.8	402	2	CQ698294	CQ698294 Sequence
C 692	43	1.8	293	5	AY270547	C 765	43	1.8	403	2	CQ519971	CQ519971 Sequence
C 693	43	1.8	293	5	AY461426	C 766	43	1.8	406	2	CQ520574	CQ520574 Sequence
C 694	43	1.8	294	7	AB145951	C 767	43	1.8	407	7	AB135990	AB135990 Homo sapi
C 695	43	1.8	298	2	AX977375	C 768	43	1.8	408	2	CQ406586	CQ406586 Sequence
C 696	43	1.8	298	2	BD112234	C 769	43	1.8	408	2	CQ505797	CQ505797 Sequence
C 697	43	1.8	298	2	AR416681	C 770	43	1.8	409	2	CQ693877	CQ693877 Sequence
C 698	43	1.8	300	2	BD212915	C 771	43	1.8	411	5	AY055358	AY055358 Cercopit
C 699	43	1.8	300	2	BD212921	C 772	43	1.8	416	2	CQ502358	CQ502358 Sequence
C 700	43	1.8	300	2	AR766509	C 773	43	1.8	416	2	CQ511220	CQ511220 Sequence
C 701	43	1.8	300	2	AR766515	C 774	43	1.8	417	2	BD032114	BD032114 Sequence
C 702	43	1.8	301	2	AX912891	C 775	43	1.8	417	2	AR732375	AR732375 Sequence
C 703	43	1.8	301	2	BD048424	C 776	43	1.8	417	2	AX270812	AX270812 Sequence
C 704	43	1.8	301	2	AR748685	C 777	43	1.8	417	2	AX272343	AX272343 Sequence
C 705	43	1.8	307	2	AX982189	C 778	43	1.8	417	2	AX896581	AX896581 Sequence
C 706	43	1.8	307	2	BD117048	C 779	43	1.8	425	2	CQ462132	CQ462132 Sequence
C 707	43	1.8	307	2	AR421495	C 780	43	1.8	425	2	AB137078	AB137078 Homo sapi
C 708	43	1.8	311	5	HUMGP1BGT	C 781	43	1.8	426	2	CQ462141	CQ462141 Sequence
C 709	43	1.8	316	5	AF344193	C 782	43	1.8	430	2	CQ433377	CQ433377 Sequence
C 710	43	1.8	318	7	HS344VA9	C 783	43	1.8	432	2	CQ522025	CQ522025 Sequence
C 711	43	1.8	327	2	CQ485049	C 784	43	1.8	435	2	CQ465379	CQ465379 Sequence
C 712	43	1.8	329	2	AX981919	C 785	43	1.8	449	5	AY879695	AY879695 Macaca si
C 713	43	1.8	329	2	BD116778	C 786	43	1.8	452	7	AB137078	AB137078 Homo sapi
C 714	43	1.8	329	2	AR421225	C 787	43	1.8	452	7	AB142628	AB142628 Homo sapi
C 715	43	1.8	332	2	CQ463743	C 788	43	1.8	453	7	AX387694	AX387694 Sequence
C 716	43	1.8	333	2	AX245330	C 789	43	1.8	453	7	AB135762	AB135762 Homo sapi
C 717	43	1.8	334	2	AX980577	C 790	43	1.8	455	2	CQ411120	CQ411120 Sequence
C 718	43	1.8	334	2	BD115436	C 791	43	1.8	455	2	CQ478473	CQ478473 Sequence
C 719	43	1.8	334	2	CQ475840	C 792	43	1.8	456	7	AB136789	AB136789 Homo sapi
C 720	43	1.8	334	2	AR419883	C 793	43	1.8	458	7	AB138404	AB138404 Homo sapi
C 721	43	1.8	335	7	AB144035	C 794	43	1.8	458	7	AB140130	AB140130 Homo sapi
C 722	43	1.8	338	5	HSU18399	C 795	43	1.8	459	7	AB137093	AB137093 Homo sapi
C 723	43	1.8	339	2	CQ460253	C 796	43	1.8	461	5	AY879663	AY879663 Naalai
C 724	43	1.8	339	2	CQ481210	C 797	43	1.8	461	5	AY879666	AY879666 Macaca ne
C 725	43	1.8	347	2	AX981808	C 798	43	1.8	462	5	AY849288	AY849288 Pongo pyg
C 726	43	1.8	347	2	BD116667	C 799	43	1.8	463	2	CQ427872	CQ427872 Sequence
C 727	43	1.8	347	2	AR421114	C 800	43	1.8	463	5	AY879726	AY879726 Trachypit
C 728	43	1.8	349	2	CQ472445	C 801	43	1.8	465	5	AB138001	AB138001 Homo sapi
C 729	43	1.8	349	7	AB142481	C 802	43	1.8	466	5	HUM2C34B10	AR086194 Homo sapi
C 730	43	1.8	354	2	AX245515	C 803	43	1.8	466	7	AB137191	AB137191 Homo sapi
C 731	43	1.8	358	2	AX978258	C 804	43	1.8	469	2	CQ680952	CQ680952 Sequence
C 732	43	1.8	358	2	BD113117	C 805	43	1.8	476	2	BD152556	BD152556 Primer fo
C 733	43	1.8	358	2	AR417564	C 806	43	1.8	476	2	AX872494	AX872494 Sequence
C 734	43	1.8	360	2	AX977566	C 807	43	1.8	477	7	HUMUT7213B	L29762 Human SRS U
C 735	43	1.8	360	2	BD112425	C 808	43	1.8	479	2	CQ488197	CQ488197 Sequence
C 736	43	1.8	360	2	AR416872	C 809	43	1.8	480	2	AX908520	AX908520 Sequence
C 737	43	1.8	369	2	CQ694519	C 810	43	1.8	480	2	BD044053	BD044053 Sequence
C 738	43	1.8	369	2	CQ695076	C 811	43	1.8	480	2	AR744314	AR744314 Sequence
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C 745	43	1.8	387	2	CQ698367	C 818	43	1.8	485	5	G34139	G34139 human SRS S
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C 832	43	1.8	500	2	AR422294	C 905	42	1.8	332	2	BD050847
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C 850	42	1.8	207	2	AX901392	C 923	42	1.8	401	7	BY198074
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C 891	42	1.8	321	2	AX981294	C 964	42	1.8	482	2	CO691900
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C 893	42	1.8	325	2	BD116153	C 966	42	1.8	486	5	AX983305
C 894	42	1.8	325	2	AR420600	C 967	42	1.8	488	2	AX983305

FEATURES	source
PUBMED REFERENCE AUTHORS TITLE JOURNAL	11351297 2 (bases 1 to 388) Tamborini, E., Pierotti, M.A., Della Torre, G., Lavarino, C., Buto, S., Della, D. and Piloti, S. Direct Submission Submitted (18-SEP-1998) Dipartimento di Anatomia Patologica, Istituto Nazionale per lo Studio e la Cura dei Tumori, Via Venezian 1, Milan, MI 20133, Italy Location/Qualifiers 1..388
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DB	121 CAAAGCCATTGCTTTGAAGTTATTAAAGTCTGTGTGACAAAGAGACCTTATACTA 180
QY	460 TGAAGAGGTCCTTTTATCTTGCCGCGATATTTATGACTTAAAGATTATATGATGGA 519
DB	181 TGAAGAGGTCCTTTTATCTTGCCGCGATATTTATGACTTAAAGATTATATGATGGA 240
QY	520 AGCAACACATATTTGATATTTGTTCAATGATCTCTAGAGATTGTTGGCGGCCAA 579
DB	241 AGCAACACATATTTGATATTTGTTCAATGATCTCTCTAGAGATTGTTGGCGGCCAA 300
QY	580 GCTTCTCTGTGAAGAGACAGAAATATATACCATGATCTACAGAACTTGATAGTA 638
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DEFINITION	Cellular immunogens useful cancer vaccines.
ACCESSION	BD005478
VERSION	BD005478.1 GI:18633849
KEYWORDS	JP 2001501909-A/8.
SOURCE	unidentified
ORGANISM	unclassified
REFERENCE	1 (bases 1 to 399)
AUTHORS	Halpern, M.S. and England, J.M.
TITLE	Cellular immunogens useful cancer vaccines
JOURNAL	Cellular immunogens useful cancer vaccines Halpern, M.S. and England, J.M. Cellular immunogens useful cancer vaccines JP 2001501909-A 8 13-FEB-2001; ALLEGHENY UNIVERSITY OF THE HEALTH SCIENCES

COMMENT	OS	Unidentified
	PN	JP 2001501909-A/8
	PD	13-FEB-2001
	PF	13-JAN-1997 JP 1997526124
	PR	19-JAN-1996 US 60/010262
	PI	MICHAEL S HALPERN, JAMES M ENGLAND
	PC	A01K63/00, A61K39/00, A61K39/38, A61K48/00, C12N5/00, C12N15/00 CC
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DB	147	AGAAGATGTGAAAGATTGAAAGGAAAGAAACCAAGACAAAGAGAGTGTGATTC 206
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DB	207	TAGTTTGGCCCTTATGATGCAATGGAACCTTGTGTGATTTGTCAAGTGCACCTAAATATGG 266
QY	1655	TTGCATTTGTCATGAGCAAAACAGGACATCTTTAGGCTCTTTACATGTGCAAAAGAGCT 1714
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QY	1715	AAAGAAAAAGAAATTAAGCCCTGCCACGATATGTAGACAAACCAATTGTAATGATTTGTCTAAC 1774
DB	327	AAAGAAAAAGAAATTAAGCCCTGCCACGATATGTAGACAAACCAATTGTAATGATTTGTCTAAC 386
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DB	387	TTATTTCCCTTAG 399
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LOCUS	AR202601	399 bp DNA linear PAT 20-JUN-2002
DEFINITION	Sequence 8 from patent US 6365151.	
ACCESSION	AR202601	
VERSION	AR202601.1	GI:21498773
KEYWORDS		
SOURCE		
ORGANISM	Unknown.	
REFERENCE	Unclonified.	
AUTHORS	1 (bases 1 to 399)	
TITLE	Halpern, M.S. and England, J.M.	
JOURNAL	Cellular immunogens comprising cognate proto-oncogenes	
FEATURES	Patent: US 6365151-A 8 02-APR-2002;	
	Location/Qualifiers	
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LOCUS Human mdm2-D (mdm2) mRNA, complete cds.
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ACCESSION U33202.1 GI:992682
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (sites)
REFERENCE Sigalas I., Calvert A.H., Anderson J.J., Neal D.B. and Lunec J.
AUTHORS Alternatively spliced mdm2 transcripts with loss of p53 binding
TITLE domain sequences: transforming ability and frequent detection in
JOURNAL human cancer
PUBMED Nat. Med. 2 (8), 912-917 (1996)
8705862
2 (bases 1 to 399)
Lunec, J.
Direct Submission
Submitted (04-AUG-1995) John Lunec, Cancer Research Unit,
University of Newcastle Upon Tyne - Medical School, Framlington
Place, Newcastle upon Tyne, NE2 4HH, U.K
LOCATION/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2,1e-165;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1775 TTATTTCCCTTAG 1787
Db 387 TTATTTCCCTTAG 399
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DEFINITION AF385327
ACCESSION AF385327
VERSION AF385327.1 GI:16033453
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 480)
Bartel, F., Taylor, A.C., Taubert, H. and Harris, L.C.
Novel mdm2 splice variants identified in pediatric rhabdomyosarcoma
tumors and cell lines
Unpublished
2 (bases 1 to 480)
Bartel, F., Taylor, A.C., Taubert, H. and Harris, L.C.
Direct Submission
Submitted (24-MAY-2001) Molecular Pharmacology, St. Jude Children's
Research Hospital, 332 N. Lauderdale, Memphis, TN 38105, USA
LOCATION/Qualifiers
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DB 216 AGATCAGTTTGAAGTATGATTTGAATTCCTCCAGTCAGGAAGATTATAGCCTTAG 275

QY 1097 TGAAGACAGACAACTCTCAGATGAGATGATGATATCAAGTTACTGTGTATCA 1156
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QY 1157 GGCAGGGAGAGTATACAGATTCAATTTGAGAGAGATCCTGAAATTTCTTACCTGACTA 1216
DB 336 GGCAGGGAGAGTATACAGATTCAATTTGAGAGAGATCCTGAAATTTCTTACCTGACTA 395

QY 1217 TTGGAATGC 1226
DB 396 TTGGAATGC 405

RESULT 7
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LOCUS Homo sapiens mRNA for p53-binding protein (MDM2 gene),
DEFINITION alternatively spliced variant PM2.
ACCESSION AJ278977
VERSION AJ278977.1 GI:10045130
KEYWORDS alternative splicing; mdm2 gene; p53-binding protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1
AUTHORS Bartel,F., Meye,A., Wurl,P., Kappler,M., Bache,M.,
Tautenschlaeger,C., Grunbaum,U., Schmidt,H. and Taubert,H.
TITLE Amplification of the MDM2 gene, but not expression of splice
variants of MDM2 mRNA, is associated with prognosis in soft tissue
sarcoma
JOURNAL Int. J. Cancer 95 (3), 168-175 (2001)
PUBMED 11307150
REFERENCE 2 (bases 1 to 393)
AUTHORS Bartel,F.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Bartel F., Institute for Pathology,
University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097
Halle, GERMANY
COMMENT Related sequences: AJ278975-AJ278978, AJ276888.
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/standard_name="human homolog of mouse double minute 2"
/experiment="experimental evidence, no additional details
recorded"
/note="alternatively spliced variant PM2"
/codon_start=1
/product="p53 binding protein"

ORIGIN
Query Match 10.3%; Score 245; DB 5; Length 393;
Best Local Similarity 100.0%; Pred. No. 1e-126;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1543 TGAAGAGTTTGAAGGGAAGAAACCCAGCAAGAGAGAGTGTGAATCTACTTGC 1602
DB 149 TGAAGAGTTTGAAGGGAAGAAACCCAGCAAGAGAGAGTGTGAATCTACTTGC 208

QY 1603 CCCTTAATGCCATTGAACCTTGTGTGATTTGTCAAGTGCACCTAAATGTTGCATTG 1662
DB 209 CCCTTAATGCCATTGAACCTTGTGTGATTTGTCAAGTGCACCTAAATGTTGCATTG 268

QY 1663 TCCATGGCAAAACAGACATCTTATGGCTGCTTACATGTGCAAGAGAGTAAAGAAA 1722
DB 269 TCCATGGCAAAACAGACATCTTATGGCTGCTTACATGTGCAAGAGAGTAAAGAAA 328

QY 1723 GGAATAGCCCTGCCAGATATGATGACCAATTCGAATGATGCTACTTATTTCC 1782
DB 329 GGAATAGCCCTGCCAGATATGATGACCAATTCGAATGATGCTACTTATTTCC 388

QY 1783 CCTAG 1787
DB 389 CCTAG 393

RESULT 8
HSA491700 318 bp mRNA linear PRI 15-APR-2005
LOCUS Homo sapiens mRNA for p53-binding protein alternatively spliced
isoform l1_15 (MDM2 gene).
DEFINITION
ACCESSION AJ491700
VERSION AJ491700.1 GI:21628670
KEYWORDS alternative splicing; MDM2 gene; p53-binding protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1
AUTHORS Bartel,F., Pinkert,D., Kappler,M., Bache,M., Schmidt,H. and
Taubert,H.
TITLE Alternatively and aberrantly spliced transcripts of the MDM2 mRNA
occur frequently in human soft tissue sarcoma and in multiple
normal tissues
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 318)
AUTHORS Bartel,F.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2002) Bartel F., Institute for Pathology,
University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097
Halle, GERMANY
COMMENT
FEATURES
SOURCE location/Qualifiers
1..318
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="lung"
1..318
/gene="MDM2"
1..318
/gene="MDM2"
/note="alternatively spliced isoform l1_15
stop codon at bp 260-262 lost due to aberrant splicing"

/codon_start=1
/product="p53-binding protein"
/protein_id="CAD36961.1"
/db_xref="GI:21628671"
/db_xref="GOA:Q8NDW0"
/db_xref="InterPro:IPR003121"
/db_xref="UniProtKB/TrEMBL:Q8NDW0"
/translation="MCDNTNMSVPTDGAATTISOIPASQEETLVREPKLLIKLKSVGAK
KDIYTKMEVLFYLGQYIMTKRLYDEKQOHYYCSNDCAHLPVLVDISIRELYISNYIT
LGI"

ORIGIN

Query Match 10.1%; Score 240; DB 5; Length 318;
Best Local Similarity 100.0%; Pred. No. 7.3e-124;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 ATGTGCATACCAACATGTCTGTACTCTGATGAGTGTCTGTAACCACTCAGATTCCA 371
Db 1 ATGTGCATACCAACATGTCTGTACTCTGATGAGTGTCTGTAACCACTCAGATTCCA 60
Qy 372 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAGTTATTAAGTCT 431
Db 61 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAGTTATTAAGTCT 120
Qy 432 GTTGTGACCAAAAAAGACCTTATATGAAAGAGTTCTTTTATCTTGCCAGAT 491
Db 121 GTTGTGACCAAAAAAGACCTTATATGAAAGAGTTCTTTTATCTTGCCAGAT 180
Qy 492 ATTATGACTAAACGATTATATGATGAGAGCAACATTTGTTATTTGTTCAATGAT 551
Db 181 ATTATGACTAAACGATTATATGATGAGAGCAACATTTGTTATTTGTTCAATGAT 240

RESULT 9
BD005479
LOCUS BD005479 309 bp DNA linear PAT 31-JAN-2002
DEFINITION Cellular immunogens useful cancer vaccines.
ACCESSION BD005479.1 GI:18633850
VERSION
KEYWORDS JP 2001501909-A/9.
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 309)
AUTHORS Halpern,M.S. and England,J.M.
TITLE Cellular immunogens useful cancer vaccines
JOURNAL Patent: JP 2001501909-A 9 13-FEB-2001;
ALLEGHENY UNIVERSITY OF THE HEALTH SCIENCES
COMMENT
OS Unidentified
PN JP 2001501909-A/9
PD 13-FEB-2001
PR 13-JAN-1997 JP 1997526124
PI 19-JAN-1996 US 60/010262
PI MICHAEL S HALPERN, JAMES M ENGLAND
PC A01K63/00,A61K39/00,A61K39/38,A61K48/00,C12N5/00,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key
FT source
FT 1..309 Location/Qualifiers
1..309 Location/Qualifiers
1..309 Location/Qualifiers
/organism="Unidentified".
/mol_type="genomic DNA"
/db_xref="taxon:32644"

FEATURES
source
1..309 Location/Qualifiers
/organism="Unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 9.5%; Score 225; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.5e-115;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 ATGTGCATACCAACATGTCTGTACTCTGATGAGTGTCTGTAACCACTCAGATTCCA 371
Db 1 ATGTGCATACCAACATGTCTGTACTCTGATGAGTGTCTGTAACCACTCAGATTCCA 60

Db 1 ATGTGCATACCAACATGTCTGTACTCTGATGAGTGTCTGTAACCACTCAGATTCCA 60
Qy 372 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAGTTATTAAGTCT 431
Db 61 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAGTTATTAAGTCT 120
Qy 432 GTTGTGACCAAAAAAGACCTTATATGAAAGAGTTCTTTTATCTTGCCAGAT 491
Db 121 GTTGTGACCAAAAAAGACCTTATATGAAAGAGTTCTTTTATCTTGCCAGAT 180
Qy 492 ATTATGACTAAACGATTATATGATGAGAGCAACATTTGTTA 536
Db 181 ATTATGACTAAACGATTATATGATGAGAGCAACATTTGTTA 225

RESULT 10

AR202602
LOCUS AR202602 309 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 9 from patent US 6365151.
ACCESSION AR202602
VERSION AR202602.1 GI:21498774
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 309)
AUTHORS Halpern,M.S. and England,J.M.
TITLE Cellular immunogens comprising cognate proto-oncogenes
JOURNAL Patent: US 6365151-A 9 02-APR-2002;
FEATURES
source
1..309 Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 9.5%; Score 225; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.5e-115;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 ATGTGCATACCAACATGTCTGTACTCTGATGAGTGTCTGTAACCACTCAGATTCCA 371
Db 1 ATGTGCATACCAACATGTCTGTACTCTGATGAGTGTCTGTAACCACTCAGATTCCA 60
Qy 372 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAGTTATTAAGTCT 431
Db 61 GCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAGTTATTAAGTCT 120
Qy 432 GTTGTGACCAAAAAAGACCTTATATGAAAGAGTTCTTTTATCTTGCCAGAT 491
Db 121 GTTGTGACCAAAAAAGACCTTATATGAAAGAGTTCTTTTATCTTGCCAGAT 180
Qy 492 ATTATGACTAAACGATTATATGATGAGAGCAACATTTGTTA 536
Db 181 ATTATGACTAAACGATTATATGATGAGAGCAACATTTGTTA 225

RESULT 11

HSU33203
LOCUS HSU33203 309 bp mRNA linear PRI 13-DEC-2001
DEFINITION Homo sapiens mdm2-E (mdm2) mRNA, complete cds.
ACCESSION U33203
VERSION U33203.1 GI:992684
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (sites)
AUTHORS Sigalas,I., Calvert,A.H., Anderson,J.J., Neal,D.E. and Lunec,J.
TITLE Alternatively spliced mdm2 transcripts with loss of p53 binding domain sequences: transforming ability and frequent detection in human cancer

JOURNAL Nat. Med. 2 (8), 912-917 (1996)
PUBMED 8705862
REFERENCE 2 (bases 1 to 309)
AUTHORS Lunec, J.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-1995) John Lunec, Cancer Research Unit,
University of Newcastle upon Tyne - Medical School, Framlington
Place, Newcastle upon Tyne, NE2 4HH, U.K.

FEATURES
SOURCE
Location/Qualifiers
1..309
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="12"
/map="12q"
/sex="female"
/tissue_type="primary ovarian tumor"
1..309
/gene="mdm2"
1..309
/gene="mdm2"
/experiment="experimental evidence, no additional details recorded"
/note="mdm2 alternatively spliced form (e)"
/codon_start=1
/product="mdm2-E"
/protein_id="AA075518.1"
/db_xref="GI:992685"
/translation="MCNTNMSVPTDGAVTTSQIPASBOETLVRPKLLKLSVGAK
KDIYTKREVLFLGQYIMTKRLYDEKQOHIVNDCANLPLVLDLSIRELYISNYITLGI
"

ORIGIN
Query Match 9.5%; Score 225; DB 5; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.5e-115;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAATCTCTGTACTCTATGATGCTGTGACCACTCAAGATTGCA 371
Db 1 ATGTGCAATACCAATCTCTGTACTCTATGATGCTGTGACCACTCAAGATTGCA 60

QY 372 GCTTCGAAACAAGAGACCTGTTAGACCAAGCATGCTTTGAAGTTATTAAGTCT 431
Db 61 GCTTCGAAACAAGAGACCTGTTAGACCAAGCATGCTTTGAAGTTATTAAGTCT 120

QY 432 GTTGTGCACAAAAGACACTTATCTATGAAAGGTTCTTTTATCTTGCCAGAT 491
Db 121 GTTGTGCACAAAAGACACTTATCTATGAAAGGTTCTTTTATCTTGCCAGAT 180

QY 492 ATTATGACTAAACGATTATGATGAGAGCAACACATATTGTA 536
Db 181 ATTATGACTAAACGATTATGATGAGAGCAACACATATTGTA 225

RESULT 12
HSA278978 297 bp mRNA linear PRI 30-MAY-2001
LOCUS Homo sapiens mRNA for p53-binding protein (MDM2 gene),
alternatively spliced variant EU2.
ACCESSION AJ278978
VERSION AJ278978.1 GI:10045132
KEYWORDS alternative splicing; mdm2 gene; p53-binding protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
AUTHORS Bartel, F., Meye, A., Wurl, P., Kappler, M., Bachle, M.,
Lauteschläger, C., Grunbaum, U., Schmidt, H. and Taubert, H.
TITLE Amplification of the MDM2 gene, but not expression of splice
variants of MDM2 mRNA, is associated with prognosis in soft tissue
sarcoma

JOURNAL Int. J. Cancer 95 (3), 168-175 (2001)
PUBMED 11307150
REFERENCE 2 (bases 1 to 297)
AUTHORS Bartel, F.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Bartel, F., Institute for Pathology,
University of Halle, Faculty of Medicine, Magdeburger Str. 14, 06097
Halle, GERMANY

COMMENT
FEATURES
SOURCE Related sequences: AJ278975-AJ278978, AJ276888.
Location/Qualifiers
1..297
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="rhabdomyosarcoma"
1..297
/gene="MDM2"
1..297
/gene="MDM2"
/product="p53 binding protein"
/note="alternatively spliced variant EU2"
1..297
/gene="MDM2"
/strand name="human homolog of mouse double minute 2"
/experiment="experimental evidence, no additional details recorded"
/note="alternatively spliced variant EU2"
/codon_start=1
/product="p53 binding protein"
/protein_id="CAC07812.1"
/db_xref="GI:10045133"
/db_xref="UniProtKB/TrEMBL:Q9H4C2"
/translation="MCNTNMSVPTDGAVTTSQIPASBOETQDKESVESLPLNAIBP
CVICQGRPKNGICVHGTGTHMACFTCAKKLKKRNKPCVCRPQIQMIVLYFP"

ORIGIN
Query Match 9.4%; Score 222; DB 5; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.3e-113;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1566 ACCCAAGCAAGAAGAGAGTGAATCTAGTTGCCCCCTTAATGCATTGAACCTTGT 1625
Db 76 ACCCAAGCAAGAAGAGAGTGAATCTAGTTGCCCCCTTAATGCATTGAACCTTGT 135

QY 1626 GTGATTGTCAAGTGCACCTTAATAATGTTGCATTGTCATGCAAAACAGACATCTT 1685
Db 136 GTGATTGTCAAGTGCACCTTAATAATGTTGCATTGTCATGCAAAACAGACATCTT 195

QY 1686 ATGGCTGCTTTACATGTGCAAGAGCTAAAGAAAGAAATTAAGCCCTGCCAGTATGT 1745
Db 196 ATGGCTGCTTTACATGTGCAAGAGCTAAAGAAAGAAATTAAGCCCTGCCAGTATGT 255

QY 1746 AGACAACCAATTCAAATGATGCTAATCTTATTTCCCTG 1787
Db 256 AGACAACCAATTCAAATGATGCTAATCTTATTTCCCTG 297

RESULT 13
HSA550516 297 bp mRNA linear PRI 19-MAR-2003
LOCUS Homo sapiens mRNA for HDM2-HD1 protein (HDM2 gene).
ACCESSION AJ550516
VERSION AJ550516.1 GI:29125740
KEYWORDS alternative splicing; HDM2 gene; HDM2-HD1 protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
AUTHORS Sturzenhecker, B., Schlotz, T., Quantin, T., Kube, D., Jung, W. and
Trumper, L.
TITLE Abundant expression of spliced HDM2 in Hodgkin Lymphoma cells does

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

not interfere with p14ARF and p53 binding
Unpublished
2 (bases 1 to 297)
Sturzenhocker B.
Direct Submission
Submitted (18-MAR-2003) Sturzenhocker B., Hematology/Oncology,
University of Goettingen, Robert-Koch-Str. 40, Goettingen, 37075,
GERMANY

FEATURES
source

location/Qualifiers
1..297
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="12"
/map="12q14.3-q15"
/cell_line="KM-H2"
/note="Hodgkin-derived human cell line"
1..297
/gene="MDM2"
1..297
/function="oncogene"
/codon_start=1
/product="MDM2-HD1 protein"
/protein_id="CAD9455.1"
/db_xref="GI:29125741"
/translation="MCNTNMSVPTDGAVTTSQIPASBOETDKESEVSSLPUNAIP
CVICGRPKNGCIVHGKTHLMACFTCAKLKKKKPCVPRQPIQMLVLPFP"

CDS

gene

ORIGIN

Query Match 9.4%; Score 222; DB 5; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.3e-113;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1566 ACCCAAGCAAGAGAGAGTGTGAATCTGTTGCCCTTAATGCCATGAACCTTGT 1625
Db 76 ACCCAAGCAAGAGAGAGTGTGAATCTGTTGCCCTTAATGCCATGAACCTTGT 135
QY 1626 GTGATTGTCAAGTGCAGCTTAATAATGGTGCATTGTCATGGCAAAACAGACATCTT 1685
Db 136 GTGATTGTCAAGTGCAGCTTAATAATGGTGCATTGTCATGGCAAAACAGACATCTT 195
QY 1686 ATGGCTGCTTTACATGTGCAAGAGAGTGAAGTAAAGAAAGAAATAGCCCTGCCAGTATGT 1745
Db 196 ATGGCTGCTTTACATGTGCAAGAGAGTGAAGTAAAGAAAGAAATAGCCCTGCCAGTATGT 255
QY 1746 AGAACAACCAATTCAATGATTTGTCTAATCTATTTCCTTAG 1787
Db 256 AGAACAACCAATTCAATGATTTGTCTAATCTATTTCCTTAG 297

RESULT 14

LOCUS

G66929 209 bp DNA linear STS 24-AUG-2000
DEFINITION csmpm2-pcr7-1 Human Homo sapiens STS genomic; sequence tagged
site.
G66929
ACCESSION G66929.1 GI:9909460
VERSION
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo
1 (bases 1 to 209)
Wong, G.K.S., Yu, J., Yang, Z., Passey, D., Kibukawa, M., Paddock, M. and
Olson, M.
Gene based polymorphism discovery
Unpublished (2000)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Gene Ka-Shu Wong
Genome Center
University of Washington

Fluke Hall, Box 352145, Seattle, WA 98195, USA
Tel: 206/685-7348
Fax: 206/685-7344
Email: gks@u.washington.edu

Primer A: ATGGCTGCTTTACATGTCC
Primer B: TGAATTAAGGCAATTTCTCAC
STS size: 209
PCR Profile:

Presoak: 92 degrees C for 1.00 minute
Denaturation: 92 degrees C for 0.16 minute
Annealing: 60-65 degrees C for 0.50 minute
Polymerization: 72 degrees C for 1.00 minute
PCR Cycles: 35
Thermal Cycler: Perkin Elmer TC
Protocol:

Template: 7 ng
Primer: each 0.5 uM
dNTPs: each 100 uM
Taq Polymerase: 0.025 units/uL
Total Vol: 10 uL

Buffer:

MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3.

FEATURES

source

location/Qualifiers
1..209
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="12q14.3-q15"
/clone_11b="Human"
1..209
/gene="MDM2"
1..209
/gene="MDM2"
1..20
primer_bind complement(189..209)

ORIGIN

Query Match 8.8%; Score 209; DB 7; Length 209;
Best Local Similarity 100.0%; Pred. No. 3.3e-106;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1686 ATGGCTGCTTTACATGTGCAAGAGAGTGAAGTAAAGAAAGAAATAGCCCTGCCAGTATGT 1745
Db 1 ATGGCTGCTTTACATGTGCAAGAGAGTGAAGTAAAGAAAGAAATAGCCCTGCCAGTATGT 60
QY 1746 AGAACAACCAATTCAATGATTTGTCTAATCTATTTCCTTAGTGAACCTGCTATAAGAG 1805
Db 61 AGAACAACCAATTCAATGATTTGTCTAATCTATTTCCTTAGTGAACCTGCTATAAGAG 120
QY 1806 AATTATATATTTCTAATCTATAATAACCTAGCAATTTGACAACTGAAATTTATTCACAT 1865
Db 121 AATTATATATTTCTAATCTATAATAACCTAGCAATTTGACAACTGAAATTTATTCACAT 180
QY 1866 AATCAAGTGAAGAAATAGCCTCAATCA 1894
Db 181 AATCAAGTGAAGAAATAGCCTCAATCA 209

RESULT 15

LOCUS

HS4550518 210 bp mRNA linear PRI 15-APR-2005
DEFINITION Homo sapiens mRNA for MDM2-HD3 protein (MDM2 gene).
AJ550518
ACCESSION AJ550518.1 GI:29125744
VERSION
KEYWORDS alternative splicing; MDM2 gene; MDM2-HD3 protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE	TITLE	JOURNAL	REFERENCE	AUTHORS	DATE
1	Homnidae; Homo.				
1	Sturzenhofecker, B., Schlott, T., Quentin, T., Kube, D., Jung, W. and Trumper, L.				
1	Abundant expression of spliced HDM2 in Hodgkin Lymphoma cells does not interfere with p14ARF and p53 binding				
1	Unpublished				
2	(bases 1 to 210)				
2	Sturzenhofecker, B.				
2	Direct Submission				
2	Submitted (18-MAR-2003) Sturzenhofecker B., Hematology/Oncology, University of Goettingen, Robert-Koch-Str. 40, Goettingen, 37075, GERMANY				
FEATURES	Location/Qualifiers				
1..210	/organism="Homo sapiens"				
1..210	/mol_type="mRNA"				
1..210	/db_xref="taxon:9606"				
1..210	/chromosome="12"				
1..210	/map="12q14.3-q15"				
1..210	/cell_line="HDLm2"				
1..210	/note="Hodgkin-derived human cell line"				
1..210	/gene="HDM2"				
1..210	/gene="HDM2"				
1..210	/function="Oncogene"				
1..210	/codon_start=1				
1..210	/product="HDM2-HD3 protein"				
1..210	/protein_id="CAD79457.1"				
1..210	/db_xref="GI:29125745"				
1..210	/db_xref="GO:086W44"				
1..210	/db_xref="InterPro:IPR003121"				
1..210	/db_xref="UniProtKB/TREMBL:Q86W44"				
1..210	/translation="MCMNMSVPDVGATGATTSQIPASEQETLVKPKPLIKLKSVGAC				
1..210	KDTYTMKEVLPLYLGQISNVTTLGI"				
ORIGIN					
Query Match	7.7%; Score 183; DB 5; Length 210;				
Best Local Similarity	100.0%; Pred. No. 2.1e-91;				
Matches	183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	312 ATGTGCAATACCAACATGTCTGTACCTACTGATGATGCTGTAAACCACTCAGATTCCA	371			
Db	1 ATGTGCATATACCAACATGTCTGTACCTACTGATGATGCTGTAAACCACTCAGATTCCA	60			
QY	372 GCTTCGGAACAAGAGACCCCTGTTTGAACCAAGCCATTGCTTTGAAGTTATTTAAAGTCT	431			
Db	61 GCTTCGGAACAAGAGACCCCTGTTTGAACCAAGCCATTGCTTTGAAGTTATTTAAAGTCT	120			
QY	432 GTTGGTGACACAAAAGACACTTATCTACTATGAAAGAGTCTTTTATCTTGGCCAGAT	491			
Db	121 GTTGGTGACACAAAAGACACTTATCTACTATGAAAGAGTCTTTTATCTTGGCCAGAT	180			
QY	492 ATT 494				
Db	181 ATT 183				
RESULT 16					
LOCUS	HSAS050519	213 bp	mRNA	linear	PRI 15-APR-2005
DEFINITION	Homo sapiens mRNA for HDM2-HD5 protein (HDM2 gene).				
ACCESSION	AJ550519				
VERSION	AJ550519.1				
KEYWORDS	alternative splicing; HDM2 gene; HDM2-HD5 protein.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Sturzenhofecker, B., Schlott, T., Quentin, T., Kube, D., Jung, W. and				

FEATURES	source	location/Qualifiers
TITLE	Trummer, L.	Abundant expression of spliced HDM2 in Hodgkin lymphoma cells does not interfere with p1ARF and p53 binding
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 213)	
AUTHORS	Sturzenhocker, B.	
TITLE	Direct Submission	
JOURNAL	Submitted (18-MAR-2003) Sturzenhocker B., Hematology/Oncology, University of Goettingen, Robert-Koch-Str. 40, Goettingen, 37075, GERMANY	
FEATURES	source	location/Qualifiers
1. 213	/organism="Homo sapiens"	
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	/db_xref="taxon:9606"	
	/chromosome="12"	
	/map="12q14.3-q15"	
	/cell_line="L1236"	
	/note="Hodgkin-derived human cell line"	
gene	1. 213	/gene="HDM2"
	1. 213	/gene="HDM2"
CDS	/function="oncogene"	
	/codon_start=1	
	/product="HDM2-HD5 protein"	
	/protein_id="CAD79458.1"	
	/db_xref="GI:29125747"	
	/db_xref="GOA:Q86WA3"	
	/db_xref="InterPro:IPR003121"	
	/db_xref="UniProtKB/TrEMBL:Q86WA3"	
	/translation="MCNTNMSVPTDGVATTSQIPASBOETLVRPKPLTLKLKSVGAQKDYTMKEVLFYGLLYMCKEAKKE"	
ORIGIN		
Query Match	7.4%; Score 175; DB 5; Length 213;	
Best Local Similarity	100.0%; Pred. No. 7.3e-87;	
Matches 175; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	312 ATGTGCAATTCACCAACATGCTCTGTACCTACCTACGATGCTGTAAACCACTTCACGATTCACA	371
Db	1 ATGTGCAATTCACCAACATGCTCTGTACCTACCTACGATGCTGTAAACCACTTCACGATTCACA	60
QY	372 GCTTCGGAACAAGAGACCTCGTGTAGACCAAGCGCATTTGTTGAAGTATTAAGTCT	431
Db	61 GCTTCGGAACAAGAGACCTCGTGTAGACCAAGCGCATTTGTTGAAGTATTAAGTCT	120
QY	432 GTTGGTGCACAAAAGACACTTATCTATGAAAAGAGTTCTTTTATCTTGGCC	486
Db	121 GTTGGTGCACAAAAGACACTTATCTATGAAAAGAGTTCTTTTATCTTGGCC	175
RESULT 17		
AF385324	224 bp	mrna linear PRI 11-OCT-2001
LOCUS	AF385324	Homo sapiens MDM2 variant FB28 (MDM2) mRNA, complete cds,
DEFINITION	AF385324	alternatively spliced.
ACCESSION	AF385324	GI:16033444
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		Homo sapiens (human)
		Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
		Hominidae; Homo.
REFERENCE		1 (bases 1 to 224)
AUTHORS		Bartel, F., Taylor, A.C., Taubert, H. and Harris, L.C.
TITLE		Novel mdm2 splice variants identified in pediatric rhabdomyosarcoma
JOURNAL		tumors and cell lines
REFERENCE		Unpublished
TITLE		2 (bases 1 to 224)
		Bartel, F., Taylor, A.C., Taubert, H. and Harris, L.C.
		Direct Submission

JOURNAL Submitted (24-MAY-2001) Molecular Pharmacology, St. Jude Children's Research Hospital, 332 N. Lauderdale, Memphis, TN 38105, USA
Location/Qualifiers

FEATURES
source
1..224
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="rhabdomyosarcoma tumor"
1..224
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1..201
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/note="alternatively spliced"
/codon_start=1
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/protein_id="AA13244.1"
/db_xref="GI:16033445"
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KDYTMKEVLFYLAQYVDNPK"

ORIGIN

Query Match 7.3%; Score 172; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.7e-85; Mismatches 0; Indels 0; Gaps 0;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTACCACTCAAGATTCCA 371
Db 1 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTACCACTCAAGATTCCA 60

Qy 372 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 431
Db 61 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 120

Qy 432 GTTGTGCACAAAAGACACTTATCTATGAAGGTTCTTTTATCTTG 483
Db 121 GTTGTGCACAAAAGACACTTATCTATGAAGGTTCTTTTATCTTG 172

RESULT 18
AP385326 288 bp mRNA linear PRI 11-OCT-2001
LOCUS Homo sapiens MDM2 variant FB30 (MDM2) mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AP385326
VERSION AP385326.1 GI:16033450
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 288)
AUTHORS Bartel,F., Taylor,A.C., Taubert,H. and Harris,L.C.
TITLE Novel mdm2 splice variants identified in pediatric rhabdomyosarcoma
tumors and cell lines
JOURNAL Unpublished
2 (bases 1 to 288)
AUTHORS Bartel,F., Taylor,A.C., Taubert,H. and Harris,L.C.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2001) Molecular Pharmacology, St. Jude Children's
Research Hospital, 332 N. Lauderdale, Memphis, TN 38105, USA
location/Qualifiers
1..288
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="rhabdomyosarcoma tumor"
/note="same sequence isolated from rhabdomyosarcoma cell
line"
1..288
/gene="MDM2"
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/db_xref="taxon:9606"
/tissue_type="rhabdomyosarcoma tumor"
/note="same sequence isolated from rhabdomyosarcoma cell
line"
1..288
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1..288
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/note="alternatively spliced"
/codon_start=1
/product="MDM2 variant FB30"
/protein_id="AA13246.1"
/db_xref="GI:16033451"
/translation="MCTNMSVPTDGAVTTSQIPASQETLVRRPKLLKLSVGAQ
KDYTMKEVLFYKGTGLMACTCAKELKRKNRCPVCPPIQIVITLTPP"

ORIGIN

Query Match 7.1%; Score 168; DB 5; Length 288;
Best Local Similarity 100.0%; Pred. No. 6.6e-83; Mismatches 0; Indels 0; Gaps 0;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 312 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTACCACTCAAGATTCCA 371
Db 1 ATGTGCAATACCAACATGTCTGTACCTAGTGTGCTGTACCACTCAAGATTCCA 60

Qy 372 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 431
Db 61 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTGCTTTGAAGTTAAAGTCT 120

Qy 432 GTTGTGCACAAAAGACACTTATCTATGAAGGTTCTTTTAT 479
Db 121 GTTGTGCACAAAAGACACTTATCTATGAAGGTTCTTTTAT 168

RESULT 19
AX587650 319 bp DNA linear PAT 10-JAN-2003
LOCUS Sequence 120 from Patent WO0246467.
DEFINITION AX587650
ACCESSION AX587650
VERSION AX587650.1 GI:27656423
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
OTHER SEQUENCES; artificial sequences.
REFERENCE 1
AUTHORS Bertucci,F., Houlgate,R., Birnbaum,D., Nguyen,C., Viens,P. and
Pert,V.
TITLE Gene expression profiling of primary breast carcinomas using arrays
of candidate genes
JOURNAL Patent: WO 0246467-A 120 13-JUN-2002;
Ipsogen (FR)
FEATURES
source
1..319
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
1..319
/note="5' terminal sequence. mouse double minute 2, human
homolog of; p53-binding protein (MDM2) gene."

ORIGIN

Query Match 7.0%; Score 167; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 2.4e-82; Mismatches 0; Indels 0; Gaps 0;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1773 ACTTATTTCCCTGTTGACCTGCTATAGAGAAATATATATTTCTTCACTATTAACCC 1832
Db 2 ACTTATTTCCCTGTTGACCTGCTATAGAGAAATATATATTTCTTCACTATTAACCC 61

Qy 1833 TAGGAATTTAGACAACCTGAAATTTATTCACATATCAAGTGAAGAAATGCTCAATT 1892
Db 62 TAGGAATTTAGACAACCTGAAATTTATTCACATATCAAGTGAAGAAATGCTCAATT 121

Qy 1893 CACATAGATTTCTTCTTTAGTAAATGACCTACTTGGTAGGG 1939
Db 122 CACATAGATTTCTTCTTTAGTAAATGACCTACTTGGTAGGG 168

RESULT 20
HSA276888

LOCUS HSA276888 364 bp mRNA linear PRI 30-MAY-2001
DEFINITION Homo sapiens non-productive mRNA for p53-binding protein,
alternatively spliced variant DS2 (MDM2 gene).
ACCESSION AJ276888
VERSION AJ276888.1 GI:7327962
KEYWORDS alternative splicing; DS2; mdm2 gene; p53-binding.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Bartel,F., Meyer,A., Wurl,P., Kappler,M., Bache,M.,
Lautenschlager,C., Grunbaum,U., Schmidt,H. and Taubert,H.
TITLE Amplification of the MDM2 gene, but not expression of splice
variants of MDM2 mRNA, is associated with prognosis in soft tissue
sarcoma
JOURNAL Int. J. Cancer 95 (3), 168-175 (2001)
PUBMED 11307150
REFERENCE 2 (bases 1 to 364)
AUTHORS Bartel,F.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2000) Bartel F., Institute for Pathology,
University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097
Halle, GERMANY
FEATURES
source location/Qualifiers
1..364
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..364
/gene="MDM2"
/pseudo
1..364
/gene="MDM2"
/note="alternatively spliced isoform DS2"
/pseudo
1..364
/gene="MDM2"
/standard_name="human homolog of mouse double minute 2"
/note="alternatively spliced isoform DS2"
/pseudo
/codon_start=1
/product="p53-binding protein"
ORIGIN
Query Match 6.6%; Score 157; DB 5; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.1e-76;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 312 ATGTGCAATACCAATGCTGTACTCTGATGCTGTACCACTCAGATTCCA 371
DB 1 ATGTGCAATACCAATGCTGTACTCTGATGCTGTACCACTCAGATTCCA 60
QY 372 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTGCTTTGAAGTATTAAAGTCT 431
DB 61 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTGCTTTGAAGTATTAAAGTCT 120
QY 432 GTTGGTGCACAAAAAGACACTTATCTATGAAAGAG 468
DB 121 GTTGGTGCACAAAAAGACACTTATCTATGAAAGAG 157
RESULT 21
LOCUS HSAS50517 198 bp mRNA linear PRI 15-APR-2005
DEFINITION Homo sapiens mRNA for HDM2-HD2 protein (HDM2 gene).
ACCESSION AJ550517
VERSION AJ550517.1 GI:29125742
KEYWORDS alternative splicing; HDM2 gene; HDM2-HD2 protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Sturzenhocker,B., Schlott,T., Quentin,T., Kube,D., Jung,W. and
Trumper,L.
TITLE Abundant expression of spliced HDM2 in Hodgkin Lymphoma cells does
not interfere with p14ARF and p53 binding
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 198)
AUTHORS Sturzenhocker,B.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-2003) Sturzenhocker B., Hematology/Oncology,
University of Goettingen, Robert-Koch-Str. 40, Goettingen, 37075,
GERMANY
FEATURES
source location/Qualifiers
1..198
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="12"
/map="12q14.3-q15"
/cell_line="KM-H2"
/note="Hodgkin-derived human cell line"
1..198
/gene="HDM2"
1..198
/gene="HDM2"
/function="Oncogene"
/codon_start=1
/product="HDM2-HD2 protein"
/protein_id="CAD79456.1"
/db_xref="GI:29125743"
/db_xref="UniProtKB/TrEMBL:O86N45"
/translation="MCNTNMSVPTDGAATTSQIPASEQETLVPRKPLLKILKSYGAQ
KDYTMKPIHIYQSEKMPQFT"
ORIGIN
Query Match 6.5%; Score 153; DB 5; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.4e-74;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 312 ATGTGCAATACCAATGCTGTACTCTGATGCTGTACCACTCAGATTCCA 371
DB 1 ATGTGCAATACCAATGCTGTACTCTGATGCTGTACCACTCAGATTCCA 60
QY 372 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTGCTTTGAAGTATTAAAGTCT 431
DB 61 GCTTCGGAACAAGAGACCCCTGTTAGACCAAGCCATTGCTTTGAAGTATTAAAGTCT 120
QY 432 GTTGGTGCACAAAAAGACACTTATCTATGAAA 464
DB 121 GTTGGTGCACAAAAAGACACTTATCTATGAAA 153
RESULT 22
LOCUS AR229721 199 bp RNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6451524.
ACCESSION AR229721
VERSION AR229721.1 GI:27269545
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 199)
AUTHORS Ecker,D.J.
TITLE Identification of disease predictive nucleic acids
JOURNAL Patent: US 6451524-A 1 17-SEP-2002;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
source location/Qualifiers
1..199
/organism="unknown"
/mol_type="unassigned RNA"


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RESULT 25
LOCUS AR229722 199 bp RNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6451524.
ACCESSION AR229722
VERSION AR229722.1 GI:27269546
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1.199
/mol_type="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 5.8%; Score 138; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 8.2e-66;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 CAGGAATGTCATACCAATGCTGTACTGTATGCTGTACCACTCACA 364
DB 62 CAGGCAATGTCATACCAATGCTGTACTGTATGCTGTACCACTCACA 121
QY 365 GATTCACGCTTGGAAACAAGAGACCTGCTGTAGCAACCAATGCTTTGAAGTTAT 424
DB 122 GATTCACGCTTGGAAACAAGAGACCTGCTGTAGCAACCAATGCTTTGAAGTTAT 181
QY 425 AAAGTCGTGTGTCACA 442
DB 182 AAAGTCGTGTGTCACA 199

RESULT 26
LOCUS HSAS50520 165 bp mRNA linear PRI 19-MAR-2003
DEFINITION Homo sapiens mRNA for HDM2-HD4 protein (HDM2 gene).
ACCESSION AJ550520
VERSION AJ550520.1 GI:29125748
KEYWORDS alternative splicing; HDM2 gene; HDM2-HD4 protein.
SOURCE
ORGANISM
Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1.165
/mol_type="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="12"
/map="12q14.3-q15"
/cell_line="HDM2"
/note="Hodgkin-derived human cell line"
1.165
/gene="HDM2"

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CDS
1.165
/gene="HDM2"
/function="oncogene"
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/product="HDM2-HD4 protein"
/protein_id="CAD79459.1"
/db_xref="GI:29125748"
/translation="MCNTNMSVPTDGAATTSQIPASQETLVPRPLKLKLSIREL
YISNTITLGI"

ORIGIN
Query Match 5.1%; Score 120; DB 5; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.5e-55;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAATGCTGTACTGTATGCTGTATGCTGTACCACTCACAATTCCA 371
DB 1 ATGTGCAATACCAATGCTGTACTGTATGCTGTATGCTGTACCACTCACAATTCCA 60
QY 372 GCTTGGAAACAAGAGACCTGCTGTAGCAACCAATGCTTTGAAGTTAAGTCT 431
DB 61 GCTTGGAAACAAGAGACCTGCTGTAGCAACCAATGCTTTGAAGTTAAGTCT 120

RESULT 27
LOCUS BV193037 401 bp DNA linear STS 10-JUN-2004
DEFINITION sqm176519 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
tagged site.
ACCESSION BV193037
VERSION BV193037.1 GI:48035762
KEYWORDS STS.
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 401.
Location/Qualifiers
1.401
/mol_type="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human DNA (Sequenom)"
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ORIGIN
Query Match 3.7%; Score 88; DB 7; Length 401;
Best Local Similarity 100.0%; Pred. No. 2e-37;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTATGACAGATGCTGCATCTCAGACCTGTCGTCGCGCCACCTC 2333
DB 289 GGGTTTACCGTGTATGACAGATGCTGCATCTCAGACCTGTCGTCGCGCGCCACCTC 348
QY 2334 GGGTCCCAAGTGTGATTAACAGC 2361

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Db 349 GGCCCTCCCAAGTCTGGATTACAGGC 376

RESULT 28
AX981948/c 397 bp DNA linear PAT 15-JAN-2004
LOCUS
DEFINITION Sequence 12751 from Patent EP1104808.
ACCESSION AX981948
VERSION AX981948.1 GI:40988088
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
ESTs and encoded human proteins
Patent: EP 1104808-A 12751 06-JUN-2001;
Genset (FR)

FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 3.3%; Score 78; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 9.7e-32;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2284 GTGTTAGCCAGAGTGTCTGATCTCTGACCTGTCGATCCGCCACCTCGGCTCCCAA 2343
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210 GTGTTAGCCAGAGTGTCTGATCTCTGACCTGTCGATCCGCCACCTCGGCTCCCAA 151
|||||

Qy 2344 AGTCTGGGATTACAGGC 2361
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150 AGTCTGGGATTACAGGC 133
|||||

Db 150 AGTCTGGGATTACAGGC 133
|||||

RESULT 29
BD116807/c 397 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION EST and encoded human protein.
ACCESSION BD116807
VERSION BD116807.1 GI:23211711
KEYWORDS JP 2002010789-A/8884.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 397)
Edwards, J.B.D.M., Jobert, S. and Giordano, J.Y.
EST and encoded human protein
Patent: JP 2002010789-A 8884 15-JAN-2002;
GENSET CORP

COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/8884
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC n=a, g, c or t location/Qualifiers
FH key misc_feature 250.
FT misc_location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 3.3%; Score 78; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 9.7e-32;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2284 GTGTTAGCCAGAGTGTCTGATCTCTGACCTGTCGATCCGCCACCTCGGCTCCCAA 2343
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210 GTGTTAGCCAGAGTGTCTGATCTCTGACCTGTCGATCCGCCACCTCGGCTCCCAA 151
|||||

Qy 2344 AGTCTGGGATTACAGGC 2361
|||||
150 AGTCTGGGATTACAGGC 133
|||||

Db 150 AGTCTGGGATTACAGGC 133
|||||

RESULT 30
AR421254/c 397 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 12751 from patent US 6639063.
ACCESSION AR421254
VERSION AR421254.1 GI:40176364
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 397)
Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 12751 28-OCT-2003;
Genset S.A.;;
WOX;

FEATURES
source location/Qualifiers
1..397
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 3.3%; Score 78; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 9.7e-32;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2284 GTGTTAGCCAGAGTGTCTGATCTCTGACCTGTCGATCCGCCACCTCGGCTCCCAA 2343
|||||
210 GTGTTAGCCAGAGTGTCTGATCTCTGACCTGTCGATCCGCCACCTCGGCTCCCAA 151
|||||

Qy 2344 AGTCTGGGATTACAGGC 2361
|||||
150 AGTCTGGGATTACAGGC 133
|||||

Db 150 AGTCTGGGATTACAGGC 133
|||||

RESULT 31
AB140799/c 427 bp DNA linear STS 27-OCT-2005
LOCUS
DEFINITION Homo sapiens DNA, STS on chromosome 11, D11S04061, sequence tagged
site.
ACCESSION AB140799
VERSION AB140799.1 GI:62161617
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
Taniya, G., Shinya, M., Imanishi, T., Ikuta, T., Makino, S., Okamoto, K.,
Furugaki, K., Matsunoto, T., Mano, S., Ando, S., Nozaki, Y., Yukawa, W.,
Nakashige, R., Yamaguchi, D., Ishibashi, H., Yonekura, M., Nakami, Y.,
Takayama, S., Endo, T., Saruwatari, T., Iegusa, M., Yoshikawa, Y.,
Fujimoto, K., Oka, A., Chiku, S., Iinsen, S.E., Giphart, M.J.,
Kulski, J.K., Fukazawa, T., Hashimoto, H., Kimura, M., Hoshina, Y.,

Suzuki,Y., Hotta,T., Mochida,J., Minezaki,T., Komai,K., Shiozawa,S., Taniguchi,A., Yamanaka,H., Kametani,N., Gojobori,T., Bahram,S. and Inoko,H.
Whole genome association study of rheumatoid arthritis using 27 039 microsatellites
Hum. Mol. Genet. 14 (16), 2305-2321 (2005)

JOURNAL PUBMED 16000323
REFERENCE 2 (bases 1 to 427)
AUTHORS Tamaya,G., Makino,S., Fujimoto,K., Oka,A., Hayashi,H., Denda,A., Linsen,S.E., Ikuta,T., Shinya,M., Endo,T., Tomizawa,M., Tokubo,E., Sato,R., Takaki,A., Nagatsuka,Y., Watanabe,H., Adachi,S., Makino,Y., Nakano,S., Yamamoto,A., Yoshida,K., Okamoto,K., Yamaguchi,D., Ishibashi,H., Yonekura,M., Takayama,S., Nakami,Y., Saruwatari,T., Brand,A., van Hilten,J.A., van de Watering,L.M., Giphart,M.J., Bahram,S., Kulski,Y.J. and Inoko,H.
Direct Submission
Submitted (12-DEC-2003) Hidetoshi Inoko, Tokai University School of Medicine, Department of Genetic Information, Bohseidai, Isehara, Kanagawa, 259-1193, Japan (E-mail:hino@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884)
Polymorphisms were confirmed by comparing with the pooled DNA typing data of 88 Dutch population or 100 Australian. When there was no significant difference between the Japanese and these Caucasians, individual typing was performed to confirm polymorphisms.

FEATURES
source location/Qualifiers
1..427
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="11"
/map="11q13.2"
/note="pooled DNA of 100 Japanese unrelated individuals sequence tagged site D11S04061"
1..22
/note="5' primer: AGGACTCTGTAAGCTGATTAG"
/PCR_conditions="denaturation 96degC 5 min, 57degC 1 min, 72degC 1 min; 40 cycles 96degC 45 sec, 57degC 45 sec, 72degC 1 min"
360..406
/note="sequence tagged site D11S04061"
/rpt_type=tandem
/rpt_unit_seg="aat"
complement(403..427)
/note="3' primer: CACACTCAGTAATGTTTAACTTAT"

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Best Local Similarity 100.0%; Pred. No. 3.5e-31;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGTCGTGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAA 2344
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DB 173 TGTAGCCAGATGTCGTGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAA 114
|||||

QY 2345 GTGCTGGATTACAGGC 2361
|||||
DB 113 GTGCTGGATTACAGGC 97
|||||

RESULT 32
ABI52167
LOCUS Homo sapiens DNA, STS on chromosome 10, D10S09061, sequence tagged site.
ACCESSION ABI52167
VERSION ABI52167.1 GI:62172985
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Tamaya,G., Shinya,M., Imanishi,T., Ikuta,T., Makino,S., Okamoto,K., Furugaki,K., Matsumoto,T., Mano,S., Ando,S., Nozaki,Y., Yukawa,W., Nakashige,R., Yamaguchi,D., Ishibashi,H., Yonekura,M., Nakami,Y., Takayama,S., Endo,T., Saruwatari,T., Yaegura,M., Yoshikawa,Y., Fujimoto,K., Oka,A., Chiku,S., Linsen,S.E., Giphart,M.J., Kulski,J.K., Fukazawa,T., Hashimoto,H., Kimura,M., Hoshina,Y., Suzuki,Y., Hotta,T., Mochida,J., Minezaki,T., Komai,K., Shiozawa,S., Taniguchi,A., Yamanaka,H., Kametani,N., Gojobori,T., Bahram,S. and Inoko,H.
Whole genome association study of rheumatoid arthritis using 27 039 microsatellites
Hum. Mol. Genet. 14 (16), 2305-2321 (2005)

JOURNAL PUBMED 16000323
REFERENCE 2 (bases 1 to 440)
AUTHORS Tamaya,G., Makino,S., Fujimoto,K., Oka,A., Hayashi,H., Denda,A., Linsen,S.E., Ikuta,T., Shinya,M., Endo,T., Tomizawa,M., Tokubo,E., Sato,R., Takaki,A., Nagatsuka,Y., Watanabe,H., Adachi,S., Makino,Y., Nakano,S., Yamamoto,A., Yoshida,K., Okamoto,K., Yamaguchi,D., Ishibashi,H., Yonekura,M., Takayama,S., Nakami,Y., Saruwatari,T., Brand,A., van Hilten,J.A., van de Watering,L.M., Giphart,M.J., Bahram,S., Kulski,Y.J. and Inoko,H.
Direct Submission
Submitted (12-DEC-2003) Hidetoshi Inoko, Tokai University School of Medicine, Department of Genetic Information, Bohseidai, Isehara, Kanagawa, 259-1193, Japan (E-mail:hino@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884)
Polymorphisms were confirmed by comparing with the pooled DNA typing data of 88 Dutch population or 100 Australian. When there was no significant difference between the Japanese and these Caucasians, individual typing was performed to confirm polymorphisms.

FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
/map="10q21.1"
/note="pooled DNA of 100 Japanese unrelated individuals sequence tagged site D10S09061"
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/PCR_conditions="denaturation 96degC 5 min, 57degC 1 min, 72degC 1 min; 40 cycles 96degC 45 sec, 57degC 45 sec, 72degC 1 min"
88..126
/note="sequence tagged site D10S09061"
/rpt_type=tandem
/rpt_unit_seg="cttg"
complement(420..440)
/note="3' primer: CTCCTCTCTCTCAGTATG"

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Query Match 3.2%; Score 77; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 3.5e-31;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGTCGTGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAA 2344
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DB 314 TGTAGCCAGATGTCGTGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAA 373
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QY 2345 GTGCTGGATTACAGGC 2361
|||||
DB 374 GTGCTGGATTACAGGC 390
|||||

RESULT 33
HS2ALU36/c
LOCUS HS2ALU36S 291 bp DNA linear PRI 18-MAR-1994
DEFINITION H.sapiens DNA for Mhc Alu elements.
ACCESSION Z30959
VERSION Z30959.1 GI:461305

KEYWORDS Ali element; major histocompatibility complex.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 291)
Mukova-Pajdlova,M., Satla,Y., O'Huigin,C., Mayer,W.E., Figuerola,F. and Klein,J.
TITLE Ali elements of the primate major histocompatibility complex
JOURNAL Mamm. Genome (1994) In press
AUTHORS 2 (bases 1 to 291)
O'Huigin,C.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1994) O'Huigin C., Max-Planck-Institut fuer Biologie, Abteilung Immunogenetik, Corrensstr. 42, 72076 Tuebingen, Germany
FEATURES
source Location/Qualifiers
1..291
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
repeat_region 1..291
Query Match 3.2%; Score 76; DB 5; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2286 GTTAGCCAGATGCTCTGATCTCTGACCTGCGATCCGCCACCTGGCCTCCCAAG 2345
Db 96 GTTAGCCAGATGCTCTGATCTCTGACCTGCGATCCGCCACCTGGCCTCCCAAG 37
Qy 2346 TGCTGGAGTTACAGGC 2361
Db 36 TGCTGGAGTTACAGGC 21
RESULT 34
BD074010/c 73 bp DNA linear PAT 27-AUG-2002
LOCUS BD074010
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074010
VERSION BD074010.1 GI:22619613
KEYWORDS JP 2001513996-A/49.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 73)
Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 49 11-SEP-2001;
HYBRIDON INC.
COMMENT OS Unidentified
PN JP 2001513996-A/49
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
JIJANDONG CHEN,SUDHIR AGRAWAL,RUTIMEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH key Location/Qualifiers
FT source 1..73
FT Location/Qualifiers
1..73
/organism="Unidentified".
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source Location/Qualifiers
1..73
/organism="unidentified"
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/db_xref="taxon:32644"
ORIGIN

Query Match 3.1%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 9.1e-29;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 665 AGGTACATCTGTGATGATGAGAACAGGTGTCACTTGAAGGTGGAGTATCAAAAGACCT 724
Db 73 AGGTACATCTGTGATGATGAGAACAGGTGTCACTTGAAGGTGGAGTATCAAAAGACCT 14
Qy 725 TGTACAGAGCTT 737
Db 13 TGTACAGAGCTT 1
RESULT 35
AR721415/c 73 bp DNA linear PAT 07-OCT-2005
LOCUS AR721415
DEFINITION Sequence 49 from patent US 6946447.
ACCESSION AR721415
VERSION AR721415.1 GI:77372938
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 73)
Chen,J., Agrawal,S. and Zhang,R.
TITLE MDM2-specific antisense oligonucleotides
JOURNAL Patent: US 6946447-A 49 20-SEP-2005;
HYBRIDON, Inc.; Cambridge, MA;
WOX;
FEATURES
source Location/Qualifiers
1..73
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/mol_type="genomic DNA"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.1e-29;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 665 AGGTACATCTGTGATGATGAGAACAGGTGTCACTTGAAGGTGGAGTATCAAAAGACCT 724
Db 73 AGGTACATCTGTGATGATGAGAACAGGTGTCACTTGAAGGTGGAGTATCAAAAGACCT 14
Qy 725 TGTACAGAGCTT 737
Db 13 TGTACAGAGCTT 1
RESULT 36
BV195288/c 401 bp DNA linear STS 10-JUN-2004
LOCUS BV195288
DEFINITION sqm184015 Human DNA (Sequenom) Homo sapiens STS genomic, sequence tagged site.
ACCESSION BV195288
VERSION BV195288.1 GI:48039039
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 401)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
TITLE Nelson,R.M., Marnell,J.G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A.
JOURNAL Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions
COMMENT Genome Res. (2004) In press
Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA

Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 401.

FEATURES
source

1..401
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human DNA (Sequenom)"
<1..>401

ORIGIN
STS

Query Match 3.1%; Score 73; DB 7; Length 401;
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Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGCTCGATCTCTGACCTCGTATCGCCGCACTCGGCTCCCAA 2344
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DB 159 TGTAGCCAGATGCTCGATCTCTGACCTCGTATCGCCGCACTCGGCTCCCAA 100
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QY 2345 GTGCTGGATTAC 2357
|||||
DB 99 GTGCTGGATTAC 87
|||||

RESULT 37
AY270309 315 bp DNA linear PRI 08-JUL-2003
LOCUS Homo sapiens clone SKT02-C5 putative promoter sequence.
DEFINITION AY270309
ACCESSION AY270309.1 GI:30720522
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 315)
Batzoglou,S. and Myers,R.M.
JOURNAL Identification of promoter regions in the human genome by using a
retroviral plasmid library-based functional reporter gene assay
Genome Res. 13 (7), 1765-1774 (2003)
PUBMED 12805274
2 (bases 1 to 315)
Khambata-Ford,S., Liu,Y., Gleason,C., Dickson,M., Altman,R.B.,
JOURNAL Direct Submission
AUTHORS Submitted (07-APR-2003) Genetics, Stanford University School of
TITLE Medicine, 300 Pasteur Drive, Stanford, CA 94305-5120, USA
JOURNAL Location/Qualifiers
1..315
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="SKT02-C5"
<1..>315
/note="contains putative promoter region; identified by
retroviral plasmid library-based functional reporter
assay"

ORIGIN

Query Match 3.0%; Score 71; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 9.7e-28;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCCAGATGCTCGATCTCTGACCTCGTATCGGCCCACTC 2333
|||||
DB 116 GGGTTTACCGTGTAGCCAGATGCTCGATCTCTGACCTCGTATCGGCCCACTC 57
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QY 2334 GGCTTCCCAA 2344
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|||||
DB 56 GGCTTCCCAA 46
|||||

RESULT 38
AX245117 353 bp DNA linear PAT 28-SEP-2001
LOCUS Sequence 47 from Patent WO0166753.
DEFINITION AX245117
ACCESSION AX245117.1 GI:15859791
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1

REFERENCE
AUTHORS Williams,L.T., Sacobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Kaasam,A., Lamson,G., Drmanac,R., Ckrvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Crain,B.
JOURNAL Human genes and gene expression products
Patent: WO 0166753-A 47 13-SEP-2001;
Chiron Corporation (US) ; Hyseq Inc. (US)
LOCATION/Qualifiers
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source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGCGGTTTACCGTGTAGCCAGATGCTCGATCTCTGACCTGCT 2319
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DB 70 TTTTAGTAGACAGCGGTTTACCGTGTAGCCAGATGCTCGATCTCTGACCTGCT 129
|||||

QY 2320 GATCGGCC 2328
|||||
DB 130 GATCGGCC 138
|||||

RESULT 39
CQ469958 426 bp DNA linear PAT 31-JAN-2004
LOCUS Sequence 1824 from Patent WO0160860.
DEFINITION CQ469958
ACCESSION CQ469958.1 GI:41435577
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
Schlegel,R., Endege,W.O. and Monahan,J.B.
JOURNAL Genes differentially expressed in human prostate cancer and their
use
Patent: WO 0160860-A 1824 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
LOCATION/Qualifiers
1..426
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source

ORIGIN

Query Match 2.9%; Score 69; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2260 TTTTAGTAGAGACAGGGTTTACCGTGTGTAACCGAGATGGTCTGATCTCCTGACTCGT 2319
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Db      91   TTTTAGTAGAGACAGGGTTTACCGTGTGTAACCGAGATGGTCTGATCTCCTGACTCGT 32
          |||||||
QY      2320 GATCCGCCC 2328
          |||||||
Db      31   GATCCGCCC 23
          |||||||

RESULT 40
CQ479126/c      CQ479126      426 bp      DNA      linear      PAT 30-JAN-2004
LOCUS           Sequence 10993 from Patent WO0160860.
DEFINITION      CQ479126
ACCESSION       CQ479126
VERSION         CQ479126.1 GI:41444745
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
REFERENCE       1
AUTHORS        Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE           Genes differentially expressed in human prostate cancer and their
                use
JOURNAL         Patent: WO 0160860-A 10993 23-AUG-2001;
                Millennium Predictive Medicine, Inc. (US)
FEATURES        Location/Qualifiers
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                                /mol_type="unassigned DNA"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2260 TTTTAGTAGAGACAGGGTTTACCGTGTGTAACCGAGATGGTCTGATCTCCTGACTCGT 2319
          |||||||
Db      91   TTTTAGTAGAGACAGGGTTTACCGTGTGTAACCGAGATGGTCTGATCTCCTGACTCGT 32
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QY      2320 GATCCGCCC 2328
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Db      31   GATCCGCCC 23
          |||||||
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Job time : 13578 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 13:45:22 ; Search time 449 Seconds
(without alignments)
9884.789 Million cell updates/sec

Title: US-09-966-724B-2

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Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 93554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 1952600

Minimum DB seq length: 5

Maximum DB seq length: 500

Post-processing: Listing first 1000 summaries

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10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	313	13.2	399	3	US-09-167-322-8
2	225	9.5	399	3	US-09-167-322-9
3	148	6.2	199	3	US-09-200-355-1
4	138	5.8	199	3	US-09-200-355-2
5	78	3.3	397	3	US-09-621-976-12751
6	73	3.1	73	3	US-09-073-567-49
7	73	3.1	73	3	US-09-541-848-49
8	67	2.8	480	3	US-09-621-976-8284
9	60	2.5	362	3	US-09-621-976-15415
10	60	2.5	441	3	US-09-621-976-17159
11	58	2.4	191	3	US-09-513-999C-18362
12	58	2.4	463	3	US-09-621-976-14420
13	55	2.3	149	3	US-09-513-999C-32581
14	55	2.3	170	3	US-09-513-999C-27025
15	55	2.3	191	3	US-09-513-999C-22797
16	55	2.3	192	3	US-09-513-999C-32123
17	55	2.3	258	5	US-09-984-429-629
18	55	2.3	266	3	US-09-621-976-13784
19	55	2.3	294	3	US-09-984-429-627
20	55	2.3	300	5	US-09-984-429-678
21	55	2.3	301	5	US-09-984-429-638
22	55	2.3	316	5	US-09-984-429-618
23	55	2.3	322	3	US-09-621-976-9777

24	2.3	322	5	US-09-984-429-679	Sequence 679, App
25	2.3	328	5	US-09-513-999C-34128	Sequence 34128, A
26	2.3	370	5	US-09-984-429-521	Sequence 521, App
27	2.3	382	3	US-09-621-976-13869	Sequence 13869, A
28	2.3	466	3	US-09-949-016-80631	Sequence 80631, A
29	2.3	411	4	US-09-880-107-445	Sequence 445, App
30	2.2	301	5	US-09-984-429-643	Sequence 643, App
31	2.2	311	3	US-09-621-976-13091	Sequence 13091, A
32	2.2	231	3	US-09-513-999C-32057	Sequence 32057, A
33	2.2	300	4	US-09-297-648-1408	Sequence 1408, App
34	2.2	315	3	US-09-621-976-14124	Sequence 14124, A
35	2.2	432	3	US-09-621-976-8313	Sequence 8313, App
36	2.1	50	3	US-10-131-827-4749	Sequence 4749, App
37	2.1	50	5	US-10-131-827-4749	Sequence 4749, App
38	2.1	95	3	US-09-513-999C-32786	Sequence 32786, A
39	2.1	133	3	US-09-513-999C-23250	Sequence 23250, A
40	2.1	215	3	US-09-513-999C-22153	Sequence 22153, A
41	2.1	252	3	US-09-513-999C-28073	Sequence 28073, A
42	2.1	252	3	US-09-513-999C-28094	Sequence 28094, A
43	2.1	288	3	US-09-973-278-870	Sequence 870, App
44	2.1	301	5	US-09-984-429-644	Sequence 644, App
45	2.1	323	5	US-09-984-429-669	Sequence 669, App
46	2.1	396	3	US-09-621-976-17326	Sequence 17326, A
47	2.1	249	3	US-09-513-999C-16980	Sequence 16980, A
48	2.1	317	3	US-09-385-982-109	Sequence 109, App
49	2.0	111	3	US-09-513-999C-18192	Sequence 18192, A
50	2.0	137	3	US-09-513-999C-27657	Sequence 27657, A
51	2.0	242	5	US-09-984-429-614	Sequence 614, App
52	2.0	243	5	US-09-984-429-675	Sequence 675, App
53	2.0	164	3	US-09-621-976-11863	Sequence 11863, A
54	2.0	204	3	US-09-513-999C-31129	Sequence 31129, A
55	2.0	281	3	US-09-621-976-1944	Sequence 1944, App
56	2.0	281	5	US-09-984-429-668	Sequence 668, App
57	2.0	294	3	US-09-621-976-1939	Sequence 1939, App
58	2.0	294	3	US-09-621-976-1940	Sequence 1940, App
59	2.0	298	3	US-09-621-976-11526	Sequence 11526, A
60	2.0	298	3	US-09-621-976-13327	Sequence 13327, A
61	2.0	302	3	US-09-621-976-1937	Sequence 1937, App
62	2.0	302	3	US-09-621-976-1942	Sequence 1942, App
63	2.0	310	3	US-09-621-976-1943	Sequence 1943, App
64	2.0	312	3	US-09-621-976-12169	Sequence 12169, A
65	2.0	314	3	US-09-621-976-11935	Sequence 11935, A
66	2.0	314	3	US-09-621-976-11969	Sequence 11969, A
67	2.0	421	3	US-09-621-976-15130	Sequence 15130, A
68	1.9	442	3	US-09-949-016-128506	Sequence 128506, A
69	1.9	227	3	US-09-513-999C-18463	Sequence 18463, A
70	1.9	237	3	US-09-513-999C-27603	Sequence 27603, A
71	1.9	279	3	US-09-513-999C-12494	Sequence 12494, A
72	1.9	303	3	US-09-513-999C-28512	Sequence 28512, A
73	1.9	387	3	US-09-621-976-2306	Sequence 2306, App
74	1.9	417	3	US-09-495-050A-282	Sequence 282, App
75	1.9	439	3	US-09-621-976-10550	Sequence 10550, A
76	1.9	440	3	US-09-621-976-16612	Sequence 16612, A
77	1.9	489	3	US-09-621-976-14080	Sequence 14080, A
78	1.9	495	3	US-09-495-050A-17	Sequence 17, App
79	1.9	76	3	US-09-513-999C-17764	Sequence 17764, A
80	1.9	102	3	US-09-973-278-939	Sequence 939, App
81	1.9	147	3	US-09-513-999C-20249	Sequence 20249, A
82	1.9	148	3	US-09-513-999C-20098	Sequence 20098, A
83	1.9	188	3	US-09-513-999C-20301	Sequence 20301, A
84	1.9	188	3	US-09-513-999C-20303	Sequence 20303, A
85	1.9	237	3	US-09-513-999C-19336	Sequence 19336, A
86	1.9	258	3	US-09-513-999C-10133	Sequence 10133, A
87	1.9	261	5	US-09-984-429-661	Sequence 661, App
88	1.9	265	3	US-09-513-999C-33210	Sequence 33210, A
89	1.9	272	3	US-09-513-999C-18392	Sequence 18392, A
90	1.9	298	3	US-09-513-999C-19939	Sequence 19939, A
91	1.9	304	5	US-09-984-429-660	Sequence 660, App
92	1.9	307	5	US-09-984-429-665	Sequence 665, App
93	1.9	316	3	US-09-621-976-11418	Sequence 11418, A
94	1.9	318	3	US-09-621-976-12699	Sequence 12699, A
95	1.9	406	3	US-09-621-976-18042	Sequence 18042, A
96	1.9	462	3	US-09-621-976-18043	Sequence 18043, A


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973 30 1.3 186 3 US-09-513-999C-26680 Sequence 26680, A
974 30 1.3 194 3 US-09-513-999C-15689, A Sequence 15689, A
975 30 1.3 198 3 US-09-513-999C-27612 Sequence 27612, A
976 30 1.3 198 3 US-09-513-999C-32043 Sequence 32043, A
977 30 1.3 207 3 US-09-621-976-9732 Sequence 9732, Ap
978 30 1.3 232 3 US-09-513-999C-19756 Sequence 19756, A
979 30 1.3 233 3 US-09-513-999C-36616 Sequence 36616, A
980 30 1.3 235 3 US-09-513-999C-9964 Sequence 9964, Ap
981 30 1.3 239 3 US-09-513-999C-8783 Sequence 8783, Ap
982 30 1.3 240 3 US-09-513-999C-17038 Sequence 17038, A
983 30 1.3 242 3 US-09-621-976-12086 Sequence 12086, A
984 30 1.3 248 3 US-09-621-976-16757 Sequence 16757, A
985 30 1.3 250 3 US-09-513-999C-26129 Sequence 26129, A
986 30 1.3 263 3 US-09-621-976-19402 Sequence 9402, Ap
987 30 1.3 267 3 US-09-513-999C-36623 Sequence 36623, A
988 30 1.3 278 3 US-09-621-976-14274 Sequence 14274, A
989 30 1.3 285 3 US-09-513-999C-13299 Sequence 13299, A
990 30 1.3 287 3 US-09-621-976-17997 Sequence 17997, A
991 30 1.3 288 3 US-09-513-999C-27561 Sequence 27561, A
992 30 1.3 297 3 US-09-621-976-12915 Sequence 12915, A
993 30 1.3 297 3 US-09-621-976-13157 Sequence 13157, A
994 30 1.3 298 3 US-09-621-976-11930 Sequence 11930, A
995 30 1.3 298 3 US-09-621-976-13112 Sequence 13112, A
996 30 1.3 299 3 US-09-621-976-12708 Sequence 12708, A
997 30 1.3 300 3 US-09-513-999C-18220 Sequence 18220, A
998 30 1.3 300 4 US-09-297-648-1504 Sequence 1504, Ap
999 30 1.3 301 3 US-09-513-999C-19859 Sequence 19859, A
1000 30 1.3 311 3 US-09-621-976-12405 Sequence 12405, A
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ALIGNMENTS

```
RESULT 1
US-09-167-322-8
; Sequence 8, Application US/09167322
; Patent No. 6365151
;
GENERAL INFORMATION:
APPLICANT: Allegheny University of the Health
Sciences, Halpern, Michael S.
England, James M.
TITLE OF INVENTION: CANCER VACCINE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavoroga & Monaco, P.C.
STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 base pairs
TYPE: nucleic acid
```

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STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-167-322-8
Query Match 13.2%; Score 313; DB 3; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.3e-132;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1475 ACAAAGAAAGAAAGCATTTCTGAGCATCACTTCTAGTAGCATTTATATAGACCCA 1534
DB 87 ACAAGAAAGAAAGCATTTCTGAGCATCACTTCTAGTAGCATTTATATAGACCCA 146
QY 1535 AGAAGATGTAAAGAGTTTGAAGAGAAAGAAACCAAGACAAAGAGAGTGTGAATC 1594
DB 147 AGAAGATGTAAAGAGTTTGAAGAGAAAGAAACCAAGACAAAGAGAGTGTGAATC 206
QY 1595 TAGTTGCCCTTAAGTCCATTGAACCTTGTGTGATTTGTCAAGGTGACCTAAATATG 1654
DB 207 TAGTTGCCCTTAAGTCCATTGAACCTTGTGTGATTTGTCAAGGTGACCTAAATATG 266
QY 1655 TTGCATTGTCCATGAGCAAAACAGACATCTTAGGCGCTTACATGTGCAAAAGAGCT 1714
DB 267 TTGCATTGTCCATGAGCAAAACAGACATCTTAGGCGCTTACATGTGCAAAAGAGCT 326
QY 1715 AAGAAAGAAATTAAGCCCTGCCAGTATGTAGCAACCAATTCAATGTATGTGCTTAC 1774
DB 327 AAGAAAGAAATTAAGCCCTGCCAGTATGTAGCAACCAATTCAATGTATGTGCTTAC 386
QY 1775 TTATTTCCCTTAG 1787
DB 387 TTATTTCCCTTAG 399
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RESULT 2
US-09-167-322-9
; Sequence 9, Application US/09167322
; Patent No. 6365151
;
GENERAL INFORMATION:
APPLICANT: Allegheny University of the Health
Sciences, Halpern, Michael S.
England, James M.
TITLE OF INVENTION: CANCER VACCINE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavoroga & Monaco, P.C.
STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
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;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-167-322-9
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Query Match          9.5%; Score 225; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.5e-92;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 312 ATGTGCAATACCAACATGCTGTACTGATGTGCTGTGTAACCACTCAGATTCCA 371
DB 1  ATGTGCAATACCAACATGCTGTACTGATGTGCTGTGTAACCACTCAGATTCCA 60
QY 372 GCTTGGCAACAAGAGACCTGTGTGACCAAGCCATTGCTTTGAAGTTAATTAAGTCT 431
DB 61  GCTTGGCAACAAGAGACCTGTGTGACCAAGCCATTGCTTTGAAGTTAATTAAGTCT 120
QY 432 GTTGTGCACAAAAAGACATTACTATGTAAGAGGTTCTTTTATCTTGCCAGTAT 491
DB 121 GTTGTGCACAAAAAGACATTACTATGTAAGAGGTTCTTTTATCTTGCCAGTAT 180
QY 492 ATTATGACTAAACGATTATATGATGAGAAAGCAACAAATATTGTA 536
DB 181 ATTATGACTAAACGATTATATGATGAGAAAGCAACAAATATTGTA 225
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RESULT 3

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US-09-200-355-1
; Sequence 1, Application US/09200355
; Patent No. 6451524
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
; FILE REFERENCE: IBIS0009
; CURRENT APPLICATION NUMBER: US/09/200,355
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 199
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-200-355-1
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Query Match          6.2%; Score 148; DB 3; Length 199;
Best Local Similarity 77.9%; Pred. No. 2.6e-57;
Matches 155; Conservative 43; Mismatches 1; Indels 0; Gaps 0;
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QY 244 GAAATGGGAGAGCTCTTAGGGAGCCCGGACCTTCGAAGCCGGAAAAACCCGGATGTGAGGA 303
DB 1  GAAACUGGGAGUCUCUGAGGGACCCCGACUCGCAAGCCGAAAAACCCGGAGUGGAGAGA 60
QY 304 GCAGGCAAAATGTGCAATACCAACATGTCGTACTGATGTGCTGTGTAACCACTCAG 363
DB 61  GCAGGCAAAATGTGCAAAUCCAAACAGUCUCUACCUACGAGUGGUCUUAACCACTCAG 120
QY 364 AGATTCGAGCTTGGACAAGAGACCTGTGTGTAACCAAGCCATTGCTTTGAAGTTAT 423
DB 121 AGAATCCAGCTTGGACAAGAGACCTGTGTGTAACCAAGCCATTGCTTTGAAGTTAT 180
QY 424 TAAAGTCTGTGTGTCACA 442
DB 181 UAAAGUCUCUGUGGCGACA 199
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RESULT 4

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US-09-200-355-2
; Sequence 2, Application US/09200355
; Patent No. 6451524
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
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; FILE REFERENCE: IBIS0009
; CURRENT APPLICATION NUMBER: US/09/200,355
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 199
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-200-355-2
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Query Match          5.8%; Score 138; DB 3; Length 199;
Best Local Similarity 73.9%; Pred. No. 9.1e-53;
Matches 102; Conservative 36; Mismatches 0; Indels 0; Gaps 0;
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QY 305 CAGGCAAAATGTGCAATACCAACATGCTGTACTGATGTGCTGTGTAACCACTCACA 364
DB 62  CAGGCAAAATGTGCAAAUCCAAACAGUCUCUACCUACGAGUGGUCUUAACCACTCACA 121
QY 365 GATTCCAGCTTGGACAAGAGACCTGTGTGACCAAAAGCCATTGCTTTGAAGTTAT 424
DB 122 GAUUCACACUCUGGAACAGAACCCUGGUUAGACCAAGCCAUUGCUUUUGAAGUUAU 181
QY 425 AAAGTCTGTGTGTCACA 442
DB 182 AAAGUCUGUGGUGCACA 199
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RESULT 5

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US-09-621-976-12751/C
; Sequence 12751, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 12751
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 250
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-12751
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Query Match          3.3%; Score 78; DB 3; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2284 GTGTTAGCAGAGAGTCTCGATCTCGACTGCTGTGATCCGCCACCTCGGCTCCCAA 2343
DB 210 GTGTTAGCAGAGAGTCTCGATCTCGACTGCTGTGATCCGCCACCTCGGCTCCCAA 151
QY 2344 AGTGCTGGATTACAGGC 2361
DB 150 AGTGCTGGATTACAGGC 133
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RESULT 6

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US-09-073-567-49/C
; Sequence 49, Application US/09073567
; Patent No. 6013786
; GENERAL INFORMATION:
; APPLICANT: Jiaodong Chen
; APPLICANT: Suhbir Agrawal
; APPLICANT: Ruwen Zhang
```

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-541-848-49
Query Match 3.1%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.5e-23;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDowell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,567
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield, Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 99,057-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 913-0001
; TELEFAX: (312) 913-0002
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; HYPOTHEICAL: NO
; ANTI-SENSE: YES
; US-09-073-567-49

Query Match 3.1%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.5e-23;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 665 AGGTACATCTGTGAGTGAAGAACAGGTGTCACCTTGAGGTGAGTGAAGAGACCT 724
; DB 73 AGGTACATCTGTGAGTGAAGAACAGGTGTCACCTTGAGGTGAGTGAAGAGACCT 14
; QY 725 TGTACAAGAGCTT 737
; DB 13 TGTACAAGAGCTT 1

RESULT 7
US-09-541-848-49/c
; Sequence 49, Application US/09541848
; Patent No. 6946447
; GENERAL INFORMATION:
; APPLICANT: CHEN, Jiansong
; APPLICANT: AGRAMAL, Sudhir
; APPLICANT: ZHANG, Ruiwen
; TITLE OF INVENTION: MD-M2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 29924/98057C
; CURRENT APPLICATION NUMBER: US/09/541,848
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 09/383,507
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/073,567
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 08/916,834
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 49
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-541-848-49
Query Match 3.1%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.5e-23;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 665 AGGTACATCTGTGAGTGAAGAACAGGTGTCACCTTGAGGTGAGTGAAGAGACCT 724
; DB 73 AGGTACATCTGTGAGTGAAGAACAGGTGTCACCTTGAGGTGAGTGAAGAGACCT 14
; QY 725 TGTACAAGAGCTT 737
; DB 13 TGTACAAGAGCTT 1

RESULT 8
US-09-621-976-8284/c
; Sequence 8284, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.in
; SEQ ID NO 8284
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-8284

Query Match 2.8%; Score 67; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 2295 GATGCTCTGATCTCTGACCTCGTGATCGGCCCACTCGGCTCCCAAAAGTCTGGAT 2354
; DB 480 GATGCTCTGATCTCTGACCTCGTGATCGGCCCACTCGGCTCCCAAAAGTCTGGAT 421
; QY 2355 TACAGGC 2361
; DB 420 TACAGGC 414

RESULT 9
US-09-621-976-15415/c
; Sequence 15415, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.in
; SEQ ID NO 15415
; LENGTH: 362
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-15415

Query Match 2.5%; Score 60; DB 3; Length 362;
Best Local Similarity 100.0%; Pred. No. 2.6e-17;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0y 2260 TTTTGTAGACAGACGGTTTCACCGTGTAGACCGATGCTCCTGACCTCGT 2313
Db 201 TTTTGTAGACAGACGGTTTCACCGTGTAGACCGATGCTCCTGACCTCGT 142

RESULT 10
US-09-621-976-17159/c
; Sequence 17159, Application US/09621976
; Patent No. 6639063

Query Match	2.5%	Score 60;	DB 3;	Length 441;
Best Local Similarity	100.0%;	Pred. No. 2.6e-17;		
Matches 60;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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US-09-513-999C-18362
SEQUENT 11
: US-09-513-999C-18362
: Sequence 18362, Application US/09513999C
: Patent No. 6783961
: GENERAL INFORMATION:
: APPLICANT: Dumas Milne Edwards, J.B.
: APPLICANT: Duclert, A.
: APPLICANT: Giordano, J.Y.
: TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
: Patent No. 6783961
: FILE REFERENCE: 59.US2.REG
: CURRENT APPLICATION NUMBER: US/09/513.999C
: CURRENT FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/122,487
: PRIOR FILING DATE: 1999-02-26
: NUMBER OF SEQ ID NOS: 36681
: SOFTWARE: Patent.pm
: SEQ ID NO 18362
: LENGTH: 191
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-513-999C-18362

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Query Match	2.4%	Score 58	DB 3	Length 191
Best Local Similarity	100.0%	Pred. No.	2.2e-16	
Matches	58	Conservative	0	Mismatches 0; Indels 0; Gaps 0
Qy	2260	TTTTAGTAGAGACACAGGGTTTCA	CGCGTTAGGCAGAGATGCTGATCTCTGACCTC	2317
Db	67	TTTTAGTAGAGACACAGGGTTTCA	CGCGTTAGGCAGAGATGCTGATCTCTGACCTC	124

RESULT 12
US-09-621-976-14420/c
; Sequence 14420, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

```

? APPLICANT: Jobert, S.
? APPLICANT: Giordano, J.Y.
? TITLE OR INVENTION: ESTs and Encoded Human Proteins
? FILE REFERENCE: GENSET.054PR2
? CURRENT APPLICATION NUMBER: US/09/621.976
? CURRENT FILING DATE: 2000-07-21
? NUMBER OF SEQ ID NOS: 19335
? SOFTWARE: Patent.pm
? SEQ ID NO 14420
? LENGTH: 463
?
? TYPE: DNA
? ORGANISM: Homo sapiens
?
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 417..454
? OTHER INFORMATION: n=a, g, c or t
US-09-621.976-14420

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Query Match	2.4%	Score 58	DB 3	Length 463
Best Local Similarity	100.0%	Pred. No.	2.1e-16	
Matches	58	Conservative	0	Mismatches 0; Indels 0; Gaps 0

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RESULT 13
US-09-513-999C-32581
/ Sequence 32581, Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclert, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ Patent No. 6783961
/ FILE REFERENCE: 59 US2, REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ CURRENT FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 32581
/ LENGTH: 149
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 149
/ OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-32581

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Query Match	2.3%	Score 55;	DB 3;	Length 149;
Best Local Similarity	100.0%;	Pred. NO. 5.1e-15;		
Matches	55;	Conservative	0;	Mismatches
			0;	Indels
				0;
				Gaps
				0;

RESULT 14
 US-09-513-999C-27025
 ; Sequence 27025; Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J. B.
 ; APPLICANT: Duclet, A.
 ; APPLICANT: Giordano, J. Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
 ; Patent No. 6783961

```
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 27025
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 162
; OTHER INFORMATION: s=g or c
;
; NAME/KEY: misc_feature
; LOCATION: 170
; OTHER INFORMATION: s=g or c
;
US-09-513-999C-27025
```

```
Query Match 2.3%; Score 55; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 5.1e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2274 GGGTTTACCGTGTAGCCAGATGTCGATCTCCGACCTCGATCCGCC 2328
Db 66 GGGTTTACCGTGTAGCCAGATGTCGATCTCCGACCTCGATCCGCC 120
```

```
RESULT 15
US-09-513-999C-22797/C
; Sequence 22797, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 22797
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-22797
```

```
Query Match 2.3%; Score 55; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 5e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2274 GGGTTTACCGTGTAGCCAGATGTCGATCTCCGACCTCGATCCGCC 2328
Db 125 GGGTTTACCGTGTAGCCAGATGTCGATCTCCGACCTCGATCCGCC 71
```

```
RESULT 16
US-09-513-999C-22123
; Sequence 22123, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
```

```
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 22123
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-22123
```

```
Query Match 2.3%; Score 55; DB 3; Length 192;
Best Local Similarity 100.0%; Pred. No. 5e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2274 GGGTTTACCGTGTAGCCAGATGTCGATCTCCGACCTCGATCCGCC 2328
Db 88 GGGTTTACCGTGTAGCCAGATGTCGATCTCCGACCTCGATCCGCC 142
```

```
RESULT 17
US-09-984-429-629/C
; Sequence 629, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 629
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-629
```

```
Query Match 2.3%; Score 55; DB 5; Length 258;
Best Local Similarity 100.0%; Pred. No. 5e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2274 GGGTTTACCGTGTAGCCAGATGTCGATCTCCGACCTCGATCCGCC 2328
Db 62 GGGTTTACCGTGTAGCCAGATGTCGATCTCCGACCTCGATCCGCC 8
```

```
RESULT 18
US-09-621-976-13784/C
; Sequence 13784, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
```

```

; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13784
; LENGTH: 266
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13784

Query Match      2.3%; Score 55; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2274 GGGTTTCAACCGTGTAGCCAGATGCTCGATCTCTGACCTCGTATCCGCC 2328
Db      125 GGGTTTCAACCGTGTAGCCAGATGCTCGATCTCTGACCTCGTATCCGCC 71

RESULT 19
US-09-984-429-627/c
; Sequence 627, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 627
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-627

Query Match      2.3%; Score 55; DB 5; Length 294;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2274 GGGTTTCAACCGTGTAGCCAGATGCTCGATCTCTGACCTCGTATCCGCC 2328
Db      102 GGGTTTCAACCGTGTAGCCAGATGCTCGATCTCTGACCTCGTATCCGCC 48

RESULT 20
US-09-984-429-678/c
; Sequence 678, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

```

```

; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 638
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-678

Query Match      2.3%; Score 55; DB 5; Length 300;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2274 GGGTTTCAACCGTGTAGCCAGATGCTCGATCTCTGACCTCGTATCCGCC 2328
Db      94 GGGTTTCAACCGTGTAGCCAGATGCTCGATCTCTGACCTCGTATCCGCC 40

RESULT 21
US-09-984-429-638/c
; Sequence 638, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 638
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens

```

US-09-984-429-638

Query Match 2.3%; Score 55; DB 5; Length 301;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2274 GGGTTTACCGGTGTTAGCCAGATGATCTCGATCTCCTGACCTCGTATCCGCC 2328
Db 107 GGGTTTACCGGTGTTAGCCAGATGATCTCGATCTCCTGACCTCGTATCCGCC 53

RESULT 22
US-09-984-429-618/c
; Sequence 618, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 618
; LENGTH: 316
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-618

US-09-984-429-618

Query Match 2.3%; Score 55; DB 5; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2274 GGGTTTACCGGTGTTAGCCAGATGATCTCGATCTCCTGACCTCGTATCCGCC 2328
Db 116 GGGTTTACCGGTGTTAGCCAGATGATCTCGATCTCCTGACCTCGTATCCGCC 62

RESULT 23
US-09-621-976-9777/c
; Sequence 9777, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9777
; LENGTH: 322
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 86
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-9777

Query Match 2.3%; Score 55; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2274 GGGTTTACCGGTGTTAGCCAGATGATCTCGATCTCCTGACCTCGTATCCGCC 2328
Db 146 GGGTTTACCGGTGTTAGCCAGATGATCTCGATCTCCTGACCTCGTATCCGCC 92

RESULT 24
US-09-984-429-679/c
; Sequence 679, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 679
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-679

Query Match 2.3%; Score 55; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2274 GGGTTTACCGGTGTTAGCCAGATGATCTCGATCTCCTGACCTCGTATCCGCC 2328
Db 109 GGGTTTACCGGTGTTAGCCAGATGATCTCGATCTCCTGACCTCGTATCCGCC 55

RESULT 25
US-09-513-999C-34128/c
; Sequence 34128, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; Patent No. 6783961
; CURRENT APPLICATION NUMBER: US/09/513,999C

```

; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 34128
; LENGTH: 328
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 190
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 293
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 299
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 305
; OTHER INFORMATION: r=a or g
; OTHER INFORMATION: r=a or g
US-09-513-999C-34128

```

```

Query Match      2.3%; Score 55; DB 3; Length 328;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2274 GGGTTTACCGGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCCGCCCC 2328
Db      282 GGGTTTACCGGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCCGCCCC 228

```

RESULT 26

```

US-09-984-429-521/c
; Sequence 521, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 521
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-521

```

```

Query Match      2.3%; Score 55; DB 5; Length 370;

```

```

Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2274 GGGTTTACCGGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCCGCCCC 2328
Db      156 GGGTTTACCGGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCCGCCCC 102

```

RESULT 27

```

US-09-621-976-13869/c
; Sequence 13869, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Joderc, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13869
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13869

```

```

Query Match      2.3%; Score 55; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 4.8e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2274 GGGTTTACCGGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCCGCCCC 2328
Db      189 GGGTTTACCGGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCCGCCCC 135

```

RESULT 28

```

US-09-949-016-80631
; Sequence 80631, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80631
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-80631

```

```

Query Match      2.3%; Score 55; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 4.8e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2274 GGGTTTACCGGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCCGCCCC 2328
Db      83 GGGTTTACCGGTGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCCGCCCC 137

```

RESULT 29

```

US-09-880-107-445

```

```
; Sequence 445, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 445
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 AA218727
; US-09-880-107-445

Query Match          2.3%; Score 54; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 1,4e-14;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2274 GGGTTACCGGTGTTAGCCAGAGATGTCGATCTCCTGACCTCGTATCCGCC 2327
Db      171 GGGTTACCGGTGTTAGCCAGAGATGTCGATCTCCTGACCTCGTATCCGCC 224

RESULT 30
US-09-984-429-643/C
; Sequence 643, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 643
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98)..(98)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-984-429-643
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Query Match          2.2%; Score 53; DB 5; Length 301;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2276 GTTTCACCGGTGTTAGCCAGAGATGTCGATCTCCTGACCTCGTATCCGCC 2328
Db      97 GTTTCACCGGTGTTAGCCAGAGATGTCGATCTCCTGACCTCGTATCCGCC 45

RESULT 31
US-09-621-976-13091/C
; Sequence 13091, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13091
; LENGTH: 311
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-13091

Query Match          2.2%; Score 53; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2275 GGTTCACCGGTGTTAGCCAGAGATGTCGATCTCCTGACCTCGTATCCGCC 2327
Db      287 GGTTCACCGGTGTTAGCCAGAGATGTCGATCTCCTGACCTCGTATCCGCC 235

RESULT 32
US-09-513-999C-32057/C
; Sequence 32057, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 32057
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 215
; OTHER INFORMATION: s=g or c
; US-09-513-999C-32057

Query Match          2.2%; Score 51; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 3.3e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2274 GGGTTACCGGTGTTAGCCAGAGATGTCGATCTCCTGACCTCGTATCC 2324
Db      75 GGGTTACCGGTGTTAGCCAGAGATGTCGATCTCCTGACCTCGTATCC 25
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RESULT 33
US-09-297-648-1408
; Sequence 1408, Application US/09297648
; Patent No. 6964868
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassan, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Cirkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, William Lee
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: No. 6964868el Human Genes and Gene Expression
; FILE REFERENCE: 2300-1481
; CURRENT APPLICATION NUMBER: US/09/297,648
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,666
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/080,515
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/105,234
; NUMBER OF SEQ ID NOS: 5252
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1408
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-297-648-1408

Query Match      2.2%; Score 51; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2274 GGGTTACCGGTGTTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 2324
Db      12 GGGTTACCGGTGTTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 62

RESULT 34
US-09-621-976-14124/c
; Sequence 14124, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
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; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14124
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14124

Query Match      2.2%; Score 51; DB 3; Length 315;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2274 GGGTTACCGGTGTTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 2324
Db      301 GGGTTACCGGTGTTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 251

RESULT 35
US-09-621-976-8313/c
; Sequence 8313, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8313
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8313

Query Match      2.2%; Score 51; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2274 GGGTTACCGGTGTTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 2324
Db      395 GGGTTACCGGTGTTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 345

RESULT 36
US-10-131-827-4749
; Sequence 4749, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Ly, Ngoc
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4749
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4749
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Query Match 2.1%; Score 50; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1747 GACACCAATTCAATGATGTTGCTAACTTATTTCCCTAGTTGACCTGT 1796
Db 1 GACACCAATTCAATGATGTTGCTAACTTATTTCCCTAGTTGACCTGT 50

RESULT 37
US-10-131-831-4749
; Sequence 4749, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE REFERENCE: 50661200121
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4749
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-4749

Query Match 2.1%; Score 50; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1747 GACACCAATTCAATGATGTTGCTAACTTATTTCCCTAGTTGACCTGT 1796
Db 1 GACACCAATTCAATGATGTTGCTAACTTATTTCCCTAGTTGACCTGT 50

RESULT 38
US-09-513-999C-32786
; Sequence 32786, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 32786
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-32786

Query Match 2.1%; Score 50; DB 3; Length 95;
Best Local Similarity 100.0%; Pred. No. 9.8e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2264 AGTAGAGACAGGGTTTACCGGTGTTAGCCAGAGATGCTCTCATCTCTCTGA 2313

Db 1 AGTAGAGACAGGGTTTACCGGTGTTAGCCAGAGATGCTCTCATCTCTCTGA 50

RESULT 39
US-09-513-999C-23250
; Sequence 23250, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 23250
; LENGTH: 133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-23250

Query Match 2.1%; Score 50; DB 3; Length 133;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2274 GGGTTACCGGTGTTAGCCAGAGATGCTCTCATCTCTGACCTGATC 2323
Db 25 GGGTTACCGGTGTTAGCCAGAGATGCTCTCATCTCTGACCTGATC 74

RESULT 40
US-09-513-999C-22153
; Sequence 22153, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 22153
; LENGTH: 215
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 140
; OTHER INFORMATION: k=g or t
US-09-513-999C-22153

Query Match 2.1%; Score 50; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 9.4e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2274 GGGTTACCGGTGTTAGCCAGAGATGCTCTCATCTCTGACCTGATC 2323
Db 152 GGGTTACCGGTGTTAGCCAGAGATGCTCTCATCTCTGACCTGATC 201

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us-09-966-724b-2.oligo.rn1

Page 19

Job time : 459 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 13:38:26 ; Search time 1481 Seconds

(without alignments)
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Title: US-09-966-724B-2

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Searched: 5244920 seqs, 3486124231 residues

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Minimum DB seq length: 5

Maximum DB seq length: 500

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	13.8	327	14	ADX15874
2	313	13.2	399	2	AA71257
3	313	13.2	399	2	AA71257
4	276	11.6	327	14	ADX15878
5	276	11.6	327	14	ADX15880
6	225	9.5	309	2	AA79994
7	225	9.5	309	2	AA79994
8	225	9.5	309	2	AA79994
9	225	9.5	309	2	AA79994
10	199	8.4	199	3	AAA62123
11	176	7.4	176	10	ADCC22295
12	167	7.0	319	6	ABV94129
13	138	5.8	199	6	AA662124
14	109	4.6	327	14	ADX15884
15	102	4.3	297	4	AAK81934
16	102	4.3	324	4	AAK81936
17	102	4.3	325	4	AAK81937
18	102	4.3	331	4	AAK81935
19	102	4.3	331	4	AAK81935
20	88	3.7	309	8	AA36256
21	88	3.7	309	8	AA36256
22	85	3.7	309	8	AA36256
23	85	3.7	309	8	AA36256
24	82	3.5	173	4	AAK85766
25	82	3.5	173	4	AAK85766
26	80	3.4	80	13	ADY59447
27	77	3.2	140	5	AAK69176
28	77	3.2	140	5	AAK69176
29	77	3.2	140	5	AAK69176
30	73	3.1	73	10	AA65023
31	73	3.1	73	10	AA65023
32	72	3.0	149	5	AA163475
33	72	3.0	149	5	AA163475
34	72	3.0	149	5	AA163475
35	72	3.0	149	5	AA163475
36	72	3.0	149	5	AA163475
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38	71	3.0	264	4	AAK81551
39	71	3.0	264	4	AAK81551
40	71	3.0	264	4	AAK81551
41	71	3.0	264	4	AAK81551
42	70	3.0	370	4	AAK70973
43	70	3.0	370	4	AAK70973
44	69	2.9	181	4	AAK32647
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96	69	2.9	181	4	AAK32647
97	69	2.9	181	4	AAK32647
98	69	2.9	181	4	AAK32647
99	69	2.9	181	4	AAK32647
100	69	2.9	181	4	AAK32647


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C 968 44 1.9 104 4 AAK69303 Human imm
C 969 44 1.9 107 4 AAK74844 Human imm
C 970 44 1.9 115 4 AAK89203 Human dig
C 971 44 1.9 115 4 AAK90088 Human dig
C 972 44 1.9 115 4 AAK80878 Human imm
C 973 44 1.9 115 4 AAL06348 Human rep
C 974 44 1.9 115 5 AAS39747 Genomic s
C 975 44 1.9 115 9 ADB32707 Human nov
C 976 44 1.9 128 4 AAS32510 Human gen
C 977 44 1.9 128 4 AAS32508 Human gen
C 978 44 1.9 128 4 AAS32513 Human gen
C 979 44 1.9 131 4 AAK80864 Human imm
C 980 44 1.9 131 4 AAK85677 Human imm
C 981 44 1.9 131 4 AAK86568 Human imm
C 982 44 1.9 131 4 AAK86094 Human imm
C 983 44 1.9 131 4 AAK72017 Human imm
C 984 44 1.9 131 4 AAK66835 Human imm
C 985 44 1.9 138 5 ABA17054 Human ner
C 986 44 1.9 138 5 ABA17055 Human ner
C 987 44 1.9 142 4 AAK84532 Human imm
C 988 44 1.9 143 4 AAK65842 Human imm
C 989 44 1.9 147 3 AAC16174 Human sec
C 990 44 1.9 148 3 AAC16023 Human sec
C 991 44 1.9 152 4 AAK87062 Human imm
C 992 44 1.9 154 4 AAK72589 Human imm
C 993 44 1.9 172 4 AAK81214 Human imm
C 994 44 1.9 172 4 AAK66061 Human imm
C 995 44 1.9 179 4 AAK66062 Human imm
C 996 44 1.9 179 4 AAK66065 Human imm
C 997 44 1.9 182 4 AAK67721 Human imm
C 998 44 1.9 182 4 AAK81143 Human imm
C 999 44 1.9 182 4 AAS32651 Human gen
C1000 44 1.9 188 3 AAC16228 Human sec
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ALIGNMENTS

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RESULT 1
AD15874
ID AD15874 standard; DNA; 327 BP.
AC AD15874;
XX
DT 05-MAY-2005 (first entry)
DE wild-type human double minute 2 protein (17-125) DNA SEQ ID NO:1.
XX
KW double minute 2; ds; cancer; cytosolic; neoplasm; X-ray crystallography;
KM protein solubilization; mutagenesis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..327
FT /tag= a
FT /product= "double minute 2"
FT /partial
FT /note= "no start/stop codon given"
XX
PN US2005037383-A1.
XX
PD 17-FEB-2005.
XX
PF 09-APR-2004; 2004US-00822254.
XX
PR 10-APR-2003; 2003US-0461787P.
PR 24-FEB-2004; 2004US-0547265P.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Taremi SS, Xie G, Hesson T, Duca JS, Strickland C, Windsor WT,
PI Madison VS, Zhang R, Reichert P;
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XX
DR WPI; 2005-180390/19.
DR P-PSDB; ADX15875.
XX
PT Novel modified human double minute 2 protein polypeptide, comprising
PT amino acid sequence differing from its corresponding wild-type, useful
PT for identifying compounds used as anticancer agents.
XX
PS Disclosure; SEQ ID NO 1; 49pp; English.
XX
CC The invention relates to a novel modified human Double Minute 2 protein
CC (Hdm2) polypeptide (1) comprising a fully defined sequence of 109 amino
CC acids (S1) as given in the specification, differing from the
CC corresponding wild-type Hdm2 (17-125) amino acid sequence (ADX15875). A
CC polypeptide of the invention is useful for identifying an agent for use
CC as an inhibitor of Hdm2. The polypeptide, crystal of the polypeptide or
CC polypeptide-compound complex (PPC) is useful for designing, selecting
CC and/or optimizing a potential inhibitor of the polypeptide. The
CC polypeptide or PPC is useful for evaluating the ability of a potential
CC inhibitor to associate with the polypeptide or PPC. The polypeptide,
CC crystal of the polypeptide or PPC is useful for identifying, selecting
CC and/or designing compounds useful as anticancer agents. The polypeptide
CC is useful in designing high affinity inhibitors of Hdm2 that are useful
CC in the treatment of cancers. The present sequence encodes the wild-type
CC human Double Minute 2 protein (Hdm2) polypeptide of the invention.
XX
SQ Sequence 327 BP; 106 A; 56 C; 69 G; 96 T; 0 U; 0 Other;
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Query Match 13.8%; Score 327; DB 14; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.3e-147;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 360 TCACAGATTCAGCTTCGGAACAAGAGACCCTGTTAGACCAAGCATTGCTTTGAAG 419
Db 1 TCACAGATTCAGCTTCGGAACAAGAGACCCTGTTAGACCAAGCATTGCTTTGAAG 60
Oy 420 TTATTAAGTCTGTTGTGACCAAAAAAGACCTTATCTATGAAAAGGTTCTTTTAT 479
Db 61 TTATTAAGTCTGTTGTGACCAAAAAAGACCTTATCTATGAAAAGGTTCTTTTAT 120
Oy 480 CTTGGCCAGTATATTAAGACATTAACGATTAATAGATGGAAGCAACAATATGTATAT 539
Db 121 CTTGGCCAGTATATTAAGACATTAACGATTAATAGATGGAAGCAACAATATGTATAT 180
Oy 540 TGTTCGAATGATCTTCTAGAGATTTGTTGGCGTGCACGCTCTCTGTGAAGAGCAC 599
Db 181 TGTTCGAATGATCTTCTAGAGATTTGTTGGCGTGCACGCTCTCTGTGAAGAGCAC 240
Oy 600 AGGAAAATATATACCATGATCTACAGAACTTGTGTAGTGCATCAGCAGGAATCATCG 659
Db 241 AGGAAAATATATACCATGATCTACAGAACTTGTGTAGTGCATCAGCAGGAATCATCG 300
Oy 660 GACTCAGGTACATCTGTGAGTGAGAAC 686
Db 301 GACTCAGGTACATCTGTGAGTGAGAAC 327
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RESULT 2
AAT71257
ID AAT71257 standard; DNA; 399 BP.
AC AAT71257;
XX
DT 30-MAR-1998 (first entry)
XX
DE Human mdm2-D gene.
XX
KW Cognate transgene; human; mdm2; lymphoma; cellular immunogen; cancer;
KW self-determinant immunoreactivity; cancer vaccination; breast carcinoma;
KW colon carcinoma; immunotherapy; proto-oncogene; ss.
XX
OS Homo sapiens.
XX
```

FN WO9725860-A1.
XX 24-JUL-1997.
XX
XX 13-JAN-1997; 97WO-US000582.
XX
XX 19-JAN-1996; 96US-0010262P.
XX
XX (UVAL-) UNIV ALLEGHENY HEALTH SCI.
XX
XX Halpern MS, England JM;
XX WPI; 1997-38493/35.
XX
XX Proto-oncogene immunogen - used in vaccine for the prevention and
XX treatment of cancer.
XX
XX Disclosure; Page 60; 81pp; English.
XX
XX This sequence represents the human mdm2-D cognate transgene (CTG).
XX Deletion of amino acids 9-155 of the encoded protein renders the CTG non-
XX transforming. This sequence can be used in the cellular immunogen of the
XX invention. The cellular immunogen of the invention is for immunising
XX against the product of a target proto-oncogene, over-expression of which
XX is associated with cancer, comprises host cells transfected with a
XX construct containing at least one transgene related to the proto-oncogene
XX and driven by a strong promoter. The product of the transgene induces
XX immunoreactivity to host self-determinants on the product of proto-
XX oncogene. The cellular immunogens are used for protective vaccination
XX against cancer (e.g. carcinoma of breast or colon, or various lymphomas)
XX and for immunotherapy of cancer. Use of the immunogen eliminates the need
XX to isolate immunogenic, HLA host-matched peptides. The method is not
XX based on immune recognition of a determinant defined by a cancer-specific
XX mutation and generates a systemic (anti-metastatic) response
XX
SQ Sequence 399 BP; 133 A; 82 C; 84 G; 100 T; 0 U; 0 Other;
Query Match 13.2%; Score 313; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.4e-140;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1475 ACAAGAAAGTGAAGCTATTCTCAGCCATCACTTCTAGTAGCATTATTATAGCAGCA 1534
DB 87 ACAAGAAAGTGAAGCTATTCTCAGCCATCACTTCTAGTAGCATTATTATAGCAGCA 146
QY 1535 AGAAGATGTGAAGAGTTTGAAGGAAAGAAACCAAGACAAAGAGAGTGTGAATC 1594
DB 147 AGAAGATGTGAAGAGTTTGAAGGAAAGAAACCAAGACAAAGAGAGTGTGAATC 206
QY 1535 TAGTTGGCCCTTATGCGATTGAACCTTGTGTGATTGTCAAGTCCAGCTTAAAGATG 1654
DB 207 TAGTTGGCCCTTATGCGATTGAACCTTGTGTGATTGTCAAGTCCAGCTTAAAGATG 266
QY 1655 TTGCATTGTCATGCGCAAAAGAGACATCTTATGCGCTTATAGTGCAAGAAAGT 1714
DB 267 TTGCATTGTCATGCGCAAAAGAGACATCTTATGCGCTTATAGTGCAAGAAAGT 326
QY 1715 AAAAGAAAGAAATAGCCCTGCCAGTATGTAGACAAACCAATTCAATGATGTCTAAC 1774
DB 327 AAAAGAAAGAAATAGCCCTGCCAGTATGTAGACAAACCAATTCAATGATGTCTAAC 386
QY 1775 TTATTTCCTCTAG 1787
DB 387 TTATTTCCTCTAG 399
RESULT 3
AAZ60819
ID AAZ60819 standard; DNA; 399 BP.
XX AAZ60819;
AC
XX 16-MAY-2000 (first entry)

XX
DE Nucleotide sequence of a cognate transgene of mdm-2.
XX
XX Cognate transgene; CTG; tumorigenic; cellular immunogen; immunisation;
XX KW proto-oncogene; malignancy; allogenic cell; vaccine; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200004927-A1.
XX
XX 03-FEB-2000.
XX
XX 08-JUL-1999; 99WO-US015594.
XX
XX 24-JUL-1998; 98US-0093965P.
XX
XX (UVAL-) UNIV ALLEGHENY HEALTH SCI.
XX (HALP/) HALPERN M S.
XX (ENGL/) ENGLAND J M.
XX
XX Halpern MS, England JM;
XX WPI; 2000-182543/16.
XX
XX Cellular immunogens comprising allogenic donor cells transfected with a
XX construct comprising a proto-oncogene cognate, useful as cancer vaccines.
XX
XX Disclosure; Page 69; 77pp; English.
XX
XX The present sequence represents a cognate transgene (CTG) which is
XX rendered non-tumorigenic by deletion of amino acids 9-155. The CTG is
XX used in the course of the invention. The specification describes a
XX cellular immunogen for immunizing a host against the effects of the
XX product of a target proto-oncogene which is associated with a
XX malignancy. The cellular immunogen comprises allogenic cells transfected
XX with transgene construct comprising a transgene cognate to target proto-
XX oncogene and a strong promoter. The cellular immunogen is useful for
XX vaccinating a host against cancer by inserting the transgene construct
XX into the body of the host for the expression of the transgene. The method
XX of the invention is designed to target mutation-driven non-self
XX determinants. The cellular immunogens induce reactivity for self-
XX expressed proto-oncogenes
XX
SQ Sequence 399 BP; 133 A; 82 C; 84 G; 100 T; 0 U; 0 Other;
Query Match 13.2%; Score 313; DB 3; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.4e-140;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1475 ACAAGAAAGTGAAGCTATTCTCAGCCATCACTTCTAGTAGCATTATTATAGCAGCA 1534
DB 87 ACAAGAAAGTGAAGCTATTCTCAGCCATCACTTCTAGTAGCATTATTATAGCAGCA 146
QY 1535 AGAAGATGTGAAGAGTTTGAAGGAAAGAAACCAAGACAAAGAGAGTGTGAATC 1594
DB 147 AGAAGATGTGAAGAGTTTGAAGGAAAGAAACCAAGACAAAGAGAGTGTGAATC 206
QY 1595 TAGTTGGCCCTTATGCGATTGAACCTTGTGTGATTGTCAAGTCCAGCTTAAAGATG 1654
DB 207 TAGTTGGCCCTTATGCGATTGAACCTTGTGTGATTGTCAAGTCCAGCTTAAAGATG 266
QY 1655 TTGCATTGTCATGCGCAAAAGAGACATCTTATGCGCTTATAGTGCAAGAAAGT 1714
DB 267 TTGCATTGTCATGCGCAAAAGAGACATCTTATGCGCTTATAGTGCAAGAAAGT 326
QY 1715 AAAAGAAAGAAATAGCCCTGCCAGTATGTAGACAAACCAATTCAATGATGTCTAAC 1774
DB 327 AAAAGAAAGAAATAGCCCTGCCAGTATGTAGACAAACCAATTCAATGATGTCTAAC 386
QY 1775 TTATTTCCTCTAG 1787
DB 387 TTATTTCCTCTAG 399

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RESULT 4
AD15878
ID AD15878 standard; DNA; 327 BP.
XX
AC AD15878;
XX
DT 05-MAY-2005 (first entry)
XX
DE Modified human double minute 2 protein Y76H encoding DNA SEQ ID NO:5.
XX
KM double minute 2; ds; cancer; cytostatic; neoplasm; X-ray crystallography;
KM protein solubilization; mutant; mutagenesis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 1..327
FT /*tag= a
FT /product= "double minute 2 variant"
FT /partial
FT /note= "no start/stop codon given"
XX
PN US2005037383-A1.
XX
PD 17-FEB-2005.
XX
PF 09-APR-2004; 2004US-00822254.
XX
PR 10-APR-2003; 2003US-0461787P.
PR 24-FEB-2004; 2004US-0547265P.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Taremi SS, Xie G, Hesson T, Duca JS, Strickland C, Windsor WT;
PI Madison VS, Zhang R, Reichert P;
XX
DR WPI; 2005-180390/19.
DR P-PSDB; ADX15879.
XX
PT Novel modified human double minute 2 protein polypeptide, comprising
PT amino acid sequence differing from its corresponding wild-type, useful
PT for identifying compounds used as anticancer agents.
XX
PS Claim 7; SEQ ID NO 5; 49pp; English.
XX
CC The invention relates to a novel modified human Double Minute 2 protein
CC (Hdm2) polypeptide (I) comprising a fully defined sequence of 109 amino
CC acids (S1) as given in the specification, differing from the
CC corresponding wild-type Hdm2 (17-125) amino acid sequence (ADX15875). A
CC polypeptide of the invention is useful for identifying an agent for use
CC as an inhibitor of Hdm2. The polypeptide, crystal of the polypeptide or
CC polypeptide-compound complex (PPC) is useful for designing, selecting
CC and/or optimizing a potential inhibitor of the polypeptide. The
CC polypeptide or PPC is useful for evaluating the ability of a potential
CC inhibitor to associate with the polypeptide or PPC. The polypeptide,
CC crystal of the polypeptide or PPC is useful for identifying, selecting
CC and/or designing compounds useful as anticancer agents. The polypeptide
CC is useful in designing high affinity inhibitors of Hdm2 that are useful
CC in the treatment of cancers. The present sequence encodes a modified
CC human Double Minute 2 protein (Hdm2) polypeptide of the invention.
XX
SQ Sequence 327 BP; 106 A; 57 C; 69 G; 95 T; 0 U; 0 Other;
Query Match 11.6%; Score 276; DB 14; Length 327;
Best Local Similarity 99.7%; Pred. No. 1.1e-122;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 360 TCACAGATTCGAGCTCGGAACAGAGACCCGTTACACCAAGCCATTGCTTTGAG 419
Db 1 TCACAGATTCGAGCTCGGAACAGAGACCCCTGTTAGACCAAGCCATTGCTTTGAG 60

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Oy 420 TTATTAAAGTCTGTGGTGACAAAGAGACCTTATATGAAAGAGTTCTTTTAT 479
Db 61 TTATTAAAGTCTGTGGTGACAAAGAGACCTTATATGAAAGAGTTCTTTTAT 120
Oy 480 CTTGGCCAGTATATTATGACTTAAACGATTATATGATGGAAGCAACATATTGTATAT 539
Db 121 CTTGGCCAGTATATTATGACTTAAACGATTATATGATGGAAGCAACATATTGTATAT 180
Oy 540 TGTTCGAATGATCTTTCAGAGATTTGTTGGCGTGCCTTCTCTGTGAAGAGCAC 599
Db 181 TGTTCGAATGATCTTTCAGAGATTTGTTGGCGTGCCTTCTCTGTGAAGAGCAC 240
Oy 600 AGGAAATATATACCATGATCTACAGAACTTGTAGTACTGATCAACAGGAATCATCG 659
Db 241 AGGAAATATATACCATGATCTACAGAACTTGTAGTACTGATCAACAGGAATCATCG 300
Oy 660 GACTCAGGTACATCTGTGAGTGAAC 686
Db 301 GACTCAGGTACATCTGTGAGTGAAC 327

RESULT 5
AD15880
ID AD15880 standard; DNA; 327 BP.
XX
AC AD15880;
XX
DT 05-MAY-2005 (first entry)
XX
DE Modified human double minute 2 protein F55Y encoding DNA SEQ ID NO:7.
XX
KM double minute 2; ds; cancer; cytostatic; neoplasm; X-ray crystallography;
KM protein solubilization; mutant; mutagenesis.
XX
OS Homo sapiens.
XX
PI Taremi SS, Xie G, Hesson T, Duca JS, Strickland C, Windsor WT;
PI Madison VS, Zhang R, Reichert P;
XX
DR WPI; 2005-180390/19.
DR P-PSDB; ADX15881.
XX
PT Novel modified human double minute 2 protein polypeptide, comprising
PT amino acid sequence differing from its corresponding wild-type, useful
PT for identifying compounds used as anticancer agents.
XX
PS Claim 7; SEQ ID NO 7; 49pp; English.
XX
CC The invention relates to a novel modified human Double Minute 2 protein
CC (Hdm2) polypeptide (I) comprising a fully defined sequence of 109 amino
CC acids (S1) as given in the specification, differing from the
CC corresponding wild-type Hdm2 (17-125) amino acid sequence (ADX15875). A
CC polypeptide of the invention is useful for identifying an agent for use
CC as an inhibitor of Hdm2. The polypeptide, crystal of the polypeptide or
CC polypeptide-compound complex (PPC) is useful for designing, selecting

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CC and/or optimizing a potential inhibitor of the polypeptide. The
CC polypeptide or PPC is useful for evaluating the ability of a potential
CC inhibitor to associate with the polypeptide or PPC. The polypeptide,
CC crystal of the polypeptide or PPC is useful for identifying, selecting
CC and/or designing compounds useful as anticancer agents. The polypeptide
CC is useful in designing high affinity inhibitors of Hdm2 that are useful
CC in the treatment of cancers. The present sequence encodes a modified
CC human Double Minute 2 protein (Hdm2) polypeptide of the invention.

XX Sequence 327 BP; 107 A; 56 C; 69 G; 95 T; 0 U; 0 Other;

Query Match 11.6%; Score 276; DB 14; Length 327;

Best Local Similarity 99.7%; Pred. No. 1.1e-122;

Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 360 TCACGATTCCAGCTTCGGAACAAGACCCCTGGTTAGCCAAAGCATGCTTTGGAAG 419
DB 1 TCACGATTCCAGCTTCGGAACAAGACCCCTGGTTAGCCAAAGCATGCTTTGGAAG 60

QY 420 TTATTAAGTCTGTGTGACAAAAGACACTTATCATGAAAGAGTCTTTTAT 479
DB 61 TTATTAAGTCTGTGTGACAAAAGACACTTATCATGAAAGAGTCTTTTAT 120

QY 480 CTTGGCCAGTATATATGACTTAACGATTATGATGAGAACAAACATATTTATAT 539
DB 121 CTTGGCCAGTATATATGACTTAACGATTATGATGAGAACAAACATATTTATAT 180

QY 540 TGTTCATATGATCTTCTAGAGATTTGTTGGCGTCCAGAGCTTCTGTGAAAGAGAC 599
DB 181 TGTTCATATGATCTTCTAGAGATTTGTTGGCGTCCAGAGCTTCTGTGAAAGAGAC 240

QY 600 AGGAAATATATATACATGATCTACAGAACTGTGATGATGATCAACAGAGATCATG 659
DB 241 AGGAAATATATATACATGATCTACAGAACTGTGATGATGATCAACAGAGATCATG 300

QY 660 GACTCAGGTACATCTGTGAGTGAAGAC 686
DB 301 GACTCAGGTACATCTGTGAGTGAAGAC 327

RESULT 6
AAT99094
ID AAT99094 standard; DNA; 309 BP.

XX AAT99094;

XX 30-MAR-1998 (first entry)

XX Human mdm2-E gene.

XX Cognate transgene; human; mdm2; lymphoma; cellular immunogen; cancer;
XX self-determinant immunoreactivity; cancer vaccination; breast carcinoma;
XX colon carcinoma; immunotherapy; proto-oncogene; ss.

OS Homo sapiens.

PN W09725860-A1.

XX 24-JUL-1997.

XX 13-JAN-1997; 97WO-US000582.

XX 19-JAN-1996; 96US-0010262P.

XX (UYAL-) UNIV ALLEGHENY HEALTH SCI.

XX Halpern MS, England JM;

XX WPI; 1997-38493/35.

XX Proto-oncogene immunogen - used in vaccine for the prevention and
XX treatment of cancer.

PS Disclosure; Page 60-61; 81pp; English.

XX This sequence represents the human mdm2-E cognate transgene (CTG).
CC Deletion of amino acids 9-155 of the encoded protein renders the CTG non-
CC transforming. This sequence can be used in the cellular immunogen of the
CC invention. The cellular immunogen of the invention is for immunising
CC against the product of a target proto-oncogene, over-expression of which
CC is associated with cancer, comprises host cells transfected with a
CC construct containing at least one transgene related to the proto-oncogene
CC and driven by a strong promoter. The product of the transgene induces
CC immunoreactivity to host self-determinants on the product of proto-
CC oncogene. The cellular immunogens are used for protective vaccination
CC against cancer (e.g. carcinoma of breast or colon, or various lymphomas)
CC and for immunotherapy of cancer. Use of the immunogen eliminates the need
CC to isolate immunogenic, HLA host-matched peptides. The method is not
CC based on immune recognition of a determinant defined by a cancer-specific
CC mutation and generates a systemic (anti-metastatic) response

XX Sequence 309 BP; 100 A; 57 C; 53 G; 99 T; 0 U; 0 Other;

Query Match 9.5%; Score 225; DB 2; Length 309;

Best Local Similarity 100.0%; Pred. No. 5.6e-98;

Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGCGAATACCAACATGCTGTACCTTATGATGCTGTGAACCACTCACAATTCGA 371
DB 1 ATGCGAATACCAACATGCTGTACCTTATGATGCTGTGAACCACTCACAATTCGA 60

QY 372 GCTTCGGAACAAGACCCCTGGTTAGACCAAGCATGCTTTGAAAGTTAAGTCT 431
DB 61 GCTTCGGAACAAGACCCCTGGTTAGACCAAGCATGCTTTGAAAGTTAAGTCT 120

QY 432 GTTGTCGCAAAAAGACACTTATATCTATGAAGAGTCTTTTATCTTGCCAGTAT 491
DB 121 GTTGTCGCAAAAAGACACTTATATCTATGAAGAGTCTTTTATCTTGCCAGTAT 180

QY 492 ATTATGACTTAACGATTATATGATGAGAACCAACATATTTGTA 536
DB 181 ATTATGACTTAACGATTATATGATGAGAACCAACATATTTGTA 225

RESULT 7
AAZ60820
ID AAZ60820 standard; DNA; 309 BP.

XX AAZ60820;

XX 16-MAY-2000 (first entry)

XX Nucleotide sequence of a cognate transgene of mdm-2.

XX Cognate transgene; CTG; tumorigenic; cellular immunogen; immunisation;
XX proto-oncogene; malignancy; allogenic cell; vaccine; cancer; ss.

OS Homo sapiens.

PN W0200004927-A1.

XX 03-FEB-2000.

XX 08-JUL-1999; 99WO-US015594.

XX 24-JUL-1998; 98US-0093965P.

XX (UYAL-) UNIV ALLEGHENY HEALTH SCI.

XX (HALP/) HALPERN M S.

XX (ENGL/) ENGLAND J M.

XX Halpern MS, England JM;
XX WPI; 2000-182543/16.
XX Cellular immunogens comprising allogenic donor cells transfected with a


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XX OS Unidentified.
XX PN DE10209071-A1.
XX PD 25-SEP-2003.
XX PF 28-FEB-2002; 2002DE-01009071.
XX PR 28-FEB-2002; 2002DE-01009071.
XX PA (ROBO-) ROBOSCREEN GRS MOLEKULARE BIOTECHNOLOGIE.
XX PI Koehler T, Rost A;
XX DR WPI; 2003-732912/70.
XX PT Standardized polynucleotide system, useful for quantitative, real-time
XX PT determination of nucleic acid, comprises stabilized standards, primers
XX PT and probe.
XX PS Claim 1; Page 7; 38pp; German.
XX CC The present invention relates to a standardized polynucleotide system,
XX CC which comprises at least one carrier nucleic acid, at least 3
XX CC oligonucleotides, as primers and target-specific, fluorescently labeled
XX CC probe and optionally at least one set of stabilized controls (standard
XX CC RNA or DNA) of known concentration and instructions. The system comprises
XX CC any of 20 sets of one control, two primers and one target-specific probe.
XX CC The standardized polynucleotide system can be used for quantitative, real-
XX CC time detection of target nucleic acids, especially analysis of genes or
XX CC gene products, e.g. for individualized medical diagnosis, in veterinary
XX CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,
XX CC pharmaceutical testing, analysis of food or environmental samples and
XX CC also for ultra-sensitive detection of proteins by immuno-PCR. The present
XX CC sequence is a polynucleotide used in the system of the invention.
XX SQ Sequence 211 BP; 73 A; 38 C; 52 G; 48 T; 0 U; 0 Other;

Query Match      8.9%; Score 211; DB 10; Length 211;
Best Local Similarity 100.0%; Pred. No. 3.4e-91;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1531 GCCAAGAGATGTGAAGATTGGAAGGAAAGAACCCAGACAAAGAGAGATGTGG 1590
Db 1 GCCAAGAGATGTGAAGATTGGAAGGAAAGAACCCAGACAAAGAGAGATGTGG 60
QY 1591 AATCTAGTTTGCCCTTATGACATTGAACCTGTGTGATTTGTCAAGGTGACCTAAA 1650
Db 61 AATCTAGTTTGCCCTTATGACATTGAACCTGTGTGTGATTTGTCAAGGTGACCTAAA 120
QY 1651 ATGTTGATTTGTCATGCGCAAAACGAGACATCTTATGCGCTCTTTCATGTGCAAGA 1710
Db 121 ATGTTGATTTGTCATGCGCAAAACGAGACATCTTATGCGCTCTTTCATGTGCAAGA 180
QY 1711 AGCTAAAGAAAGAAATTAAGCCCTGCCCACT 1741
Db 181 AGCTAAAGAAAGAAATTAAGCCCTGCCCACT 211

RESULT 10
AAA62123
ID AAA62123 standard; RNA; 199 BP.
XX
XX AAA62123;
XX AC
XX 20-JUN-2001 (first entry)
XX DT
XX mdm2 long transcript found in cancerous cells.
XX DE
XX mdm2; disease prediction; cancer; p53; human; ss.
XX KW
XX Homo sapiens.
XX OS
```

```
XX Key
XX Key Location/Qualifiers
XX misc_structure 5..50
XX /tag= f
XX /standard_name= "Unique Exon1 structure"
XX 5..10
XX /tag= a
XX /bound_moiety= "mdm2 long transcript"
XX /note= "Forms double-stranded region with bases 45-50 of
XX mdm2 long transcript"
XX 13..17
XX /tag= b
XX /bound_moiety= "mdm2 long transcript"
XX /note= "Forms double-stranded region with bases 37-41 of
XX mdm2 long transcript"
XX 20..33
XX /tag= c
XX /tag= d
XX /bound_moiety= "mdm2 long transcript"
XX /note= "Forms double-stranded region with bases 13-17 of
XX mdm2 long transcript"
XX 45..50
XX /tag= e
XX /bound_moiety= "mdm2 long transcript"
XX /note= "Forms double-stranded region with bases 5-10 of
XX mdm2 long transcript"
XX 53..98
XX /tag= g
XX /standard_name= "Unique Exon1/ Exon3 junction structure"
XX 101..114
XX /tag= h
XX 116..118
XX /tag= i
XX /bound_moiety= "mdm2 long transcript"
XX /note= "Forms double-stranded region with bases 141-143
XX of mdm2 long transcript"
XX 124..137
XX /tag= j
XX 141..143
XX /tag= k
XX /bound_moiety= "mdm2 long transcript"
XX /note= "Forms double-stranded region with bases 116-118
XX of mdm2 long transcript"
XX 148..158
XX /tag= l
XX 161..164
XX /tag= m
XX /bound_moiety= "mdm2 long transcript"
XX /note= "Forms double-stranded region with bases 191-194
XX of mdm2 long transcript"
XX 169..185
XX /tag= n
XX 191..194
XX /tag= o
XX /bound_moiety= "mdm2 long transcript"
XX /note= "Forms double-stranded region with bases 161-164
XX of mdm2 long transcript"
XX WO200031110-A1.
XX 02-JUN-2000.
XX
XX 22-NOV-1999; 99WO-US027710.
XX
XX 25-NOV-1998; 98US-0020035.
XX 25-NOV-1998; 98US-0110024P.
XX (ISIS-) ISIS PHARM INC.
XX Ecker DJ;
XX WPI; 2000-400027/34.
XX
```

XX Identifying a target nucleic acid sequence predictive of preselected
PT disease states such as a cancerous state, by comparing members of a set
PT of mRNA molecules, from a common gene, containing different sequences and
PT structures.
XX
XX Example 1; Fig 2; 38pp; English.
XX
CC The mdm2 oncogene is implicated in a variety of human cancers. The
CC protein encoded by mdm2 gene binds to p53 protein and thereby inhibits
CC p53's function. p53 is a tumour suppressor. Cancer cells contain a
CC specific form of mdm2 RNA, which is not found in normal cells. The
CC present sequence is the cancer-specific mdm2 RNA. The present sequence
CC has two unique structures: "unique Exon1 structure", and "unique Exon1/
CC Exon3 junction structure". These structures are not found in the mdm2 RNA
CC of normal cells (see ABA62124). The present sequence is predictive of
CC cancer and detection of the present sequence may therefore be used as a
CC method of predicting disease. Other diseases which may be identified by
CC using a similar method to detect other RNA molecules are
CC hyperproliferative conditions, lupus erythematosus, psoriasis,
CC inflammation, cardiovascular disease, pain, arthritis, obesity, trauma,
CC Huntington's disease or neurological disorders
XX
SQ Sequence 199 BP; 56 A; 49 C; 51 G; 0 T; 43 U; 0 Other;
Query Match 8.4%; Score 199; DB 3; Length 199;
Best Local Similarity 78.4%; Pred. No. 2.2e-85;
Matches 156; Conservative 43; Mismatches 0; Indels 0; Gaps 0;
OY 244 GAAACTGGGAGCTTGAAGGAGACCCCGATCCAAAGCCGAGATGCTGAGGA 303
DB 1 GAACTGGGAGCTTGAAGGAGACCCCGATCCAAAGCCGAGATGCTGAGGA 60
OY 304 GCAAGCAATGTCATCCAAATGCTGATACCTGATGATGCTGATACCTGATAC 363
DB 61 GCAAGCAATGTCATCCAAATGCTGATACCTGATGATGCTGATACCTGATAC 120
OY 364 AGATTCCAGCTTCGGAACAAGACCCCTGTTAGACCAAGCATTCCTTTGAAGTTAT 423
DB 121 AGAATCCAGCTTCGGAACAAGACCCCTGTTAGACCAAGCATTCCTTTGAAGTTAT 180
OY 424 TAAAGTCTGTTGTGACACA 442
DB 181 UAAAGUCUGUUGUGACACA 199
RESULT 11
ADC22295
ID ADC22295 standard; DNA; 176 BP.
XX
XX ADC22295;
XX
DT 18-DEC-2003 (first entry)
XX
XX Protein binding domain nucleotide sequence SEQ ID NO:144.
XX
XX recombinant fusion protein; fusion protein; binding; detection;
KW localisation domain; binding domain;
KW subcellular compartment localisation; gene; ds.
XX
XX Homo sapiens.
XX
XX WO2003012068-A2.
XX
XX 13-FEB-2003.
XX
XX 01-AUG-2002; 2002WO-US024572.
XX
XX 01-AUG-2001; 2001US-0309395P.
XX
XX 13-DEC-2001; 2001US-0341589P.
XX
XX (CELL-) CELLOMICS INC.
XX

PI Bright G, Premkumar DR, Chen Y;
XX
XX WPI: 2003-248174/24.
DR P-PSDB; ADC22294.
XX
XX New recombinant fusion protein comprising detection and first
PT localisation domains and a binding domain for the molecule of interest,
PT useful for detecting binding of a molecule of interest.
XX
XX Disclosure; SEQ ID NO 144; 101pp; English.
XX
XX The present invention describes a recombinant fusion protein (1) for
CC detecting binding of a molecule of interest. (1) comprises: (a) a
CC detection domain; (b) a first localisation domain; and (c) a binding
CC domain for the molecule of interest. The detection domain, the first
CC localisation domain and the binding domain for the molecule of interest
CC constituting the recombinant fusion protein for detecting binding of a
CC molecule of interest are operably linked. The binding domain for the
CC molecule of interest is separated from the first localisation domain by 0
CC -20 amino acid residues. The first localisation domain and the binding
CC domain for the molecule of interest both do not occur in a single non-
CC recombinant protein with the same spacing as in the recombinant fusion
CC protein for detecting binding of a molecule of interest. Also described:
CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;
CC (2) a recombinant expression vector comprising the nucleic acid control
CC sequences operably linked to the recombinant nucleic acid molecule; (3) a
CC genetically engineered host cell transfected with the recombinant
CC expression vector; (4) a kit for detecting binding of the molecule of
CC interest; and (5) a method for identifying compounds that alter the
CC binding of the molecule of interest. The recombinant fusion protein is
CC useful for detecting binding of a molecule of interest. The recombinant
CC fusion protein eliminates the need to construct two or more chimeric
CC proteins and enables the monitoring of biochemical events in live, intact
CC or fixed cells. The present sequence is used in the exemplification of
CC the present invention.
XX
SQ Sequence 176 BP; 60 A; 25 C; 35 G; 56 T; 0 U; 0 Other;
Query Match 7.4%; Score 176; DB 10; Length 176;
Best Local Similarity 100.0%; Pred. No. 3e-74;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 435 GGTGCACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGGCAGTATAT 494
DB 1 GTGCACAAAAGACACTTATCTATGAAAGAGTCTTTTATCTTGGCAGTATAT 60
OY 495 ATGACTAAAGATTTATGATGAGAACACAAATATTTGTTCAAAAGATCTT 554
DB 61 ATGACTAAAGATTTATGATGAGAACACAAATATTTGTTCAAAAGATCTT 120
OY 555 CTAGAGATTTGTTGGCGTGCCAAAGCTTCTGTGAAAGACACAGAAATATATA 610
DB 121 CTAGAGATTTGTTGGCGTGCCAAAGCTTCTGTGAAAGACACAGAAATATATA 176
RESULT 12
ABV94129
ID ABV94129 standard; cDNA; 319 BP.
XX
XX ABV94129;
XX
DT 08-JAN-2003 (first entry)
XX
XX Breast carcinoma related nucleotide sequence SEQ ID NO:120.
XX
XX Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
KW ss.
XX
XX Homo sapiens.
XX
XX WO200246467-A2.
XX
XX 13-JUN-2002.
XX

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XX 07-DEC-2001; 2001WO-1B002811.
PF 08-DEC-2000; 2000US-0254090P.
PR 07-DEC-2001; 2001US-00007926.
XX (IPSO-) IPSOGEN.
XX Bertucci F, Houlgate R, Birnbaum D, Nguyen C, Viens P, Fert V,
XX WPI; 2002-619023/66.
XX
XX Novel polynucleotide library useful in molecular characterization of a
XX carcinoma, comprising a pool of polynucleotide sequences or its
XX subsequences which are either underexpressed or overexpressed in tumor
XX cells.
XX
XX Claim 1; Page 189; 401pp; English.
XX
XX The present invention describes a polynucleotide library (I) useful in
XX the molecular characterization of a carcinoma, comprising a pool of
XX polynucleotides or its subsequences which are either underexpressed or
XX overexpressed in tumor cells, and correspond to any of the
XX polynucleotide sequences chosen from the 468 sequences given in ABY94010
XX to ABY94477. Also described: (1) a polynucleotide array (II) useful for
XX the prognosis or diagnostic of tumor, comprising (I); and (2) detecting
XX (M1) differentially expressed polynucleotide sequences which are
XX correlated with a cancer, involves obtaining a polynucleotide sample from
XX a patient, and reacting the polynucleotide sample obtained with a probe
XX immobilised on a solid support, where the probe comprises any combination
XX of the polynucleotide sequences of (I) or its expression products encoded
XX by polynucleotide sequences of (I), and detecting the reaction product.
XX (I) have cytostatic activities and can be used as anti-tumour agents. (I)
XX is useful in molecular characterization of a carcinoma. (I) and (II) are
XX useful for the prognosis or diagnostic of tumour, in differentiating a
XX normal cell from a cancer cell, detecting a hormone sensitive tumour
XX cell, differentiating a tumour with lymph nodes from a tumour without
XX lymph nodes, differentiating antitaxylene-sensitive tumours from
XX antitaxylene-insensitive tumours, and classifying good and poor prognosis
XX primary breast tumours. (I) is useful for large-scale molecular
XX characterisation of breast cancer that help in prediction, prognosis and
XX cancer treatment, and for detecting differentially expressed genes that
XX correlated with a cancer
XX
XX Sequence 319 BP; 100 A; 50 C; 44 G; 123 T; 0 U; 2 Other;
XX
XX Query Match 7.0%; Score 167; DB 6; Length 319;
XX Best Local Similarity 100.0%; Pred. No. 6.7e-70;
XX Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1773 ACTTATTTCCCTAGTGAAGTCTCTATPAGAAATTAATATTTCTAATATATACCC 1832
XX Db 2 ACTTATTTCCCTAGTGAAGTCTCTATPAGAAATTAATATTTCTAATATATACCC 61
XX
XX 1833 TAGGAATTTAGCAACCTGAATTTATTCACATATATCAAAAGTGAAGAAATGCCCAATT 1892
XX Db 62 TAGGAATTTAGCAACCTGAATTTATTCACATATATCAAAAGTGAAGAAATGCCCAATT 121
XX
XX 1893 CACATAGATTTCTTCTTTAGTATATATGACCTACTTTGGTAGGG 1939
XX Db 122 CACATAGATTTCTTCTTTAGTATATATGACCTACTTTGGTAGGG 168
XX
XX RESULT 13
XX AAA62124
XX ID AAA62124 standard; RNA; 199 BP.
XX AC AAA62124;
XX XX
XX DT 20-JUN-2001 (first entry)
XX XX
XX DE mdm2 short transcript found in normal cells.
XX XX

```

```

KM mdm2; disease prediction; cancer; p53; human; ss.
XX
XX Homo sapiens.
XX
XX Key
XX misc_binding
XX 2..8
XX /tag= a
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 10..28
XX /tag= b
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 29..38
XX /tag= c
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 40..46
XX /tag= d
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 54..67
XX /tag= e
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 72..110
XX /tag= f
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 116..118
XX /tag= g
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 124..137
XX /tag= h
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 141..143
XX /tag= i
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 148..158
XX /tag= j
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 161..164
XX /tag= k
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 169..185
XX /tag= l
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX 191..194
XX /tag= m
XX /bound_moiety= "mdm2 short transcript"
XX /note= "Forms double-stranded region with bases 40-46 of
XX mdm2 short transcript"
XX
XX WO200031110-A1.
XX
XX 02-JUN-2000.
XX
XX 22-NOV-1999; 99WO-US027710.
XX
XX 25-NOV-1998; 98US-00200355.
XX
XX 25-NOV-1998; 98US-0110024P.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ;
XX
XX WPI; 2000-400027/34.
XX
XX Identifying a target nucleic acid sequence predictive of preselected
XX disease states such as a cancerous state, by comparing members of a set
XX of mRNA molecules, from a common gene, containing different sequences and
XX structures.
XX
XX Example 1; Fig 2; 38pp; English.
XX
XX The mdm2 oncogene is implicated in a variety of human cancers. The
XX

```

CC protein encoded by mdm2 gene binds to p53 protein and thereby inhibits
CC p53's function. p53 is a tumour suppressor. Cancer cells contain a
CC specific form of mdm2 RNA, which is not found in normal cells (AA62123).
CC The present sequence is the mdm2 RNA which is found in normal cells. The
CC present sequence has a unique structure: "Exon2/ Exon3 junction
CC structure". These structures are not found in the mdm2 RNA of cancerous
CC cells. The sequence of AA62123 is predictive of cancer and detection of
CC the sequence of AA62123 may therefore be used as a method of predicting
CC disease. Other diseases which may be identified by using a similar method
CC to detect other RNA molecules are hyperproliferative conditions, lupus
CC erythematosus, psoriasis, inflammation, cardiovascular disease, pain,
CC arthritis, obesity, trauma, Huntington's disease or neurological
CC disorders
XX
SQ Sequence 199 BP; 50 A; 49 C; 49 G; 0 T; 51 U; 0 Other;
Query Match 5.8%; Score 138; DB 3; Length 199;
Best Local Similarity 73.9%; Pred. No. 7.4e-56;
Matches 102; Conservative 36; Mismatches 0; Indels 0; Gaps 0;
QY 305 CAGGCAATGTGCATACCAATGCTGTACCTACTGATGTGTACCACTCACA 364
Db 62 CAGGCAAAUGUGCAADUACCAUGUCUGUACCUAGUGUGUAAACCCUACA 121
QY 365 GATTCAGACTTCGGAACAAGAGACCCCTGTTAGACCAAGCATGCTTTGAAGTAT 424
Db 122 GAUUCGACGUCUGGAACAAGAGACCCUGUUAAGCAAGCAUUGCUUUGAAGUUAU 181
QY 425 AAAGCTGTTGTTGTCACA 442
Db 182 AAAGUCUGUGUGUGACA 199
RESULT 14
ADX15884
ID ADX15884 standard; DNA; 327 BP.
XX
AC ADX15884;
XX
DT 05-MAY-2005 (first entry)
XX
DE Modified human double minute 2 protein HK5 encoding DNA SEQ ID NO:11.
XX
KM double minute 2; ds; cancer; cytostatic; neoplasm; X-ray crystallography;
KM protein solubilization; mutant; mutagenesis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..327
FT /tag= a
FT /product= "double minute 2 variant"
FT /partial
FT /note= "no start/stop codon given"
XX
PN US2005037383-A1.
XX
PD 17-FEB-2005.
XX
PR 09-APR-2004; 2004US-00822254.
XX
PR 10-APR-2003; 2003US-0461787P.
PR 24-FEB-2004; 2004US-0547265P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Taremi SS, Xie G, Hesson T, Duca JS, Strickland C, Windsor WT;
PI Madison VS, Zhang R, Reichert P;
XX
XX WPI; 2005-180390/19.
DR P-PSDB; ADX15885.
XX
PT Novel modified human double minute 2 protein polypeptide, comprising

PT amino acid sequence differing from its corresponding wild-type, useful
XX for identifying compounds used as anticancer agents.
XX
PS Claim 7; SEQ ID NO 11; 49pp; English.
XX
XX The invention relates to a novel modified human Double Minute 2 protein
CC (Hdm2) polypeptide (I) comprising a fully defined sequence of 109 amino
CC acids (S1) as given in the specification, differing from the
CC corresponding wild-type Hdm2 (117-125) amino acid sequence (ADX15875). A
CC polypeptide of the invention is useful for identifying an agent for use
CC as an inhibitor of Hdm2. The polypeptide, crystal of the polypeptide or
CC polypeptide-compound complex (PPC) is useful for designing, selecting
CC and/or optimizing a potential inhibitor of the polypeptide. The
CC polypeptide or PPC is useful for evaluating the ability of a potential
CC inhibitor to associate with the polypeptide or PPC. The polypeptide,
CC crystal of the polypeptide or PPC is useful for identifying, selecting
CC and/or designing compounds useful as anticancer agents. The polypeptide
CC is useful in designing high affinity inhibitors of Hdm2 that are useful
CC in the treatment of cancers. The present sequence encodes a modified
CC human Double Minute 2 protein (Hdm2) polypeptide of the invention.
XX
SQ Sequence 327 BP; 117 A; 53 C; 70 G; 87 T; 0 U; 0 Other;
Query Match 4.6%; Score 109; DB 14; Length 327;
Best Local Similarity 100.0%; Pred. No. 8e-42;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 578 AAGCTTCTGTGTGAAGAAGCAGCAAGAAATATATACCATGATCTACAGGAATGTTAGT 637
Db 219 AAGCTTCTGTGTGAAGAAGCAGCAAGAAATATATACCATGATCTACAGGAATGTTAGT 278
QY 638 AGTCATCAGCAGGAATCATCGACTCAGTACATCTGTGAGTGAAC 686
Db 279 AGTCATCAGCAGGAATCATCGACTCAGTACATCTGTGAGTGAAC 327
RESULT 15
AAK81934/C
ID AAK81934 standard; DNA; 297 BP.
XX
AC AAK81934;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36746.
XX
KM Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.

PR	26-JUL-2000	2000US-0220963P.
PR	26-JUL-2000	2000US-0220964P.
PR	14-AUG-2000	2000US-0224518P.
PR	14-AUG-2000	2000US-0224519P.
PR	14-AUG-2000	2000US-0224521P.
PR	14-AUG-2000	2000US-0225216P.
PR	14-AUG-2000	2000US-0225266P.
PR	14-AUG-2000	2000US-0225267P.
PR	14-AUG-2000	2000US-0225268P.
PR	14-AUG-2000	2000US-0225270P.
PR	14-AUG-2000	2000US-0225447P.
PR	14-AUG-2000	2000US-0225757P.
PR	14-AUG-2000	2000US-0225758P.
PR	14-AUG-2000	2000US-0225759P.
PR	18-AUG-2000	2000US-0226279P.
PR	22-AUG-2000	2000US-0226681P.
PR	22-AUG-2000	2000US-0226868P.
PR	22-AUG-2000	2000US-0227182P.
PR	23-AUG-2000	2000US-0227009P.
PR	30-AUG-2000	2000US-0228924P.
PR	01-SEP-2000	2000US-0229287P.
PR	01-SEP-2000	2000US-0229343P.
PR	01-SEP-2000	2000US-0229344P.
PR	01-SEP-2000	2000US-0229345P.
PR	05-SEP-2000	2000US-0229509P.
PR	05-SEP-2000	2000US-0239513P.
PR	06-SEP-2000	2000US-0230437P.
PR	06-SEP-2000	2000US-0230438P.
PR	08-SEP-2000	2000US-0231242P.
PR	08-SEP-2000	2000US-0231243P.
PR	08-SEP-2000	2000US-0231244P.
PR	08-SEP-2000	2000US-0231413P.
PR	08-SEP-2000	2000US-0231414P.
PR	08-SEP-2000	2000US-0232080P.
PR	12-SEP-2000	2000US-0231968P.
PR	14-SEP-2000	2000US-0232397P.
PR	14-SEP-2000	2000US-0232398P.
PR	14-SEP-2000	2000US-0232399P.
PR	14-SEP-2000	2000US-0232400P.
PR	14-SEP-2000	2000US-0232401P.
PR	14-SEP-2000	2000US-0233063P.
PR	14-SEP-2000	2000US-0233064P.
PR	21-SEP-2000	2000US-0234223P.
PR	21-SEP-2000	2000US-0234274P.
PR	25-SEP-2000	2000US-0234997P.
PR	25-SEP-2000	2000US-0234998P.
PR	26-SEP-2000	2000US-0235484P.
PR	27-SEP-2000	2000US-0235834P.
PR	27-SEP-2000	2000US-0235836P.
PR	29-SEP-2000	2000US-0236327P.
PR	29-SEP-2000	2000US-0236367P.
PR	29-SEP-2000	2000US-0236368P.
PR	29-SEP-2000	2000US-0236369P.
PR	29-SEP-2000	2000US-0236370P.
PR	02-OCT-2000	2000US-0236802P.
PR	02-OCT-2000	2000US-0237037P.
PR	02-OCT-2000	2000US-0237038P.
PR	02-OCT-2000	2000US-0237039P.
PR	02-OCT-2000	2000US-0237040P.
PR	13-OCT-2000	2000US-0239955P.
PR	13-OCT-2000	2000US-0239957P.
PR	20-OCT-2000	2000US-0240960P.
PR	20-OCT-2000	2000US-0241221P.
PR	20-OCT-2000	2000US-0241785P.
PR	20-OCT-2000	2000US-0241786P.
PR	20-OCT-2000	2000US-0241787P.
PR	20-OCT-2000	2000US-0241808P.
PR	20-OCT-2000	2000US-0241809P.
PR	20-OCT-2000	2000US-0241826P.
PR	01-NOV-2000	2000US-0244617P.
PR	08-NOV-2000	2000US-0244674P.
PR	08-NOV-2000	2000US-0246475P.
PR	08-NOV-2000	2000US-0246476P.
PR	08-NOV-2000	2000US-0246477P.
PR	08-NOV-2000	2000US-0246478P.
PR	08-NOV-2000	2000US-0246523P.
PR	08-NOV-2000	2000US-0246524P.
PR	08-NOV-2000	2000US-0246525P.
PR	08-NOV-2000	2000US-0246526P.
PR	08-NOV-2000	2000US-0246527P.
PR	08-NOV-2000	2000US-0246528P.
PR	08-NOV-2000	2000US-0246532P.
PR	08-NOV-2000	2000US-0246609P.
PR	08-NOV-2000	2000US-0246610P.
PR	08-NOV-2000	2000US-0246611P.
PR	17-NOV-2000	2000US-0246613P.
PR	17-NOV-2000	2000US-0249207P.
PR	17-NOV-2000	2000US-0249208P.
PR	17-NOV-2000	2000US-0249209P.
PR	17-NOV-2000	2000US-0249210P.
PR	17-NOV-2000	2000US-0249211P.
PR	17-NOV-2000	2000US-0249212P.
PR	17-NOV-2000	2000US-0249213P.
PR	17-NOV-2000	2000US-0249215P.
PR	17-NOV-2000	20

CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169
XX represent sequences used in the exemplification of the present invention
SQ Sequence 297 BP, 93 A; 68 C; 88 G; 48 T; 0 U; 0 Other;

Query Match 4.3%; Score 102; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2260 TTTTAGTAGACACGAGGTTTACCGTGTAGCCAGAGTGTCTGATCTCTGACCTCGT 2319
Db 110 TTTTAGTAGACACGAGGTTTACCGTGTAGCCAGAGTGTCTGATCTCTGACCTCGT 51

OY 2320 GATCGCGCCACCTGCGCTCCCAAGTGTGGGATTACAGGC 2361
Db 50 GATCGCGCCACCTGCGCTCCCAAGTGTGGGATTACAGGC 9

RESULT 16
AAK81936/C
ID AAK81936 standard; DNA; 324 BP.

AC AAK81936;

DT 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36748.

DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

OS WO200157182-A2.

PN 09-AUG-2001.

PD 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205151P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225265P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226688P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 08-SEP-2000; 2000US-0232081P.

PR 12-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

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XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM,
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 36748; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytosstatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK7694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention
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Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 07-NOV-2001 (first entry)
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XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
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PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
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XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 36749; 3071bp + Sequence listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK67694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention
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XX Sequence 325 BP; 100 A; 71 C; 97 G; 57 T; 0 U; 0 Other;
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XX Query Match 4.3%; Score 102; DB 4; Length 325;
XX Best Local Similarity 100.0%; Pred. No. 2e-38;
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DE Human immune/haematopoietic; immune/haematopoietic antigen; cancer;
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
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OS Homo sapiens.
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(HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 36747; 3071bp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytotoxic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 331 BP; 102 A; 72 C; 99 G; 58 T; 0 U; 0 Other;

Query Match 4.3%; Score 102; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2320 GATCCGCCACCTCGGCTCCCAAGTGTGCGATTACAGC 2361
Db 78 GATCCGCCACCTCGGCTCCCAAGTGTGCGATTACAGC 37

RESULT 19
AAK81933/C
ID AAK81933 standard; DNA; 331 BP.
XX
AC AAK81933;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36745.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytotoxic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN MO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225269P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
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PR 05-SEP-2000; 2000US-0229509P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
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PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
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PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234224P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
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PR 29-SEP-2000; 2000US-0236337P.
PR 29-SEP-2000; 2000US-0236338P.
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PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
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PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.

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PR	08-NOV-2000	2000US-0246532P	PR
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PR	08-NOV-2000	2000US-0246610P	PR
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PR	17-NOV-2000	2000US-0249209P	PR
PR	17-NOV-2000	2000US-0249210P	PR
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PR	17-NOV-2000	2000US-0249212P	PR
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PR	17-NOV-2000	2000US-0249216P	PR
PR	17-NOV-2000	2000US-0249217P	PR
PR	17-NOV-2000	2000US-0249218P	PR
PR	17-NOV-2000	2000US-0249244P	PR
PR	17-NOV-2000	2000US-0249245P	PR
PR	17-NOV-2000	2000US-0249264P	PR
PR	17-NOV-2000	2000US-0249265P	PR
PR	17-NOV-2000	2000US-0249297P	PR
PR	17-NOV-2000	2000US-0249299P	PR
PR	01-DEC-2000	2000US-0250160P	PR
PR	01-DEC-2000	2000US-0250391P	PR
PR	05-DEC-2000	2000US-0251030P	PR
PR	05-DEC-2000	2000US-0251988P	PR
PR	05-DEC-2000	2000US-0256719P	PR
PR	06-DEC-2000	2000US-0251479P	PR
PR	08-DEC-2000	2000US-0251856P	PR
PR	08-DEC-2000	2000US-0251868P	PR
PR	08-DEC-2000	2000US-0251869P	PR
PR	08-DEC-2000	2000US-0251889P	PR
PR	08-DEC-2000	2000US-0251907P	PR
PR	11-DEC-2000	2000US-0254097P	PR
PR	05-JAN-2001	2001US-0259678P	PR
XX	(HUMA-) HUMAN GENOME SCI INC.		
XX	Rosen CA, Barash SC, Ruben SM;		
PI	WPI, 2001-483426/52.		
DR			
XX			
XX			
PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,		
XX	useful for preventing, diagnosing and/or treating cancers and metastasis		
XX			
PS	Disclosure; SEQ ID NO 36745; 3071pp + Sequence Listing; English.		
XX			
CC	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)		
CC	amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic		
CC	activity, and can be used in gene therapy and vaccine production. (I)		
CC	proteins and polynucleotides may be used in the prevention, diagnosis and		
CC	treatment of diseases associated with inappropriate (I) expression. For		
CC	example, they may be used to treat disorders associated with decreased		
CC	expression by rectifying mutations or deletions in a patient's genome		
CC	that affect the activity of (I) by expressing inactive proteins or to		
CC	supplement the patients own production of (I). Additionally, (I)		

CC	polynucleotides may be used to produce the secreted (1), by inserting the
CC	nucleic acids into a host cell and culturing the cell to express the
CC	protein. (1) proteins and polynucleotides may be used to prevent.
CC	diagnose and treat immune/haematopoietic-related diseases, especially
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC	to AAK67694 represent human immune/haematopoietic antigen genomic
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC	represent sequences used in the exemplification of the present invention
XX	
SQ	Sequence 331 BP; 102 A; 72 C; 99 G; 58 T; 0 U; 0 Other;
Query Match	4.3%; Score 102; DB 4; Length 331;
Best Local Similarity	100.0%; Pred. No. 2e-38;
Matches 102; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Oy	2260 TTTTAGTGAAGACGAGCGTTTCACCGGTATTAGCAGAGATGCTCCATCTCGAAGCTCGT 2311
Dd	 138 TTTTAGTGAAGACGAGCGTTTCACCGGTATTAGCAGAGATGCTCCATCTCGAAGCTCGT 79
Oy	2320 GATCGGCCACCTCGGCCTCCCAAGTGCTGGATTACAGGC 2361 Db 78 GATCGGCCACCTCGGCCTCCCAAGTGCTGGATTACAGGC 37
RESULT 20	
ID	AALJ6256 standard; DNA; 309 BP.
AC	AALJ6256;
XX	
DT	08-JAN-2002 (first entry)
XX	
DE	Human musculoskeletal system related polynucleotide SEQ ID NO 2621.
XX	
KW	Cytostatic; immunosuppressive; nocotropic; neuroprotective; antiviral;
KM	antiallergic; hepatocytic; antidiabetic; antiinflammatory; anticancer;
KM	vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KM	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KM	neurological disease; infection; human; secreted protein;
KM	musculoskeletal system; ds.
OS	Homo sapiens.
XX	
PN	WO20015367-A1.
XX	
PD	02-AUG-2001.
PF	17-JAN-2001; 2001WO-US001338.
PR	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.
PR	07-JUN-2000; 2000US-0209467P.
PR	28-JUN-2000; 2000US-0214886P.
PR	30-JUN-2000; 2000US-0215135P.
PR	07-JUL-2000; 2000US-0216647P.
PR	07-JUL-2000; 2000US-0216880P.
PR	11-JUL-2000; 2000US-0217487P.
PR	11-JUL-2000; 2000US-0217496P.
PR	14-JUL-2000; 2000US-0218290P.
PR	26-JUL-2000; 2000US-0220963P.
PR	26-JUL-2000; 2000US-0220964P.
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PR	14-AUG-2000; 2000US-0224519P.
PR	14-AUG-2000; 2000US-0225213P.
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PR	14-AUG-2000	2000US-02254477
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PR	14-AUG-2000	2000US-02257588
PR	14-AUG-2000	2000US-02257598
PR	18-AUG-2000	2000US-02252579
PR	18-AUG-2000	2000US-02262799
PR	22-AUG-2000	2000US-02266619
PR	22-AUG-2000	2000US-02271888
PR	22-AUG-2000	2000US-02277182
PR	23-AUG-2000	2000US-02270099
PR	30-AUG-2000	2000US-02289249
PR	01-SEP-2000	2000US-02292879
PR	01-SEP-2000	2000US-02293439
PR	01-SEP-2000	2000US-02293449
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PR	05-SEP-2000	2000US-02295099
PR	05-SEP-2000	2000US-02295139
PR	06-SEP-2000	2000US-02304479
PR	06-SEP-2000	2000US-02304589
PR	08-SEP-2000	2000US-02312429
PR	08-SEP-2000	2000US-02312439
PR	08-SEP-2000	2000US-02312449
PR	08-SEP-2000	2000US-02314139
PR	08-SEP-2000	2000US-02314149
PR	08-SEP-2000	2000US-02320819
PR	08-SEP-2000	2000US-02320819
PR	12-SEP-2000	2000US-02319689
PR	14-SEP-2000	2000US-02323979
PR	14-SEP-2000	2000US-02323989
PR	14-SEP-2000	2000US-02323999
PR	14-SEP-2000	2000US-02324009
PR	14-SEP-2000	2000US-02324019
PR	14-SEP-2000	2000US-02330639
PR	14-SEP-2000	2000US-02330649
PR	14-SEP-2000	2000US-02330659
PR	21-SEP-2000	2000US-02342239
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PR	25-SEP-2000	2000US-02349989
PR	25-SEP-2000	2000US-02354649
PR	25-SEP-2000	2000US-02358949
PR	27-SEP-2000	2000US-02358949
PR	27-SEP-2000	2000US-02358969
PR	29-SEP-2000	2000US-02363379
PR	29-SEP-2000	2000US-02363679
PR	29-SEP-2000	2000US-02363689
PR	29-SEP-2000	2000US-02363699
PR	29-SEP-2000	2000US-02363709
PR	02-OCT-2000	2000US-02368029
PR	02-OCT-2000	2000US-02370379
PR	02-OCT-2000	2000US-02370389
PR	02-OCT-2000	2000US-02370399
PR	02-OCT-2000	2000US-02370409
PR	13-OCT-2000	2000US-02399359
PR	13-OCT-2000	2000US-02399379
PR	13-OCT-2000	2000US-02409609
PR	20-OCT-2000	2000US-02412219
PR	20-OCT-2000	2000US-02417859
PR	20-OCT-2000	2000US-02417869
PR	20-OCT-2000	2000US-02417879
PR	20-OCT-2000	2000US-02418089
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PR	20-OCT-2000	2000US-02418269
PR	01-NOV-2000	2000US-02464579
PR	08-NOV-2000	2000US-02464749
PR	08-NOV-2000	2000US-02464759
PR	08-NOV-2000	2000US-02464769
PR	08-NOV-2000	2000US-02464779
PR	08-NOV-2000	2000US-02464789
PR	08-NOV-2000	2000US-02465239
PR	08-NOV-2000	2000US-02465249
PR	08-NOV-2000	2000US-02465259
PR	08-NOV-2000	2000US-02465269

XX	08-NOV-2000	2000US-0246527P	
PR	08-NOV-2000	2000US-0246528P	
PR	08-NOV-2000	2000US-0246532P	
PR	08-NOV-2000	2000US-0246609P	
PR	08-NOV-2000	2000US-0246610P	
PR	08-NOV-2000	2000US-0246611P	
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PR	17-NOV-2000	2000US-0249264P	
PR	17-NOV-2000	2000US-0249265P	
PR	17-NOV-2000	2000US-0249297P	
PR	17-NOV-2000	2000US-0249299P	
PR	17-NOV-2000	2000US-0249300P	
PR	01-DEC-2000	2000US-0250160P	
PR	01-DEC-2000	2000US-0250391P	
PR	05-DEC-2000	2000US-0251030P	
PR	05-DEC-2000	2000US-0251988P	
PR	05-DEC-2000	2000US-0256719P	
PR	06-DEC-2000	2000US-0251479P	
PR	08-DEC-2000	2000US-0251856P	
PR	08-DEC-2000	2000US-0251868P	
PR	08-DEC-2000	2000US-0251869P	
PR	08-DEC-2000	2000US-0251989P	
PR	08-DEC-2000	2000US-0251990P	
PR	11-DEC-2000	2000US-0254097P	
PR	05-JAN-2001	2001US-0259678P	
XX	(HUMA-) HUMAN GENOME SCI INC.		
PA	Rosen CA, Barash SC, Ruben SW;		
XX	WPI; 2001-451937/48.		
XX			
DR			
XX			
XX			
PT	Isolated polypeptide for treating, preventing and/ or prognosing		
PT	disorders related to the musculoskeletal system including musculoskeletal		
PT	cancers and also for testing and detection e.g. diagnosis.		
XX			
PS	Example 2; SEQ ID NO 2621; 781bp + Sequence Listing; English.		
XX			
CC	The invention relates to novel genes (AAL34669-AAL37666) and proteins		
CC	(AAB03087-AAB04109) associated with the musculoskeletal system useful for		
CC	preventing, treating or ameliorating medical conditions e.g. by protein		
CC	or gene therapy. The genes are isolated from a range of human tissues		
CC	disclosed in the specification. The nucleic acids, proteins, antibodies		
CC	and (ant)agonists are useful in the diagnosis, treatment and prevention		
CC	of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the		
CC	adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,		
CC	lung, or urogenital; (b) immune disorders e.g. Addison's disease,		
CC	allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,		
CC	diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid		
CC	arthritis and ulcerative colitis; (c) cardiovascular disorders such as		
CC	myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g.		
CC	cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,		
CC	bacterial, fungal and parasitic infections. Note: The sequence data for		
CC	this patent did not form part of the printed specification, but was		
CC	obtained in electronic format directly from WIPO at		
CC	ftp.wipo.int/pub/published_pat_sequences		
XX			
XX	Sequence 309 BP; 42 A; 95 C; 80 G; 92 T; 0 U; 0 Other;		

Query Match 3.7%; Score 88; DB 4; Length 309;
Best Local Similarity 100.0%; Pred.No.1.2e-31;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGGTTCAGGATGTCATTCCTGACCTCGTGATCCGCCACCTC 2333
|||||
DB 200 GGGTTTCACCGGTTCAGGATGTCATTCCTGACCTCGTGATCCGCCACCTC 259
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QY 2334 GGCCTCCCAAGTGCCTGGGATTCACAGGC 2361
|||||
DB 260 GGCCTCCCAAGTGCCTGGGATTCACAGGC 287
|||||

RESULT 21
ABX59244
ID ABX59244 standard; cDNA; 309 BP.
XX
XX ABX59244;
XX
XX 26-FEB-2003 (first entry)
XX
XX cDNA encoding novel human musculoskeletal system antigen #1588.
XX
XX Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;
KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
KW post-operative tissue repair; limb regeneration; neuronal growth;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW AIDS-related complex; chondrocyte growth; bone regeneration;
KW periodontal regeneration; tissue transport; bone graft; skin aging;
KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
KW cell growth; organ transplant; cell differentiation; body height; weight;
KW hair colour; eye colour; skin; percentage of adipose tissue;
KW pigmentation; cosmetic surgery; metabolism; biohythm; cardiac rhythm;
KW depression; tendency for violence; pain; reproductive capability;
KW hormone level; endocrine level; appetite; libido; memory; stress;
KW storage capability; fat content; lipid content; protein content;
KW carbohydrate content; vitamin content; cofactor content;
KW nutritional component.
XX
XX Homo sapiens.
OS
XX US2002147140-A1.
XX
XX 10-OCT-2002.
XX
XX 17-JAN-2001; 2001US-00764877.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-021886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0226868P.
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PR 01-SEP-2000; 2000US-0228287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
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PR 05-SEP-2000; 2000US-0229513P.
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PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 01-NOV-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX
XX (ROSE/) ROSEN C A.
PA (RUBE/) ROSEN S M.
PA (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI, 2003-128199/12.
XX
XX Isolated nucleic acid molecules encoding musculoskeletal system
XX associated polypeptides, useful for detecting disorders, e.g. cancer.
XX
XX Disclosure, SEQ ID NO 2621, 321pp, English.
XX
XX The invention describes an isolated nucleic acid molecule comprising a
XX sequence encoding musculoskeletal system associated polypeptides useful
XX for detecting disorders, e.g., cancer or cancer metastases, in animals or
XX humans. The nucleic acid stimulates re-vascularisation of ischemic
XX tissues associated with conditions such as thrombosis, arteriosclerosis,
XX and other cardiovascular conditions; treats wounds due to injuries,
XX burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
XX and limb regeneration; stimulates neuronal growth; can treat and prevent
XX neuronal damage occurring in certain disorders or neurodegenerative
XX conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-
XX related complex; stimulates chondrocyte growth, thus they can be used to
XX enhance bone and periodontal regeneration and aid in tissue transports or
XX bone grafts; prevents skin aging due to sunburn by stimulating
XX keratinocyte growth; prevents hair loss, since FGF family members
XX activate hair-forming cells and promotes melanocyte growth; stimulates
XX growth and differentiation of hematopoietic cells and bone marrow cells
XX when used in combination with other cytokines; maintains organs before
XX transplantation or for supporting cell culture of primary tissues;
XX induces tissue of mesodermal origin to differentiate in early embryos;
XX increases or decreases the differentiation or proliferation of embryonic
XX stem cells, besides, haematopoietic lineage; modulates mammalian
XX characteristics, such as, body height, weight, hair colour, eye colour,
XX skin, percentage of adipose tissue, pigmentation, size, and shape (e.g.,
XX cosmetic surgery); modulates mammalian metabolism; changes mammal's metal
XX state or physical state by influencing biohythms; cardiac rhythms,
XX depression, tendency for violence, tolerance for pain, reproductive
XX capabilities, hormonal or endocrine levels, appetite, libido, memory, or
XX stress; increases or decreases storage capabilities, fat content, lipid,
XX protein, carbohydrate, vitamins, minerals, cofactors or other nutritional
XX components. This sequence encodes a novel human musculoskeletal system
XX antigen. Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?docID=20020147140

XX SQ Sequence 309 BP; 42 A; 95 C; 80 G; 92 T; 0 U; 0 Other;
Query Match 3.7%; Score 88; DB 8; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTACCGTGTATAGCAGATGATGTCGATCTCCGACTCGATCCGACCTC 2333
DB 200 GGGTTTACCGTGTATAGCAGATGATGTCGATCTCCGACTCGATCCGACCTC 259
QY 2334 GGGCTCCCAAGTCTGGGATTACAGGC 2361
DB 260 GGCCTCCCAAGTCTGGGATTACAGGC 287
RESULT 22
ADJ2994
ID ADJ2994 standard; DNA; 309 BP.
XX AC ADJ2994;
XX DT 20-MAY-2004 (first entry)
XX DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2621.
XX KW musculoskeletal system; cytosratic; osteopathic; cancer; osteoporosis;
XX KM gene therapy; vaccine; human; ds.
XX OS Homo sapiens.
XX PN US2004009488-A1.
XX PD 15-JAN-2004.
XX PF 13-SEP-2002; 2002US-00242515.
XX PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 23-AUG-2000; 2000US-0227182P.
PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
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PR 29-SEP-2000; 2000US-0236357P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236399P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.

Query Match	3.7% Score 88; DB 12; Length 309;
Best Local Similarity 100.0%; Pred. No. 1,2e-31;	
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
2274 GGGTTTCAACCGCTGTTACCCAGAGATGTCGATCTCCTGACCTCGTATCCGCCACCTC	2333
200 GGGTTTCAACCGCTGTTACCCAGAGATGTCGATCTCCTGACCTCGTATCCGCCACCTC	259
2334 GGCCTCCCAAGTGTCTGGATTACAGCC	2361
260 GGCCTCCCAAGTGTCTGGATTACAGCC	287

RESULT 23

AEF22010

ID AEF22010 standard; DNA; 140 BP.

XX AEF22010;

XX

DT	09-MAR-2006	(first entry)
XX		
DE	Human non-basal transcription modulator splice variant DNA #152.	
XX		
KM	Cycostatic; diagnosis; transcription factor; neoplasm; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2006005042-A2.	
XX		
PD	12-JAN-2006.	
XX		
PF	30-JUN-2005; 2005WO-US023708.	
XX		
PR	30-JUN-2004; 2004US-0584784P.	
XX		
PA	(CEMI-) CEMINES INC.	
XX		
PI	Shen D, Neuman T, Palm K;	
DR	WPI; 2006-100776/10.	
XX		
PT	Diagnosing cancer, useful for treating cancer, e.g. lung, breast,	
PT	prostate, skin, gastrointestinal cancer, comprises determining the	
PT	expression of at least one splice variant of each of the basal	
PT	transcription factors.	
XX		
PS	Disclosure; Page 68; 131pp; English.	
XX		
CC	The invention relates to a method of diagnosing cancer which comprises	
CC	determining the expression of at least one splice variant of each of the	
CC	basal transcription factors, where expression of each of the basal	
CC	transcription factor splice variants is distinguished from expression of	
CC	its wildtype isoform, and where the expression pattern of the basal	
CC	transcription factor splice variants is indicative of cancer. The methods	
CC	and bioactive agents are useful for treating cancer, e.g. lung cancer,	
CC	gastrointestinal cancer, breast cancer, prostate cancer, skin cancer,	
CC	sarcoma, endocrine cancer, neural cancer, bladder cancer, cervical	
CC	cancer, renal cancer and hematopoietic cancer. The present sequence	
CC	represents a human non-basal transcription modulator splice variant DNA.	
XX		
SQ	Sequence 140 BP; 50 A; 26 C; 26 G; 38 T; 0 U; 0 Other;	
XX		
Query Match	3.6%; Score 85; DB 15; Length 140;	
Best Local Similarity	100.0%; Pred. No. 3.3e-30;	
Matches	85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1387 TTCCCTGATTGTAACAACTATAGTGATGATTCAGAGAGTCATGTGTGAGGAAATG 1446	
DB	56 TTCTGTATTGTAACAAAACTATAGTGATGATTCAGAGAGTCATGTGTGAGGAAATG 115	
QY	1447 ATGATTAATTTACACAGCTTCACA 1471	
DB	116 ATGATTAATTTACACAGCTTCACA 140	
XX		
RESULT 24		
AAK85766/c		
ID	AAK85766 standard; DNA; 173 BP.	
XX		
AC	AAK85766;	
XX		
DT	07-NOV-2001 (first entry)	
XX		
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40578.	
XX		
DE	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;	
KW	cycostatic; gene therapy; vaccine; metastasis; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200157182-A2.	
XX		

PD 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
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PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
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PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
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PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
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PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
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PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
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PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250319P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI, 2001-483426/52.
DR

XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure: SEQ ID NO 40578; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I) may be
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK67694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169,
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 173 BP; 41 A; 47 C; 56 G; 29 T; 0 U; 0 Other;

Query Match 3.5%; Score 82; DB 4; Length 173;
Best Local Similarity 100.0%; Pred. No. 9.5e-29;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCAGATGTCGATCCTGACCTCGTATCGGCCACCTC 2333
|||
Db 103 GGGTTTCACCGTGTAGCAGATGTCGATCCTGACCTCGTATCGGCCACCTC 44
|||
QY 2334 GGGCTCCCAAGTGTGGATT 2355
|||
Db 43 GGGCTCCCAAGTGTGGATT 22
|||

RESULT 25
AAK5765/c
ID AAK85765 standard; DNA; 173 BP.
XX
AC AAK85765;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40577.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KM cytosolic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 26-JUL-2000; 2000US-0220963P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
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PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
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PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
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PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
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PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
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PR 20-OCT-2000; 2000US-0241809P.

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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure; SEQ ID NO 40577; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (1)
CC amino acid sequences given in AAM82170 to AAM91921. (1) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (1)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (1) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (1) by expressing inactive proteins or to
CC supplement the patients own production of (1). Additionally, (1)
CC polynucleotides may be used to produce the secreted (1), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the

CC protein. (1) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 173 BP; 41 A; 47 C; 56 G; 29 T; 0 U; 0 Other;
Query Match 3.5%; Score 82; DB 4; Length 173;
Best Local Similarity 100.0%; Pred. No. 9.5e-29;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTACCGTGTAGCCAGATGGTCTGATCTCTGACCTGATGATCCGCCACCTC 2333
DB 103 GGGTTTACCGTGTAGCCAGATGGTCTGATCTCTGACCTGATGATCCGCCACCTC 44
QY 2334 GGCCTCCCAAAGTGTGGATT 2355
DB 43 GGCCTCCCAAAGTGTGGATT 22
RESULT 26
ADY59447
ID ADY59447 standard; cDNA; 80 BP.
XX
AC ADY59447;
XX
DT 19-MAY-2005 (first entry)
XX
DE Polynucleotide of the invention SD36.
XX
XX ss; diagnosis; tumor; cytostatic; neoplasm; DNA microarray.
XX
OS Unidentified.
XX
PN CN1472338-A.
XX
PD 04-FEB-2004.
XX
PF 01-AUG-2002; 2002CN-00125892.
XX
PR 01-AUG-2002; 2002CN-00125892.
XX
XX (JUNXUAN) JUNXUAN BIOLOGICAL TECHNOLOGY CO LTD SHE.
XX
PA Liang P, Ding Y, Zhang X;
XX
PI WPI; 2004-317417/30.
XX
XX Tumor related gene testing method.
XX
PS Disclosure; Page 7; 14pp; Chinese.
XX
XX The invention relates to a novel process for detecting a tumor associated
CC gene in order to diagnose early tumor. The method comprises artificially
CC synthesizing a specific cDNA fragment as a probe, on a solid support to
CC form a DNA array of a tumor associated gene, reverse transcription and
CC labelling, hybridizing the labeled specimen cDNA fragment and tumor
CC associated gene DNA array, and direct quantitative analysis. The present
CC sequence is used in the invention.
XX
SQ Sequence 80 BP; 26 A; 17 C; 15 G; 22 T; 0 U; 0 Other;
Query Match 3.4%; Score 80; DB 13; Length 80;
Best Local Similarity 100.0%; Pred. No. 8.8e-28;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 827 AGATGATTATTCGTGTAACGACAAAGAAAGCGCACAAATCTGATTTCCCTTC 886
DB 1 AGATGATTATTCGTGTAACGACAAAGAAAGCGCACAAATCTGATTTCCCTTC 60
QY 887 CTTGATGAAAGCTGGCTC 906

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Db          61 CTTGATGAAGCCTGCCTC 80
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RESULT 27
AAK69176/c
ID AAK69176 standard; DNA; 140 BP.
XX
XX AAK69176;
AC
XX
XX 06-NOV-2001 (first entry)
DT
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23988.
DE
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytoskeletal; gene therapy; vaccine; metastasis; ds.
OS
XX Homo sapiens.
XX
XX MO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
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PR 05-DEC-2000; 2000US-0251988P.
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PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 23988; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK4702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention
XX
SQ Sequence 140 BP; 36 A; 38 C; 42 G; 24 T; 0 U; 0 Other;
Query Match 3.2%; Score 77; DB 4; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2285 TGTTAGCCAGATGCTCTGATCTCTGACTCTGATCCGCCACCTCGGCTCCCAAA 2344
DB 96 TGTTAGCCAGATGCTCTGATCTCTGACTCTGATCCGCCACCTCGGCTCCCAAA 37
QY 2345 GTGCTGGGATTACAGGC 2361
DB 36 GTGCTGGGATTACAGGC 20
RESULT 28
ID ABA18531/C
XX ABA18531 standard; DNA; 140 BP.
XX
XX ABA18531;
XX
XX 23-JAN-2002 (first entry)
XX
XX Human nervous system related polynucleotide SEQ ID NO 10862.
XX
XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
XX immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnary;
XX antiparkinsonian; antisticking; antianemic; antiarthritic; cancer;

KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; de-
OS Homo sapiens.
XX
XX WO200159063-A2.
XX
XX 16-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001334.
XX
XX 31-JAN-2000; 2000US-0179065P.
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 PR 05-DEC-2000; 2000US-0251033P.
 PR 05-DEC-2000; 2000US-0251988P.
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PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 DR
 XX
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system cancers
 PT and metastases.
 XX
 PS Disclosure; SEQ ID NO 10862; 1701bp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (AB114678-AB118001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 CC (e) neurological diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
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 SQ Sequence 140 BP; 36 A; 38 C; 42 G; 24 T; 0 U; 0 Other;
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 Db 36 GTGCTGGGATTACAGGC 20
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 ID ABA19693 standard; DNA; 140 BP.
 XX
 AC ABA19693;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Human nervous system related polynucleotide SEQ ID NO 12024.
 XX
 KW Human; nootropic; neuroprotective; cytoskeletal; dermatological; virucide;
 KW immunosuppressive; anti-inflamatory; anti-HIV; antibacterial; vulnerary;
 KW antiparasitic; antidiabetic; antitubercular; antitumor; cancer;
 KW antineoplastic; hepatoprotective; cerebroprotective; anti-inflammation;
 KW antiallergic; antidiabetic; antitubercular; anticonvulsant; antifungal;
 KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotoxic; gene therapy; vaccine; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200159063-A2.
 XX
 PD 16-AUG-2001.
 XX

PR	17-JAN-2001,	2001WO-US001334,
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PR	24-FEB-2000,	2000US-0186466P,
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PR	06-DEC-2000;	2000US-0251479P.
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PR	05-JAN-2001;	2001US-0259678P.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI, 2001-541565/60.	
PT	Nucleic acids encoding 3224 human nervous system antigen polypeptides	

PT useful for preventing, diagnosing and/or treating nervous system cancers
PT and metastases.
XX
XX
PS Disclosure; SEQ ID NO 12024; 1701bp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (AB14678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC anemia, autoimmune thyroiditis, diabetes mellitus, autoimmune haemolytic
CC anemias, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 140 BP; 36 A; 38 C; 42 G; 24 T; 0 U; 0 Other;
Query Match 3.2%; Score 77; DB 5; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2285 TGTAGCCAGATGTCCTGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAAA 2344
DB 96 TGTAGCCAGATGTCCTGATCTCTGACCTCGTATCCGCCACCTCGGCTCCCAAA 37
QY 2345 GTGCTGGATTACAGCC 2361
DB 36 GTGCTGGATTACAGCC 20
RESULT 30
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ID AA35141 standard; DNA; 73 BP.
AC AA35141;
XX
XX
DT 01-JUN-1999 (first entry)
XX
DE Nucleotide sequence SEQ ID 49.
XX
KM MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KM inhibition; tumour growth; DNA-damaging agent; camptothecin;
KM DNA/RNA hybrid; ss.
XX
OS Synthetic.
XX
FN WO9910486-A2.
XX
PD 04-MAR-1999.
XX
PF 18-AUG-1998; 98WO-US017147.
XX
XX 22-AUG-1997; 97US-00916384.
PR 06-MAY-1998; 98US-00073567.
XX
PA (HYBR-) HYBRIDON INC.
XX
PI Chen J, Agrawal S, Zhang R;
XX
DR WPI; 1999-254219/21.
XX
XX New MDM2-specific antisense oligonucleotides.
XX
PS Disclosure; Page 57; 59pp; English.
XX

CC The specification describes antisense oligonucleotides that inhibit MDM2
CC protein expression. The antisense oligonucleotides can be used to
CC activate a tumour suppressor. The antisense oligonucleotides are used to
CC inhibit tumour growth in a mammal, including a human, particularly in
CC conjunction with a DNA-damaging agent such as camptothecin. The present
CC sequence appears in the specification
XX
SQ Sequence 73 BP; 17 A; 23 C; 11 G; 22 T; 0 U; 0 Other;
Query Match 3.1%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 73 AGTACATCTGATGAGACAGGTGTCACCTGAAGTGGAGTGCATCAAGACCT 14
QY 725 TGTACAGAGCTT 737
DB 13 TGTACAGAGCTT 1
RESULT 31
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ID AAD65023 standard; DNA; 73 BP.
AC AAD65023;
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XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) non-coding antisense oligonucleotide.
XX
KM MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KM therapeutic; antisense therapy; human; antisense; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
FN US2003119765-A1.
XX
PD 26-JUN-2003.
XX
PF 03-APR-2000; 2000US-00541848.
XX
XX 22-AUG-1997; 97US-00916384.
PR 06-MAY-1998; 98US-00073567.
PR 26-AUG-1999; 99US-00383507.
XX
PA (CHEN/) CHEN J.
PA (AGRA/) AGRAWAL S.
PA (ZHANG/) ZHANG R.
PI Chen J, Agrawal S, Zhang R;
XX
DR WPI; 2003-863445/80.
XX
XX Inhibiting expression of mouse double-minute (MDM2) using anti-MDM2
XX PT antisense oligonucleotides, useful for screening potential therapeutic
XX PT agents and evaluating therapeutic effectiveness in treating tumors and/or
XX PT cancers.
XX
PS Disclosure; SEQ ID NO 49; 0pp; English.
XX
XX The present invention provides methods for inhibiting expression of mouse
XX CC double-minute (MDM2) using anti-MDM2 antisense oligonucleotides. The
XX CC methods and compositions of the present invention are useful as
XX analytical and diagnostic tools for screening potential therapeutic

CC agents in the treatment of tumours and/or cancers. They may also be
CC useful in evaluating the therapeutic effectiveness of anti-human-MDM2
CC antisense oligonucleotides in the treatment of human colorectal cancers.
CC The present sequence is human mouse double minute (MDM2) non-coding
CC oligonucleotide
CC
SQ Sequence 73 BP; 17 A; 23 C; 11 G; 22 T; 0 U; 0 Other;
Query Match 3.1%; Score 73; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 665 AGGTACATCTGTAGTGAAGACAGTGTCACTTGAAGTGGAGTCAAAAGACCT 724
Db 73 AGGTACATCTGTAGTGAAGACAGTGTCACTTGAAGTGGAGTCAAAAGACCT 14
QY 725 TGTACAGAGCCTT 737
Db 13 TGTACAGAGCCTT 1
AC AAI99125;
XX AAI99125 standard; DNA; 149 BP.
ID AAI99125/c
XX AAI99125;
XX 07-JAN-2002 (first entry)
DE Human excretory related polynucleotide SEQ ID NO 889.
XX
XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virocidic;
XX immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnery;
XX antiparkinsonian; antisticking; antianaemic; antitubercic; cancer;
XX antitumour; hepatotropic; cerebroprotective; antiinflammatory;
XX antiallergic; antidiabetic; antituber; anticonvulsant; antifungal;
XX antiparasitic; cardiac; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotropic; gene therapy; vaccine;
XX excretory system; ds.
XX
OS Homo sapiens.
XX
PN MO20015513-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001323.
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PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCT INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465569/50.
XX
XX WPI; 2001-465569/50.
PT Isolated nucleic acid molecule encoding excretory system antigen is used
PT in preventing, treating or ameliorating a medical condition.
XX
XX Example 2; SEQ ID NO 889; 574pp + Sequence Listing; English.
XX
XX The invention relates to novel excretory system related human
XX polynucleotides (AA198667-AA199503) and the encoded proteins (AAM99594-
XX AAM99913) useful for preventing, treating or ameliorating medical
XX conditions e.g. by protein or gene therapy, especially disorders related
XX to the excretory system. The genes are isolated from a range of human
XX tissues disclosed in the specification. The nucleic acids, proteins,
XX antibodies and (ant)agonists are useful in the diagnosis, treatment and
XX prevention of: (a) cancer, e.g. breast and ovarian cancer and other
XX cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal
XX tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's
XX disease, allergies, autoimmune haemolytic anaemia, autoimmune
XX thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis,
XX rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders
XX such as myocardial ischaemias; (d) wound healing; (e) neurological
XX diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases
XX such as viral, bacterial, fungal and parasitic infections. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pat_sequences
SQ Sequence 149 BP; 47 A; 35 C; 41 G; 26 T; 0 U; 0 Other;

Query Match

3.0%; Score 72; DB 4; Length 149;

Best Local Similarity 100.0%; Pred. No. 6,66-24;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2284 GTGTAGCCAGAGTGTCTCGATCTCTGACCTGTGATCCGCCACCTCGGCTCCCA 2343
DB 116 GTGTAGCCAGAGTGTCTCGATCTCTGACCTGTGATCCGCCACCTCGGCTCCCA 57
QY 2344 AGTGCTGGGATT 2355
DB 56 AGTGCTGGGATT 45
RESULT 33
AA163475/C
ID AA163475 standard; DNA; 149 BP.
XX
XX AA163475;
AC
XX
DT 22-OCT-2001 (first entry)
XX
XX Human kidney related polynucleotide SEQ ID NO 790.
DE
XX
XX Human; kidney antigen; immunosuppressive; antiarthritic; anti-rheumatic;
XX antiproliferative; cytostatic; cardiact; vasotropic; cerebroprotective;
XX neurotropic; neuroprotective; antibacterial; virucide; fungicide;
XX ophthalmological; antiallergic; hepatotropic; antidiabetic;
XX antiinflammatory; anticancer; immune disorder; cardiovascular disorder;
XX gene therapy; cancer; immune disorder; infection; ds.
OS Homo sapiens.
XX
XX WO20015323-A2.
FN
XX
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001343.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214866P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218299P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.

Db 56 AGTCTGGGATT 45

RESULT 34

ABK42381
ID ABK42381 standard; DNA; 308 BP.

XX ABK42381;

DT 21-MAY-2002 (first entry)

XX Genomic sequence #280 encoding novel human connective tissue polypeptide.

KW Human; connective tissue related disorder; cancer; gene therapy;
XX cytosstatic; gene; ds.

OS Homo sapiens.

XX W020015343-A1.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US001322.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 11-JUL-2000; 2000US-0217487P.

PR 14-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 14-AUG-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 16-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.

PR 23-AUG-2000; 2000US-0227182P.

PR 30-AUG-2000; 2000US-0227009P.

PR 01-SEP-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 06-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0232402P.
PR 14-SEP-2000; 2000US-0232403P.
PR 14-SEP-2000; 2000US-0232404P.
PR 14-SEP-2000; 2000US-0232405P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
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PR 25-SEP-2000; 2000US-0234999P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
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PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
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PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239933P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
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PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
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PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.

PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-565190/63.
XX
XX Nucleic acid encoding novel connective tissue associated polypeptides,
XX used in diagnosing, preventing, treating or ameliorating a disorder such
XX as cancer or rheumatoid arthritis.
XX
XX Disclosure; SEQ ID NO 1268; 673pp; English.
XX
XX The present invention relates to the isolation of novel human connective
XX tissue related polypeptides (AUB6435-AUB6923) and the polynucleotide
XX (cDNA and genomic) sequences encoding them. The sequences of the
XX invention are useful in the diagnosis, treatment, prevention and/or
XX prognosis of diseases associated with connective tissue(s), including
XX cancer. The polynucleotide sequences of the invention are also useful in
XX gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the
XX novel human connective tissue related polypeptides. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 308 BP; 48 A; 97 C; 72 G; 91 T; 0 U; 0 Other;
XX
XX
XX Query Match 3.0%; Score 72; DB 4; Length 308;
XX Best Local Similarity 100.0%; Pred. No. 6,6e-24;
XX Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGATGCTCGATCTCTGACCTGATCGGCCACCTCGGCTCCCAAGTCT 2349
Db 213 GCCAGATGCTCGATCTCTGACCTGATCGGCCACCTCGGCTCCCAAGTCT 272

QY 2350 GGGATTACAGC 2361
Db 273 GGGATTACAGC 284

RESULT 35
ADB60537
ID ADB60537 standard; DNA; 308 BP.
XX
XX ADB60537;
XX
XX 04-DEC-2003 (first entry)
XX
XX Connective tissue related genomic DNA #280.
XX
XX cytosolic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;
XX antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic;
XX antiinflammatory; antiallergic; antisthmatic; dermatological;
XX nephrotropic; virucide; fungicide; antibacterial; antiparasitic;
XX gene therapy; ds; connective tissues disorder; rheumatoid arthritis;
XX systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;
XX cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;
XX Alzheimer's disease; Parkinson's disease; cardiovascular disease;

KW atherosclerosis; myocarditis; cardiopulmonary bypass complication;
KW autoimmune disease; multiple sclerosis; allergic reaction; asthma;
KW rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;
KW gastrointestinal disorder; inflammatory bowel disease;
KW organ transplant rejection; immune system disorder; Bruton's disease;
KW X-linked lymphoproliferative syndrome;
KW B-cell lymphoproliferative disorder; HIV, AIDS, infection;
KW chromosome identification; chromosome mapping;
KW connective tissue related polynucleotide; gene; ds.
XX
OS Homo sapiens.
XX
XX US2003054375-A1.
XX
XX 20-MAR-2003.
XX
XX 07-MAR-2002; 2002US-00092154.
XX
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
XX 02-MAR-2000; 2000US-0186350P.
XX 16-MAR-2000; 2000US-0189874P.
XX 17-MAR-2000; 2000US-0190076P.
XX 18-APR-2000; 2000US-0198123P.
XX 19-MAY-2000; 2000US-0205515P.
XX 07-JUN-2000; 2000US-0209467P.
XX 26-JUN-2000; 2000US-0214886P.
XX 30-JUN-2000; 2000US-0215135P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
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XX 14-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
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XX 26-JUL-2000; 2000US-0220964P.
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XX 14-AUG-2000; 2000US-0225213P.
XX 14-AUG-2000; 2000US-0225214P.
XX 14-AUG-2000; 2000US-0225266P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
XX 14-AUG-2000; 2000US-0225270P.
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XX 14-AUG-2000; 2000US-0225757P.
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XX 18-AUG-2000; 2000US-0226279P.
XX 22-AUG-2000; 2000US-0226681P.
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XX 23-AUG-2000; 2000US-0227009P.
XX 30-AUG-2000; 2000US-0228924P.
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XX 14-SEP-2000; 2000US-0232398P.
XX 14-SEP-2000; 2000US-0232399P.

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 PR 29-SEP-2000; 2000US-0236368P.
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 PR 17-NOV-2000; 2000US-0249213P.
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 PR 17-NOV-2000; 2000US-0249217P.
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 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249246P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.

PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251889P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0251990P.
 PR 05-JAN-2001; 2000US-0254097P.
 PR 17-JAN-2001; 2001US-00764847.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI, 2003-634869/60.
 DR P-PSDB; ADB59434.
 XX
 PT New connective tissue-related polypeptides and polynucleotides, useful
 PT for treating, preventing and/or prognosing e.g. disorders of connective
 PT tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or
 PT neoplasias.
 XX
 PS Disclosure; SEQ ID NO 1268; 248bp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I), which
 CC comprises a sequence that is at least 95 % identical to a connective
 CC tissue-related polynucleotide encoding connective tissue antigens (CTA).
 CC The polypeptide or polynucleotide is useful for preventing, treating, or
 CC ameliorating medical conditions in a mammal. The connective tissue
 CC polypeptides, polynucleotides and antibodies are particularly useful for
 CC treating, preventing and/or prognosing disorders of connective tissues
 CC (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus,
 CC scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or
 CC neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g.
 CC Alzheimer's disease, or Parkinson's disease), cardiovascular diseases
 CC (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass
 CC complications), autoimmune diseases (e.g. systemic lupus erythematosus,
 CC rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.
 CC

Query Match 3.0%; Score 72; DB 9; Length 308;
 Best Local Similarity 100.0%; Pred. No. 6.6e-24;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 2290 GCCAGATGCTCTGATCTCTGACCTGTCGATCGCCACCTGCGCTCCCAAGTCT 2349
 Db 213 GCCAGATGCTCTGATCTCTGACCTGTCGATCGCCACCTGCGCTCCCAAGTCT 272

Gy 2350 GGGATTACAGGC 2361
 Db 273 GGGATTACAGGC 284

RESULT 36
 ABR42380
 ID ABR42380 standard; DNA; 312 BP.
 XX
 AC ABR42380;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Genomic sequence #279 encoding novel human connective tissue polypeptide.
 XX
 KW Human; connective tissue related disorder; cancer; gene therapy;
 KW cytoskeletal; gene; de.
 XX
 OS Homo sapiens.
 XX
 PN W0200155343-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001322.
 XX

XX PS Disclosure; SEQ ID NO 1267; 673bp; English.
XX CC The present invention relates to the isolation of novel human connective
CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide
CC (cDNA and genomic) sequences encoding them. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with connective tissue(s), including
CC cancer. The polynucleotide sequences of the invention are also useful in
CC gene therapy. ABRK2102-ABK4116 represent genomic sequences encoding the
CC novel human connective tissue related polypeptides. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 312 BP; 49 A; 98 C; 72 G; 93 T; 0 U; 0 Other;

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QY 2350 GGGATTACAGGC 2361
Db 277 GGGATTACAGGC 288

RESULT 37
ADB60536
ID ADB60536 standard; DNA; 312 BP.
XX AC ADB60536;
XX DT 04-DEC-2003 (first entry)
XX DE Connective tissue related genomic DNA #279.
XX KW cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;
KW antileukemic; immunosuppressive; antirheumatic; antiarthritic;
KW antiinflammatory; antiallergic; antibacterial; dermatological;
KW nephrotropic; virucide; fungicide; antibacterial; antiparasitic;
KW gene therapy; ds; connective tissues disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;
KW cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disease;
KW atherosclerosis; myocarditis; cardiopulmonary bypass complication;
KW autoimmune disease; multiple sclerosis; allergic reaction; asthma;
KW rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;
KW gastrointestinal disorder; inflammatory bowel disease;
KW organ transplant rejection; immune system disorder; Bruton's disease;
KW X-linked lymphoproliferative syndrome;
KW B-cell lymphoproliferative disorder; HIV; AIDS; infection;
KW chromosome identification; chromosome mapping;
KW connective tissue related polynucleotide; gene; ds.
XX OS Homo sapiens.
XX US2003054375-A1.
XX PD 20-MAR-2003.
XX PF 07-MAR-2002; 2002US-00092154.
XX PR 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
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XX PR 18-APR-2000; 2000US-0196123P.

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DT	07-NOV-2001 (first entry)			
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KM	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;			
KW	cytostatic; gene therapy; vaccine; metastasis; ds.			
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OS	Homo sapiens.			
XX				
PN	WO200157182-A2.			
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PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0253678P.

(PDMA-) HUMAN GENOME SCI INC.
XX
PA
XX
Rosen CA, Barash SC, Ruben SM;
PI
XX
WPI; 2001-483426/52.
XX
DR
XX
Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT
XX
useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS
Disclousre; SEQ ID NO 41440; 3071bp + Sequence Listing; English.
XX
CC
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostratic
CC
activity, and can be used in gene therapy and vaccine production. (I)
CC
proteins and polynucleotides may be used in the prevention, diagnosis and
CC
treatment of diseases associated with inappropriate (I) expression. For
CC
example, they may be used to treat disorders associated with decreased
CC
expression by rectifying mutations or deletions in a patient's genome
CC
that affect the activity of (I) by expressing inactive proteins or to
CC
supplement the patients own production of (I). Additionally, (I)
CC
polynucleotides may be used to produce the secreted (I), by inserting the
CC
nucleic acids into a host cell and culturing the cell to express the
CC
protein. (I) proteins and polynucleotides may be used to prevent,
CC
diagnose and treat immune/haematopoietic-related diseases, especially
CC
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC
to AAK67694 represent human immune/haematopoietic antigen genomic
CC
sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC
represent sequences used in the exemplification of the present invention
XX
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DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35963.		
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KM	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		
KM	cytotoxic; gene therapy; vaccine; metatlas; ds.		
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OS	Homo sapiens.		
PN	MO200157182-A2.		
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PA (HUMA-) HUMAN GENOME SCI INC.
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PI Rosen CA, Barash SC, Ruben SM;
XX WPI, 2001-483426/52.
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PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure; SEQ ID NO 35963; 3071pp + Sequence Listing; English.
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CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK67694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
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 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-483426/52.
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 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
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 PS Disclosure; SEQ ID NO 38875; 3071pp + Sequence listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAm82170 to AAm91921. (I) have cytostatic
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 CC example, they may be used to treat disorders associated with decreased
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 CC that affect the activity of (I) by expressing inactive proteins or to
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 CC polynucleotides may be used to produce the secreted (I), by inserting the
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 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAm82169
 CC represent sequences used in the exemplification of the present invention
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GenCore version 5.1.9
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C 95	59	2.5	201	16	US-11-124-367A-1930	Sequence 1930, Ap	C 168	57	2.4	285	6	US-10-091-504-1569	Sequence 1569, Ap
C 96	59	2.5	201	16	US-11-124-367A-17823	Sequence 17823, A	C 169	57	2.4	285	7	US-10-227-577-1569	Sequence 1569, Ap
C 97	59	2.5	201	16	US-11-124-367A-17825	Sequence 17825, A	C 170	57	2.4	287	3	US-09-796-692-8599	Sequence 8599, Ap
C 98	59	2.5	201	16	US-11-124-367A-18137	Sequence 18137, A	C 171	57	2.4	287	6	US-10-040-862-8599	Sequence 8599, Ap
C 99	59	2.5	201	16	US-11-124-367A-18139	Sequence 18139, A	C 172	57	2.4	287	7	US-10-057-475B-8599	Sequence 8599, Ap
C 100	59	2.5	374	3	US-09-814-353-14963	Sequence 14963, A	C 173	57	2.4	287	7	US-10-154-884B-8599	Sequence 8599, Ap
C 101	59	2.5	421	3	US-09-814-353-14897	Sequence 14897, A	C 174	57	2.4	287	9	US-10-764-324-8599	Sequence 8599, Ap
C 102	59	2.5	453	3	US-09-814-353-2239	Sequence 2239, Ap	C 175	57	2.4	315	7	US-10-242-515-2515	Sequence 2515, Ap
C 103	59	2.5	453	3	US-09-814-353-8579	Sequence 8579, Ap	C 176	57	2.4	315	7	US-10-242-515-2515	Sequence 2515, Ap
C 104	59	2.5	470	4	US-09-925-065A-733661	Sequence 733661, A	C 177	57	2.4	341	3	US-09-918-595-18053	Sequence 18053, A
C 105	59	2.5	470	4	US-09-925-065A-733661	Sequence 733661, A	C 178	57	2.4	346	6	US-10-040-862-8335	Sequence 8335, Ap
C 106	59	2.5	478	4	US-09-925-065A-733497	Sequence 733497, A	C 179	57	2.4	346	6	US-10-040-862-8335	Sequence 8335, Ap
C 107	59	2.5	478	4	US-09-925-065A-812339	Sequence 812339, A	C 180	57	2.4	346	7	US-10-057-475B-8335	Sequence 8335, Ap
C 108	59	2.5	478	4	US-09-925-065A-733497	Sequence 733497, A	C 181	57	2.4	346	7	US-10-154-884B-8335	Sequence 8335, Ap
C 109	59	2.5	478	4	US-09-925-065A-733497	Sequence 733497, A	C 182	57	2.4	346	9	US-10-764-324-8335	Sequence 8335, Ap
C 110	58	2.4	126	3	US-09-764-860-1020	Sequence 812339, A	C 183	57	2.4	415	3	US-09-814-353-3788	Sequence 3788, Ap
C 111	58	2.4	126	6	US-10-074-095-1020	Sequence 1020, Ap	C 184	57	2.4	415	3	US-09-814-353-10097	Sequence 10097, A
C 112	58	2.4	126	6	US-10-212-872-1020	Sequence 1020, Ap	C 185	57	2.4	424	9	US-10-674-124A-16064	Sequence 16064, A
C 113	58	2.4	126	7	US-10-212-872-1020	Sequence 1020, Ap	C 186	57	2.4	429	6	US-10-027-632-104325	Sequence 104325, A
C 114	58	2.4	169	7	US-10-227-646-168	Sequence 168, App	C 187	57	2.4	429	6	US-10-027-632-325337	Sequence 325337, A
C 115	58	2.4	170	8	US-10-227-646-168	Sequence 168, App	C 188	57	2.4	429	7	US-10-027-632-104325	Sequence 104325, A
C 116	58	2.4	181	3	US-10-085-783A-51616	Sequence 51616, A	C 189	57	2.4	429	9	US-10-027-632-325337	Sequence 325337, A
C 117	58	2.4	181	6	US-09-764-869-2122	Sequence 2122, Ap	C 190	57	2.4	429	9	US-10-357-930-10393	Sequence 10393, A
C 118	58	2.4	181	6	US-10-091-504-2122	Sequence 2122, Ap	C 191	57	2.4	463	3	US-09-814-353-16481	Sequence 16481, A
C 119	58	2.4	181	7	US-10-227-577-2122	Sequence 2122, Ap	C 192	57	2.4	463	3	US-09-764-891-6194	Sequence 6194, Ap
C 120	58	2.4	185	9	US-10-357-930-31210	Sequence 31210, A	C 193	57	2.4	469	9	US-10-357-930-31551	Sequence 31551, A
C 121	58	2.4	185	9	US-10-357-930-40180	Sequence 40180, A	C 194	57	2.4	478	3	US-09-918-995-13035	Sequence 13035, A
C 122	58	2.4	201	15	US-10-995-561-54793	Sequence 54793, A	C 195	57	2.4	486	9	US-10-357-930-13804	Sequence 13804, A
C 123	58	2.4	201	15	US-11-124-368A-7727	Sequence 7727, Ap	C 196	57	2.4	489	9	US-10-357-930-52421	Sequence 52421, A
C 124	58	2.4	201	15	US-11-124-368A-7814	Sequence 7814, Ap	C 197	57	2.4	490	5	US-09-925-065A-8656	Sequence 8656, Ap
C 125	58	2.4	201	15	US-11-124-368A-7904	Sequence 7904, Ap	C 198	57	2.4	490	5	US-09-925-065A-8656	Sequence 8656, Ap
C 126	58	2.4	201	15	US-11-124-368A-7939	Sequence 7939, Ap	C 199	57	2.4	490	12	US-10-301-480-109893	Sequence 109893, A
C 127	58	2.4	239	7	US-09-860-670-198	Sequence 198, App	C 200	57	2.4	490	12	US-10-301-480-109893	Sequence 109893, A
C 128	58	2.4	239	7	US-10-227-646-198	Sequence 198, App	C 201	56	2.4	145	3	US-09-860-670-192	Sequence 723302, A
C 129	58	2.4	270	3	US-09-764-847-1216	Sequence 1216, Ap	C 202	56	2.4	145	7	US-10-227-646-192	Sequence 192, App
C 130	58	2.4	270	3	US-09-764-847-1217	Sequence 1217, Ap	C 203	56	2.4	201	8	US-10-741-601-19311	Sequence 19311, A
C 131	58	2.4	270	6	US-10-092-154-1216	Sequence 1216, Ap	C 204	56	2.4	201	8	US-10-741-601-23793	Sequence 23793, A
C 132	58	2.4	270	6	US-10-092-154-1217	Sequence 1217, Ap	C 205	56	2.4	201	9	US-10-741-600-24883	Sequence 24883, A
C 133	58	2.4	281	9	US-10-357-930-4635	Sequence 4635, A	C 206	56	2.4	201	9	US-10-741-600-53079	Sequence 53079, A
C 134	58	2.4	326	9	US-10-357-930-49979	Sequence 49979, A	C 207	56	2.4	201	9	US-10-741-600-64494	Sequence 64494, A
C 135	58	2.4	354	9	US-10-357-930-217	Sequence 217, App	C 208	56	2.4	201	10	US-10-995-561-31556	Sequence 31556, A
C 136	58	2.4	384	9	US-10-357-930-19852	Sequence 19852, A	C 209	56	2.4	201	16	US-11-124-367A-18608	Sequence 18608, A
C 137	58	2.4	388	9	US-10-357-930-10578	Sequence 10578, A	C 210	56	2.4	282	3	US-09-764-891-9298	Sequence 9298, Ap
C 138	58	2.4	399	10	US-10-779-543-11917	Sequence 11917, A	C 211	56	2.4	282	6	US-10-091-572-859	Sequence 859, App
C 139	58	2.4	407	9	US-10-357-930-9883	Sequence 9883, Ap	C 212	56	2.4	298	6	US-09-764-878-594	Sequence 394, App
C 140	58	2.4	407	9	US-10-357-930-13596	Sequence 13596, A	C 213	56	2.4	397	10	US-10-779-543-20099	Sequence 20099, A
C 141	58	2.4	412	3	US-09-814-353-1505	Sequence 1505, Ap	C 214	56	2.4	401	3	US-09-867-701-6438	Sequence 6438, Ap
C 142	58	2.4	412	3	US-09-814-353-7864	Sequence 7864, Ap	C 215	56	2.4	401	3	US-10-741-601-11011	Sequence 11011, A
C 143	58	2.4	422	9	US-10-357-930-18494	Sequence 18494, A	C 216	55	2.3	201	8	US-10-741-601-14838	Sequence 24838, A
C 144	58	2.4	425	9	US-10-357-930-34737	Sequence 34737, A	C 217	55	2.3	201	8	US-10-741-601-14838	Sequence 24838, A
C 145	58	2.4	427	9	US-10-357-930-31775	Sequence 31775, A	C 218	55	2.3	201	9	US-10-719-993-12945	Sequence 12945, A
C 146	58	2.4	430	9	US-10-674-124A-7055	Sequence 7055, Ap	C 219	55	2.3	201	9	US-10-719-993-12945	Sequence 12945, A
C 147	58	2.4	430	9	US-10-357-930-10612	Sequence 10612, A	C 220	55	2.3	201	9	US-10-741-600-26506	Sequence 26506, A
C 148	58	2.4	431	9	US-10-357-930-1440	Sequence 1440, Ap	C 221	55	2.3	201	9	US-10-741-600-29821	Sequence 29821, A
C 149	58	2.4	446	9	US-10-357-930-31084	Sequence 31084, A	C 222	55	2.3	201	9	US-10-741-600-61888	Sequence 61808, A
C 150	58	2.4	450	9	US-10-357-930-10010	Sequence 10010, A	C 223	55	2.3	201	9	US-10-741-600-65605	Sequence 65605, A
C 151	58	2.4	460	9	US-10-357-930-1443	Sequence 1443, Ap	C 224	55	2.3	201	10	US-10-995-561-23484	Sequence 23484, A
C 152	58	2.4	460	9	US-10-357-930-31809	Sequence 31809, A	C 225	55	2.3	201	15	US-11-124-368A-20112	Sequence 20112, A
C 153	58	2.4	460	9	US-10-357-930-31809	Sequence 31809, A	C 226	55	2.3	201	15	US-11-124-368A-20186	Sequence 20186, A
C 154	58	2.4	467	9	US-10-357-930-30589	Sequence 30589, A	C 227	55	2.3	201	16	US-11-124-367A-10535	Sequence 10535, A
C 155	58	2.4	467	9	US-10-357-930-30589	Sequence 30589, A	C 228	55	2.3	201	16	US-11-124-367A-10535	Sequence 10535, A
C 156	57	2.4	468	3	US-10-357-930-48305	Sequence 48305, A	C 229	55	2.3	201	16	US-11-124-367A-15753	Sequence 15753, A
C 157	57	2.4	488	3	US-09-764-860-602	Sequence 602, App	C 230	55	2.3	201	16	US-11-124-367A-15960	Sequence 15960, A
C 158	57	2.4	488	3	US-09-764-860-602	Sequence 602, App	C 231	55	2.3	201	16	US-11-124-367A-15970	Sequence 15970, A
C 159	57	2.4	188	6	US-10-074-095-602	Sequence 602, App	C 232	55	2.3	201	16	US-11-124-367A-16023	Sequence 16023, A
C 160	57	2.4	188	6	US-10-074-095-602	Sequence 602, App	C 233	55	2.3	201	16	US-11-124-367A-16023	Sequence 16023, A
C 161	57	2.4	189	7	US-10-212-872-602	Sequence 602, App	C 234	55	2.3	201	16	US-11-124-367A-17231	Sequence 17231, A
C 162	57	2.4	189	7	US-10-357-930-34943	Sequence 34943, A	C 235	55	2.3	222	6	US-09-920-300A-345	Sequence 345, App
C 163	57	2.4	193	3	US-09-764-877-2685	Sequence 2685, Ap	C 236	55	2.3	222	7	US-10-033-528-345	Sequence 345, App
			193	7	US-10-242-515-2685	Sequence 2685, Ap							

C 237	55	2.3	222	10	US-10-961-527-345	Sequence 345, App	310	55	2.3	385	9	US-10-357-930-14860	Sequence 14860, A
C 238	55	2.3	228	3	US-09-860-670-208	Sequence 208, App	311	55	2.3	404	3	US-09-967-768A-43	Sequence 43, Appl
C 239	55	2.3	228	7	US-10-227-646-208	Sequence 208, App	312	55	2.3	404	10	US-10-843-681A-6188	Sequence 6188, Ap
C 240	55	2.3	247	3	US-09-860-670-200	Sequence 200, App	313	55	2.3	408	9	US-10-357-930-34623	Sequence 34623, A
C 241	55	2.3	247	7	US-10-227-646-200	Sequence 200, App	314	55	2.3	413	8	US-10-242-533A-37825	Sequence 37825, A
C 242	55	2.3	249	3	US-09-860-670-173	Sequence 173, App	315	55	2.3	413	8	US-10-085-783A-37825	Sequence 37825, A
C 243	55	2.3	249	7	US-10-227-646-173	Sequence 173, App	316	55	2.3	427	4	US-09-925-065A-732335	Sequence 732335,
C 244	55	2.3	250	3	US-09-860-670-197	Sequence 197, App	317	55	2.3	427	5	US-09-925-065A-732335	Sequence 732335,
C 245	55	2.3	250	7	US-10-227-646-197	Sequence 197, App	318	55	2.3	429	3	US-09-814-353-2660	Sequence 2560, Ap
C 246	55	2.3	258	3	US-09-984-429-629	Sequence 629, App	319	55	2.3	432	3	US-09-814-353-8895	Sequence 8895, Ap
C 247	55	2.3	264	3	US-09-764-891-8680	Sequence 8680, Ap	320	55	2.3	432	6	US-10-027-633-277790	Sequence 277790,
C 248	55	2.3	267	7	US-09-860-670-196	Sequence 196, App	321	55	2.3	432	6	US-10-027-633-277791	Sequence 277791,
C 249	55	2.3	267	7	US-10-227-646-196	Sequence 196, App	322	55	2.3	432	6	US-10-027-633-277792	Sequence 277792,
C 250	55	2.3	276	3	US-09-860-670-202	Sequence 202, App	323	55	2.3	432	7	US-10-027-633-277790	Sequence 277790,
C 251	55	2.3	276	7	US-10-227-646-202	Sequence 202, App	324	55	2.3	432	7	US-10-027-633-277791	Sequence 277791,
C 252	55	2.3	279	3	US-09-860-670-180	Sequence 180, App	325	55	2.3	432	7	US-10-027-633-277792	Sequence 277792,
C 253	55	2.3	279	7	US-10-227-646-180	Sequence 180, App	326	55	2.3	432	8	US-10-242-533A-37824	Sequence 37824, A
C 254	55	2.3	282	7	US-09-764-891-9438	Sequence 9438, Ap	327	55	2.3	432	8	US-10-085-783A-37824	Sequence 37824, A
C 255	55	2.3	282	7	US-10-091-414-306	Sequence 306, App	328	55	2.3	439	12	US-10-085-783A-37824	Sequence 37824, A
C 256	55	2.3	282	10	US-10-984-180-3	Sequence 3, Appl	329	55	2.3	439	12	US-10-301-480-235599	Sequence 235599,
C 257	55	2.3	283	3	US-09-860-670-219	Sequence 219, App	330	55	2.3	439	12	US-10-301-480-235600	Sequence 235600,
C 258	55	2.3	283	7	US-10-227-646-219	Sequence 219, App	331	55	2.3	439	12	US-10-301-480-235601	Sequence 235601,
C 259	55	2.3	287	6	US-10-115-278-6	Sequence 6, Appl	332	55	2.3	439	12	US-10-301-480-235602	Sequence 235602,
C 260	55	2.3	287	9	US-10-762-966-6	Sequence 6, Appl	333	55	2.3	439	12	US-10-301-480-849008	Sequence 849008,
C 261	55	2.3	287	10	US-10-673-575-7	Sequence 7, Appl	334	55	2.3	439	12	US-10-301-480-849010	Sequence 849010,
C 262	55	2.3	288	7	US-10-229-058B-14	Sequence 14, Appl	335	55	2.3	443	9	US-10-301-480-849011	Sequence 849011,
C 263	55	2.3	290	3	US-09-860-670-223	Sequence 223, App	336	55	2.3	441	3	US-09-764-891-6748	Sequence 6748, Ap
C 264	55	2.3	290	7	US-10-227-646-223	Sequence 223, App	337	55	2.3	441	3	US-09-764-891-6749	Sequence 6749, Ap
C 265	55	2.3	293	3	US-09-860-670-169	Sequence 169, App	338	55	2.3	441	6	US-10-091-572-598	Sequence 598, App
C 266	55	2.3	293	7	US-10-227-646-169	Sequence 169, App	339	55	2.3	441	6	US-10-091-572-599	Sequence 599, App
C 267	55	2.3	294	3	US-09-984-429-627	Sequence 627, App	340	55	2.3	441	9	US-10-357-930-5691	Sequence 5691, Ap
C 268	55	2.3	297	3	US-09-764-877-2183	Sequence 2183, Ap	341	55	2.3	442	3	US-09-918-995-1943	Sequence 11943, A
C 269	55	2.3	297	7	US-09-860-670-191	Sequence 191, App	342	55	2.3	443	4	US-09-925-065A-140617	Sequence 140617,
C 270	55	2.3	297	7	US-10-227-646-191	Sequence 191, App	343	55	2.3	443	4	US-09-925-065A-140618	Sequence 140618,
C 271	55	2.3	297	7	US-10-242-515-2183	Sequence 2183, Ap	344	55	2.3	443	4	US-09-925-065A-140619	Sequence 140619,
C 272	55	2.3	299	3	US-09-860-670-226	Sequence 226, App	345	55	2.3	443	4	US-09-925-065A-140620	Sequence 140620,
C 273	55	2.3	299	7	US-10-074-024-602	Sequence 602, App	346	55	2.3	443	5	US-09-925-065A-140620	Sequence 140620,
C 274	55	2.3	299	7	US-10-227-646-226	Sequence 226, App	347	55	2.3	443	5	US-09-925-065A-140618	Sequence 140618,
C 275	55	2.3	300	3	US-09-764-891-5511	Sequence 5511, Ap	348	55	2.3	443	5	US-09-925-065A-140619	Sequence 140619,
C 276	55	2.3	300	3	US-09-984-429-678	Sequence 678, App	349	55	2.3	443	5	US-09-925-065A-140620	Sequence 140620,
C 277	55	2.3	301	3	US-09-860-670-181	Sequence 181, App	350	55	2.3	443	6	US-10-027-632-277793	Sequence 277793,
C 278	55	2.3	301	3	US-09-860-670-181	Sequence 181, App	351	55	2.3	443	6	US-10-027-632-277793	Sequence 277793,
C 279	55	2.3	301	3	US-09-984-429-638	Sequence 638, App	352	55	2.3	447	4	US-09-925-065A-46720	Sequence 46720, A
C 280	55	2.3	301	7	US-10-227-646-181	Sequence 181, App	353	55	2.3	447	4	US-09-925-065A-46720	Sequence 46720, A
C 281	55	2.3	301	7	US-10-227-646-181	Sequence 181, App	354	55	2.3	447	10	US-10-779-543-17814	Sequence 17814, A
C 282	55	2.3	301	7	US-10-227-646-183	Sequence 183, App	355	55	2.3	447	10	US-10-779-543-17814	Sequence 17814, A
C 283	55	2.3	304	7	US-09-764-891-8441	Sequence 8441, Ap	356	55	2.3	447	12	US-10-301-480-147958	Sequence 147958,
C 284	55	2.3	308	7	US-10-074-024-587	Sequence 587, App	357	55	2.3	449	9	US-10-301-480-761367	Sequence 761367,
C 285	55	2.3	310	7	US-09-860-670-224	Sequence 224, App	358	55	2.3	449	9	US-10-357-930-53755	Sequence 38875, A
C 286	55	2.3	310	7	US-10-227-646-224	Sequence 224, App	359	55	2.3	449	3	US-10-357-930-53755	Sequence 38875, A
C 287	55	2.3	311	7	US-09-860-670-199	Sequence 199, App	360	55	2.3	451	3	US-09-814-353-12957	Sequence 12957, A
C 288	55	2.3	311	7	US-10-227-646-199	Sequence 199, App	361	55	2.3	459	4	US-09-925-065A-472633	Sequence 472633,
C 289	55	2.3	314	3	US-09-860-670-217	Sequence 217, App	362	55	2.3	459	5	US-09-925-065A-472633	Sequence 472633,
C 290	55	2.3	314	3	US-09-764-891-9014	Sequence 9014, Ap	363	55	2.3	460	4	US-09-925-065A-564331	Sequence 564331,
C 291	55	2.3	314	7	US-10-227-646-217	Sequence 217, App	364	55	2.3	460	5	US-09-925-065A-564331	Sequence 564331,
C 292	55	2.3	316	7	US-09-984-429-618	Sequence 618, App	365	55	2.3	463	3	US-09-764-891-1978	Sequence 1978, Ap
C 293	55	2.3	316	7	US-10-074-024-607	Sequence 607, App	366	55	2.3	463	3	US-09-764-891-1978	Sequence 1978, Ap
C 294	55	2.3	322	3	US-09-764-887-506	Sequence 506, App	367	55	2.3	463	6	US-10-091-504-1978	Sequence 1978, Ap
C 295	55	2.3	322	3	US-09-764-891-5613	Sequence 5613, App	368	55	2.3	463	7	US-10-091-504-1978	Sequence 1978, Ap
C 296	55	2.3	322	3	US-09-984-429-679	Sequence 679, App	369	55	2.3	463	7	US-10-227-577-1979	Sequence 1979, Ap
C 297	55	2.3	322	6	US-10-073-961-506	Sequence 506, App	370	55	2.3	465	4	US-09-925-065A-947399	Sequence 947399,
C 298	55	2.3	322	7	US-10-074-024-585	Sequence 585, App	371	55	2.3	465	4	US-09-925-065A-947399	Sequence 947399,
C 299	55	2.3	324	7	US-09-764-891-9012	Sequence 9012, App	372	55	2.3	466	5	US-09-925-065A-508845	Sequence 508845,
C 300	55	2.3	324	3	US-09-764-891-8700	Sequence 8700, Ap	373	55	2.3	466	4	US-09-925-065A-508845	Sequence 508845,
C 301	55	2.3	337	3	US-09-764-877-3785	Sequence 3785, App	374	55	2.3	466	4	US-09-925-065A-508846	Sequence 508846,
C 302	55	2.3	337	7	US-10-242-515-3785	Sequence 3785, App	375	55	2.3	466	4	US-09-925-065A-508847	Sequence 508847,
C 303	55	2.3	353	4	US-09-925-065A-689267	Sequence 689267, A	376	55	2.3	466	5	US-09-925-065A-508847	Sequence 508847,
C 304	55	2.3	353	5	US-09-925-065A-689267	Sequence 689267, A	377	55	2.3	466	5	US-09-925-065A-508847	Sequence 508847,
C 305	55	2.3	358	3	US-09-918-995-37710	Sequence 37710, A	378	55	2.3	466	5	US-09-925-065A-508845	Sequence 508845,
C 306	55	2.3	370	3	US-09-984-429-521	Sequence 521, App	379	55	2.3	466	5	US-09-925-065A-508847	Sequence 508847,
C 307	55	2.3	370	9	US-10-357-930-13481	Sequence 13481, A	380	55	2.3	466	6	US-10-027-632-114651	Sequence 114651,
C 308	55	2.3	382	4	US-09-925-065A-506709	Sequence 506709, A	381	55	2.3	466	7	US-10-027-632-114651	Sequence 114651,
C 309	55	2.3	382	5	US-09-925-065A-506709	Sequence 506709, A	382	55	2.3	467	4	US-09-925-065A-949560	Sequence 949560,

383	55	2.3	467	5	US-09-925-065A-949560	Sequence 949560,	C 456	54	2.3	311	8	US-10-085-783A-30969	Sequence 30969, A
384	55	2.3	475	8	US-10-242-535A-44241	Sequence 44241, A	457	54	2.3	332	9	US-10-674-124A-23797	Sequence 23797, A
385	55	2.3	475	8	US-10-085-783A-44241	Sequence 44241, A	458	54	2.3	335	9	US-10-357-930-30785	Sequence 30785, A
386	55	2.3	479	9	US-10-674-124A-1220	Sequence 1220, Ap	459	54	2.3	375	5	US-10-357-930-33975	Sequence 33975, A
387	55	2.3	480	3	US-09-814-353-20881	Sequence 20881, A	460	54	2.3	388	8	US-10-242-535A-18717	Sequence 18717, A
388	55	2.3	482	4	US-09-925-065A-941604	Sequence 941604, A	461	54	2.3	398	8	US-10-085-783A-18717	Sequence 18717, A
389	55	2.3	482	5	US-09-925-065A-941604	Sequence 941604, A	462	54	2.3	407	9	US-10-357-930-12797	Sequence 12797, A
390	55	2.3	486	9	US-10-357-930-50010	Sequence 50010, A	463	54	2.3	411	3	US-09-954-456-1450	Sequence 1450, Ap
391	55	2.3	489	5	US-09-925-065A-935799	Sequence 935799, A	464	54	2.3	411	3	US-09-880-107-445	Sequence 445, App
392	55	2.3	489	5	US-09-925-065A-935799	Sequence 935799, A	465	54	2.3	411	10	US-10-843-641A-4477	Sequence 4477, App
393	55	2.3	494	4	US-09-925-065A-558062	Sequence 558062, A	466	54	2.3	412	9	US-09-918-995-16264	Sequence 16264, A
394	55	2.3	494	4	US-09-925-065A-558063	Sequence 558062, A	467	54	2.3	447	9	US-10-357-930-3628	Sequence 3628, Ap
395	55	2.3	494	4	US-09-925-065A-740820	Sequence 740820, A	468	54	2.3	453	4	US-09-925-065A-673493	Sequence 673493, A
396	55	2.3	494	5	US-09-925-065A-558062	Sequence 558062, A	469	54	2.3	453	5	US-09-925-065A-673493	Sequence 673493, A
397	55	2.3	494	5	US-09-925-065A-558063	Sequence 558062, A	470	54	2.3	458	9	US-10-357-930-33953	Sequence 33953, A
398	55	2.3	494	5	US-09-925-065A-740820	Sequence 740820, A	471	54	2.3	458	9	US-10-357-930-42827	Sequence 42827, A
399	55	2.3	496	10	US-10-450-763-1682	Sequence 1682, Ap	472	54	2.3	463	6	US-10-073-961-112	Sequence 112, App
400	55	2.3	497	3	US-09-918-995-14827	Sequence 14827, A	473	54	2.3	463	6	US-10-073-961-112	Sequence 112, App
401	54	2.3	101	3	US-09-764-887-454	Sequence 454, App	474	54	2.3	463	10	US-10-779-543-16254	Sequence 16254, A
402	54	2.3	101	3	US-09-764-847-2002	Sequence 2002, Ap	475	54	2.3	467	4	US-09-925-065A-618091	Sequence 618091, A
403	54	2.3	101	6	US-10-092-154-2002	Sequence 2002, Ap	476	54	2.3	467	5	US-09-925-065A-618091	Sequence 618091, A
404	54	2.3	101	6	US-10-073-961-454	Sequence 454, App	477	54	2.3	468	12	US-10-301-480-19675	Sequence 19675, A
405	54	2.3	158	3	US-09-860-670-167	Sequence 167, App	478	54	2.3	468	12	US-10-301-480-633084	Sequence 633084, A
406	54	2.3	158	7	US-10-227-646-167	Sequence 167, App	479	54	2.3	468	12	US-10-301-480-633085	Sequence 633085, A
407	54	2.3	201	8	US-10-741-601-11015	Sequence 11015, A	480	54	2.3	468	12	US-10-301-480-633085	Sequence 633085, A
408	54	2.3	201	8	US-10-741-601-15537	Sequence 15537, A	481	54	2.3	476	3	US-09-998-598-1168	Sequence 1168, Ap
409	54	2.3	201	8	US-10-741-601-15541	Sequence 15541, A	482	54	2.3	485	12	US-10-301-480-305380	Sequence 305380, A
410	54	2.3	201	8	US-10-741-601-15550	Sequence 15550, A	483	54	2.3	485	12	US-10-301-480-918789	Sequence 918789, A
411	54	2.3	201	8	US-10-741-601-23751	Sequence 23751, A	484	54	2.3	489	5	US-09-925-065A-219683	Sequence 219683, A
412	54	2.3	201	8	US-10-741-601-23753	Sequence 23753, A	485	54	2.3	489	5	US-09-925-065A-219683	Sequence 219683, A
413	54	2.3	201	9	US-10-719-993-12566	Sequence 12566, A	486	54	2.3	490	6	US-10-027-632-90218	Sequence 90218, A
414	54	2.3	201	9	US-10-719-993-14541	Sequence 14541, A	487	54	2.3	490	7	US-10-027-632-90218	Sequence 90218, A
415	54	2.3	201	9	US-10-719-993-14543	Sequence 14543, A	488	54	2.3	490	7	US-10-027-632-90218	Sequence 90218, A
416	54	2.3	201	9	US-10-741-600-64416	Sequence 64416, A	489	54	2.3	491	6	US-10-027-632-904188	Sequence 304188, A
417	54	2.3	201	9	US-10-741-600-26510	Sequence 26510, A	490	54	2.3	491	6	US-10-027-632-904188	Sequence 304188, A
418	54	2.3	201	9	US-10-741-600-44935	Sequence 44935, A	491	54	2.3	491	7	US-10-027-632-304188	Sequence 304188, A
419	54	2.3	201	9	US-10-741-600-44939	Sequence 44939, A	492	54	2.3	491	7	US-10-027-632-304188	Sequence 304188, A
420	54	2.3	201	9	US-10-741-600-44948	Sequence 44948, A	493	54	2.3	493	7	US-10-027-632-307766	Sequence 307766, A
421	54	2.3	201	9	US-10-741-600-59211	Sequence 59211, A	494	54	2.3	493	7	US-09-925-065A-91897	Sequence 91897, A
422	54	2.3	201	9	US-10-741-600-64416	Sequence 64416, A	495	54	2.3	493	5	US-09-925-065A-91897	Sequence 91897, A
423	54	2.3	201	9	US-10-741-600-64418	Sequence 64418, A	496	54	2.3	495	8	US-10-242-535A-8661	Sequence 8661, Ap
424	54	2.3	201	10	US-10-995-561-20705	Sequence 20705, A	497	54	2.3	495	8	US-10-085-783A-8661	Sequence 8661, Ap
425	54	2.3	201	10	US-10-995-561-23486	Sequence 23486, A	498	54	2.3	497	4	US-09-925-065A-902221	Sequence 90222, A
426	54	2.3	201	10	US-10-995-561-69440	Sequence 69440, A	499	54	2.3	497	5	US-09-925-065A-902221	Sequence 90222, A
427	54	2.3	201	10	US-10-995-561-71599	Sequence 71599, A	500	53	2.2	201	8	US-10-741-601-74706	Sequence 24706, A
428	54	2.3	201	10	US-10-995-561-72296	Sequence 72296, A	501	53	2.2	201	9	US-10-741-600-66219	Sequence 66219, A
429	54	2.3	201	10	US-10-995-561-72298	Sequence 72298, A	502	53	2.2	201	16	US-10-995-561-20773	Sequence 20773, A
430	54	2.3	201	15	US-11-124-368A-12658	Sequence 12658, A	503	53	2.2	201	16	US-11-124-367A-15389	Sequence 15389, A
431	54	2.3	201	15	US-11-124-368A-12668	Sequence 12668, A	504	53	2.2	293	3	US-09-764-872-777	Sequence 777, App
432	54	2.3	201	15	US-11-124-368A-12670	Sequence 12670, A	505	53	2.2	293	3	US-09-764-872-777	Sequence 777, App
433	54	2.3	201	15	US-11-124-368A-12671	Sequence 12671, A	506	53	2.2	339	3	US-10-357-930-18786	Sequence 18786, A
434	54	2.3	201	15	US-11-124-368A-12671	Sequence 12671, A	507	53	2.2	339	3	US-10-357-930-18786	Sequence 18786, A
435	54	2.3	201	16	US-11-124-367A-15638	Sequence 15638, A	508	53	2.2	343	6	US-10-027-632-26505	Sequence 26505, A
436	54	2.3	201	16	US-11-124-367A-15638	Sequence 15638, A	509	53	2.2	343	7	US-10-027-632-26505	Sequence 26505, A
437	54	2.3	280	3	US-09-764-872-549	Sequence 549, App	510	53	2.2	394	7	US-10-357-930-18182	Sequence 18182, A
438	54	2.3	283	3	US-09-764-872-5523	Sequence 5523, App	511	53	2.2	414	4	US-09-925-065A-2830	Sequence 2830, Ap
439	54	2.3	283	6	US-10-091-572-478	Sequence 478, App	512	53	2.2	414	4	US-09-925-065A-2830	Sequence 2830, Ap
440	54	2.3	303	3	US-09-764-860-776	Sequence 776, App	513	53	2.2	414	12	US-10-301-480-104067	Sequence 104067, A
441	54	2.3	303	3	US-09-764-877-2535	Sequence 2535, App	514	53	2.2	414	12	US-10-301-480-71786	Sequence 71786, A
442	54	2.3	303	3	US-09-764-877-2543	Sequence 2543, App	515	53	2.2	416	9	US-10-357-930-18368	Sequence 18368, A
443	54	2.3	303	6	US-10-074-095-776	Sequence 776, App	516	53	2.2	416	9	US-10-357-930-18368	Sequence 18368, A
444	54	2.3	303	7	US-10-212-872-776	Sequence 776, App	517	53	2.2	449	9	US-10-674-124A-19448	Sequence 19448, Ap
445	54	2.3	303	7	US-10-242-515-2535	Sequence 2535, App	518	53	2.2	449	9	US-10-674-124A-19448	Sequence 19448, Ap
446	54	2.3	303	7	US-10-242-515-2543	Sequence 2543, App	519	53	2.2	465	4	US-09-925-065A-126480	Sequence 126480, A
447	54	2.3	308	10	US-10-472-553-642	Sequence 642, App	520	53	2.2	465	4	US-09-925-065A-126480	Sequence 126480, A
448	54	2.3	309	7	US-09-764-877-2197	Sequence 2197, App	521	53	2.2	465	4	US-09-925-065A-231973	Sequence 231973, A
449	54	2.3	317	8	US-10-242-515-2197	Sequence 2197, App	522	53	2.2	465	4	US-09-925-065A-231973	Sequence 231973, A
450	54	2.3	317	8	US-10-242-535A-20968	Sequence 20968, A	523	53	2.2	465	5	US-09-925-065A-126480	Sequence 126480, A
451	54	2.3	317	8	US-10-085-783A-20968	Sequence 20968, A	524	53	2.2	465	5	US-09-925-065A-231973	Sequence 231973, A
452	54	2.3	324	6	US-09-764-891-5520	Sequence 5520, App	525	53	2.2	465	5	US-09-925-065A-231974	Sequence 231974, A
453	54	2.3	324	6	US-10-091-572-435	Sequence 435, App	526	53	2.2	498	3	US-09-925-065A-231974	Sequence 231974, A
454	54	2.3	326	9	US-10-357-930-9582	Sequence 9582, App	527	53	2.2	500	10	US-09-918-995-30641	Sequence 30641, A
455	54	2.3	341	8	US-10-242-535A-30969	Sequence 30969, A	528	53	2.2	500	10	US-10-779-543-20070	Sequence 20070, A

C 529	52	2.2	201	9	US-10-741-600-58922	Sequence 58922, A	602	51	2.2	362	4	US-09-925-065A-88288	Sequence 88288, A
C 530	52	2.2	201	10	US-10-995-561-52323	Sequence 52323, A	603	51	2.2	362	5	US-09-925-065A-88288	Sequence 88288, A
C 531	52	2.2	201	16	US-11-124-367A-17786	Sequence 17786, A	604	51	2.2	362	12	US-10-301-480-189329	Sequence 189329, A
C 532	52	2.2	238	7	US-10-242-355-875	Sequence 875, App	605	51	2.2	362	12	US-10-301-480-802938	Sequence 802938, A
C 533	52	2.2	389	4	US-09-925-065A-554407	Sequence 554407, A	606	51	2.2	364	10	US-10-972-024-406	Sequence 406, App
C 534	52	2.2	389	5	US-09-925-065A-554407	Sequence 554407, A	607	51	2.2	392	9	US-10-357-930-40676	Sequence 40676, A
C 535	52	2.2	395	10	US-10-779-543-10976	Sequence 10976, A	608	51	2.2	392	9	US-10-357-930-44084	Sequence 44084, A
C 536	52	2.2	407	3	US-09-867-701-6885	Sequence 6885, App	609	51	2.2	400	8	US-10-242-535A-8804	Sequence 8804, App
C 537	52	2.2	428	4	US-09-925-065A-819737	Sequence 819737, A	610	51	2.2	400	8	US-10-085-783A-8804	Sequence 8804, App
C 538	52	2.2	428	5	US-09-925-065A-819737	Sequence 819737, A	611	51	2.2	401	3	US-09-795-668-421	Sequence 421, App
C 539	52	2.2	451	9	US-10-674-124A-21367	Sequence 21367, A	612	51	2.2	401	3	US-09-795-668-421	Sequence 421, App
C 540	52	2.2	461	9	US-10-357-930-58379	Sequence 58379, A	613	51	2.2	401	3	US-09-946-807-421	Sequence 421, App
C 541	52	2.2	471	9	US-10-674-124A-3661	Sequence 3661, App	614	51	2.2	401	10	US-10-995-011-421	Sequence 421, App
C 542	52	2.2	474	9	US-10-674-124A-24199	Sequence 24199, A	615	51	2.2	421	3	US-09-918-995-35835	Sequence 35835, A
C 543	52	2.2	487	9	US-10-357-930-48292	Sequence 48292, A	616	51	2.2	424	9	US-10-357-930-35261	Sequence 35261, A
C 544	51	2.2	118	3	US-09-764-891-8324	Sequence 8324, App	617	51	2.2	454	10	US-10-756-149-152	Sequence 152, App
C 545	51	2.2	194	3	US-09-764-877-2426	Sequence 2426, App	618	51	2.2	461	9	US-09-867-701-8502	Sequence 8502, App
C 546	51	2.2	194	7	US-10-242-515-2426	Sequence 2426, App	619	51	2.2	479	9	US-10-674-124A-1118	Sequence 1118, App
C 547	51	2.2	201	8	US-10-741-601-24633	Sequence 24633, A	620	51	2.2	480	5	US-09-925-065A-32025	Sequence 32025, A
C 548	51	2.2	201	8	US-10-741-601-25926	Sequence 25926, A	621	51	2.2	480	5	US-09-925-065A-32025	Sequence 32025, A
C 549	51	2.2	201	8	US-10-741-601-25927	Sequence 25927, A	622	51	2.2	480	5	US-09-925-065A-32025	Sequence 32025, A
C 550	51	2.2	201	9	US-10-719-993-18970	Sequence 18970, A	623	51	2.2	480	6	US-10-027-632-137719	Sequence 137719, A
C 551	51	2.2	201	9	US-10-719-993-18976	Sequence 18976, A	624	51	2.2	480	7	US-10-027-632-137719	Sequence 137719, A
C 552	51	2.2	201	9	US-10-719-993-22269	Sequence 22269, A	625	51	2.2	480	12	US-10-301-480-133263	Sequence 133263, A
C 553	51	2.2	201	9	US-10-719-993-34818	Sequence 34818, A	626	51	2.2	482	4	US-09-925-065A-737314	Sequence 737314, A
C 554	51	2.2	201	9	US-10-719-993-35022	Sequence 35022, A	627	51	2.2	482	4	US-09-925-065A-741639	Sequence 741639, A
C 555	51	2.2	201	9	US-10-719-993-42762	Sequence 42762, A	628	51	2.2	482	4	US-09-925-065A-741640	Sequence 741640, A
C 556	51	2.2	201	9	US-10-719-993-50196	Sequence 50196, A	629	51	2.2	482	4	US-09-925-065A-817268	Sequence 817268, A
C 557	51	2.2	201	9	US-10-719-993-53042	Sequence 53042, A	630	51	2.2	482	5	US-09-925-065A-737314	Sequence 737314, A
C 558	51	2.2	201	9	US-10-741-600-38805	Sequence 38805, A	631	51	2.2	482	5	US-09-925-065A-741639	Sequence 741639, A
C 559	51	2.2	201	9	US-10-741-600-39631	Sequence 39631, A	632	51	2.2	482	5	US-09-925-065A-741640	Sequence 741640, A
C 560	51	2.2	201	9	US-10-741-600-42102	Sequence 42102, A	633	51	2.2	482	5	US-09-925-065A-817268	Sequence 817268, A
C 561	51	2.2	201	9	US-10-741-600-62096	Sequence 62096, A	634	51	2.2	484	9	US-10-357-930-57692	Sequence 57692, A
C 562	51	2.2	201	9	US-10-741-600-66146	Sequence 66146, A	635	51	2.2	489	3	US-09-918-995-578	Sequence 578, App
C 563	51	2.2	201	9	US-10-741-600-67344	Sequence 67344, A	636	51	2.2	489	4	US-09-925-065A-75000	Sequence 75000, A
C 564	51	2.2	201	9	US-10-741-600-68776	Sequence 68776, A	637	51	2.2	489	4	US-09-925-065A-75000	Sequence 75000, A
C 565	51	2.2	201	9	US-10-995-561-17457	Sequence 17457, A	638	51	2.2	489	5	US-09-925-065A-75001	Sequence 75001, A
C 566	51	2.2	201	10	US-10-995-561-17470	Sequence 17470, A	639	51	2.2	489	5	US-09-925-065A-75001	Sequence 75001, A
C 567	51	2.2	201	10	US-10-995-561-10721	Sequence 30721, A	640	51	2.2	489	12	US-10-301-480-176239	Sequence 176239, A
C 568	51	2.2	201	10	US-10-995-561-10744	Sequence 30741, A	641	51	2.2	489	12	US-10-301-480-176240	Sequence 176240, A
C 569	51	2.2	201	10	US-10-995-561-33927	Sequence 33927, A	642	51	2.2	489	12	US-10-301-480-789648	Sequence 789648, A
C 570	51	2.2	201	10	US-10-995-561-33929	Sequence 33929, A	643	51	2.2	489	12	US-10-301-480-789649	Sequence 789649, A
C 571	51	2.2	201	10	US-10-995-561-39465	Sequence 39465, A	644	51	2.2	490	7	US-10-074-024-154	Sequence 154, App
C 572	51	2.2	201	10	US-10-995-561-42456	Sequence 42456, A	645	51	2.2	491	4	US-09-925-065A-938715	Sequence 938715, A
C 573	51	2.2	201	10	US-10-995-561-6763	Sequence 42456, A	646	51	2.2	491	5	US-09-925-065A-938715	Sequence 938715, A
C 574	51	2.2	201	10	US-10-995-561-70504	Sequence 70504, A	647	51	2.2	491	5	US-10-450-763-8417	Sequence 8417, App
C 575	51	2.2	201	10	US-10-995-561-76757	Sequence 76757, A	648	51	2.2	491	7	US-10-131-827-7449	Sequence 7449, App
C 576	51	2.2	201	10	US-10-995-561-78840	Sequence 78840, A	649	51	2.2	50	16	US-11-222-526-147	Sequence 147, App
C 577	51	2.2	201	10	US-10-995-561-79439	Sequence 79439, A	650	51	2.2	105	3	US-09-764-891-7259	Sequence 7259, App
C 578	51	2.2	201	10	US-10-995-561-79444	Sequence 79444, A	651	51	2.2	148	7	US-10-074-024-589	Sequence 589, App
C 579	51	2.2	201	10	US-10-995-561-80595	Sequence 80595, A	652	51	2.2	201	8	US-10-741-601-19652	Sequence 19652, A
C 580	51	2.2	201	15	US-11-124-368A-9993	Sequence 9993, App	653	51	2.2	201	9	US-10-719-993-11378	Sequence 11378, A
C 581	51	2.2	201	15	US-11-124-368A-13844	Sequence 13844, A	654	51	2.2	201	9	US-10-719-993-11804	Sequence 11804, A
C 582	51	2.2	201	15	US-11-124-368A-13856	Sequence 13856, A	655	51	2.2	201	9	US-10-719-993-24883	Sequence 24883, A
C 583	51	2.2	201	16	US-11-124-367A-19570	Sequence 19570, A	656	51	2.2	201	9	US-10-741-600-46183	Sequence 46183, A
C 584	51	2.2	201	16	US-11-124-367A-19570	Sequence 19570, A	657	51	2.2	201	9	US-10-741-600-53651	Sequence 53651, A
C 585	51	2.2	201	16	US-11-124-367A-29640	Sequence 29640, A	658	51	2.2	201	9	US-10-741-600-53651	Sequence 53651, A
C 586	51	2.2	201	16	US-11-124-367A-32804	Sequence 32804, A	659	51	2.2	201	10	US-10-995-561-40948	Sequence 40948, A
C 587	51	2.2	229	7	US-09-860-670-225	Sequence 225, App	660	51	2.2	201	10	US-10-995-561-40948	Sequence 40948, A
C 588	51	2.2	229	7	US-10-227-646-225	Sequence 225, App	661	51	2.2	201	10	US-10-995-561-42844	Sequence 42844, A
C 589	51	2.2	254	3	US-09-764-864-1696	Sequence 1696, App	662	51	2.2	201	10	US-10-995-561-52962	Sequence 52962, A
C 590	51	2.2	292	3	US-09-764-847-1844	Sequence 1847, App	663	51	2.2	201	10	US-10-995-561-52962	Sequence 52962, A
C 591	51	2.2	292	3	US-09-764-847-1847	Sequence 1847, App	664	51	2.2	201	10	US-10-995-561-52962	Sequence 52962, A
C 592	51	2.2	292	6	US-10-092-154-1844	Sequence 1844, App	665	51	2.2	201	10	US-10-995-561-63220	Sequence 63220, A
C 593	51	2.2	300	10	US-10-092-154-1847	Sequence 1847, App	666	51	2.2	201	10	US-10-995-561-76204	Sequence 76204, A
C 594	51	2.2	300	10	US-10-779-543-8252	Sequence 8252, App	667	51	2.2	201	10	US-10-995-561-78577	Sequence 78577, A
C 595	51	2.2	310	8	US-10-242-535A-39440	Sequence 29440, A	668	51	2.2	201	10	US-10-995-561-83651	Sequence 83651, A
C 596	51	2.2	310	8	US-10-085-783A-39440	Sequence 29440, A	669	51	2.2	201	15	US-11-124-367A-19552	Sequence 19552, A
C 597	51	2.2	326	3	US-09-764-891-6088	Sequence 6088, App	670	51	2.2	201	15	US-11-124-367A-81953	Sequence 81953, App
C 598	51	2.2	326	3	US-09-764-891-6090	Sequence 6090, App	671	51	2.2	201	16	US-11-124-367A-10993	Sequence 10993, A
C 599	51	2.2	329	7	US-09-764-877-3390	Sequence 3390, App	672	51	2.2	201	16	US-11-124-367A-15954	Sequence 15954, A
C 600	51	2.2	335	7	US-10-242-355-8840	Sequence 840, App	673	51	2.2	201	16	US-11-124-367A-15955	Sequence 15955, A
C 601	51	2.2	342	3	US-09-867-701-8277	Sequence 8277, App	674	51	2.2	201	16	US-11-124-367A-28679	Sequence 28679, A

675	50	2.1	201	16	US-11-124-367A-31777	Sequence 31777, A	748	50	2.1	494	4	US-09-925-065A-869357	Sequence 869377, A
C 676	50	2.1	201	16	US-11-124-367A-33263	Sequence 33263, A	749	50	2.1	494	5	US-09-925-065A-869357	Sequence 869357, A
677	50	2.1	223	3	US-09-860-670-220	Sequence 220, App	C 750	50	2.1	499	4	US-09-925-065A-842223	Sequence 842223, A
678	50	2.1	223	7	US-10-227-546-220	Sequence 220, App	C 751	50	2.1	499	5	US-09-925-065A-842223	Sequence 842223, A
679	50	2.1	239	9	US-10-674-124A-21646	Sequence 21646, A	C 752	49	2.1	111	8	US-10-242-535A-38990	Sequence 38990, A
680	50	2.1	252	3	US-09-764-847-1033	Sequence 1033, App	C 753	49	2.1	111	8	US-10-085-783A-38990	Sequence 38990, A
681	50	2.1	252	6	US-10-092-154-1033	Sequence 1033, App	C 754	49	2.1	111	8	US-10-085-783A-38990	Sequence 38990, A
C 682	50	2.1	262	6	US-10-357-930-18436	Sequence 18436, A	C 755	49	2.1	201	8	US-10-741-601-21194	Sequence 21194, A
C 683	50	2.1	264	3	US-09-764-891-8746	Sequence 8746, App	C 756	49	2.1	201	9	US-10-719-993-7133	Sequence 7133, App
C 684	50	2.1	272	3	US-09-764-891-8747	Sequence 8747, App	C 757	49	2.1	201	9	US-10-719-993-7133	Sequence 7133, App
C 685	50	2.1	272	3	US-10-242-535A-55757	Sequence 55757, A	C 758	49	2.1	201	9	US-10-741-600-29595	Sequence 29595, A
C 686	50	2.1	273	8	US-10-085-783A-55757	Sequence 55757, A	C 759	49	2.1	201	9	US-10-741-600-29595	Sequence 29595, A
C 687	50	2.1	288	3	US-09-973-278-870	Sequence 870, App	C 760	49	2.1	201	9	US-10-741-600-50959	Sequence 50959, A
C 688	50	2.1	288	6	US-10-205-428-929	Sequence 929, App	C 761	49	2.1	201	10	US-10-995-561-26409	Sequence 26409, A
C 689	50	2.1	301	3	US-09-984-429-644	Sequence 644, App	C 762	49	2.1	201	15	US-10-995-561-70515	Sequence 70515, A
C 690	50	2.1	317	3	US-09-764-891-7588	Sequence 7588, App	C 763	49	2.1	201	15	US-10-995-561-70515	Sequence 70515, A
C 691	50	2.1	323	3	US-09-984-429-669	Sequence 669, App	C 764	49	2.1	201	15	US-10-995-561-70515	Sequence 70515, A
C 692	50	2.1	337	3	US-10-357-930-48248	Sequence 48248, A	C 765	49	2.1	276	3	US-09-764-891-5817	Sequence 5817, App
C 693	50	2.1	361	3	US-09-803-719-115	Sequence 115, App	C 766	49	2.1	276	3	US-09-764-891-5817	Sequence 5817, App
C 694	50	2.1	361	10	US-10-779-543-13385	Sequence 13385, A	C 767	49	2.1	276	3	US-09-764-891-5817	Sequence 5817, App
C 695	50	2.1	364	3	US-09-803-719-110	Sequence 110, App	C 768	49	2.1	276	3	US-09-764-891-5817	Sequence 5817, App
C 696	50	2.1	364	10	US-10-779-543-13380	Sequence 13380, A	C 769	49	2.1	301	9	US-10-357-930-841	Sequence 841, App
C 697	50	2.1	366	8	US-10-242-535A-7668	Sequence 7668, App	C 770	49	2.1	317	3	US-09-871-161-109	Sequence 109, App
C 698	50	2.1	366	8	US-10-085-783A-7668	Sequence 7668, App	C 771	49	2.1	317	3	US-09-871-161-109	Sequence 109, App
C 699	50	2.1	377	9	US-10-357-930-10372	Sequence 10372, A	C 772	49	2.1	334	3	US-09-867-701-9936	Sequence 9936, App
C 700	50	2.1	378	6	US-10-027-632-142956	Sequence 142956, A	C 773	49	2.1	364	3	US-09-867-701-9936	Sequence 9936, App
C 701	50	2.1	378	7	US-10-027-632-142956	Sequence 142956, A	C 774	49	2.1	371	9	US-10-914-037-919	Sequence 919, App
C 702	50	2.1	378	7	US-10-357-930-9873	Sequence 9873, App	C 775	49	2.1	374	9	US-10-357-930-554	Sequence 554, App
C 703	50	2.1	378	9	US-10-357-930-19220	Sequence 19220, A	C 776	49	2.1	378	9	US-10-357-930-554	Sequence 554, App
C 704	50	2.1	380	9	US-10-357-930-9718	Sequence 9718, App	C 777	49	2.1	389	4	US-09-925-065A-492995	Sequence 492995, A
C 705	50	2.1	380	9	US-10-357-930-10919	Sequence 10919, A	C 778	49	2.1	389	4	US-09-925-065A-492995	Sequence 492995, A
C 706	50	2.1	393	9	US-10-357-930-9723	Sequence 9723, App	C 779	49	2.1	389	5	US-09-925-065A-492995	Sequence 492995, A
C 707	50	2.1	396	4	US-09-925-065A-62856	Sequence 62856, A	C 780	49	2.1	389	5	US-09-925-065A-492995	Sequence 492995, A
C 708	50	2.1	396	4	US-09-925-065A-62856	Sequence 62856, A	C 781	49	2.1	413	6	US-10-027-632-130553	Sequence 130553, A
C 709	50	2.1	396	12	US-10-301-480-164094	Sequence 164094, A	C 782	49	2.1	413	6	US-10-027-632-130553	Sequence 130553, A
C 710	50	2.1	396	12	US-10-301-480-777503	Sequence 777503, A	C 783	49	2.1	448	12	US-10-301-480-21884	Sequence 21884, A
C 711	50	2.1	400	9	US-10-357-930-39031	Sequence 39031, A	C 784	49	2.1	448	12	US-10-301-480-21884	Sequence 21884, A
C 712	50	2.1	411	3	US-09-764-891-7754	Sequence 7754, App	C 785	49	2.1	453	12	US-10-301-480-634693	Sequence 634693, A
C 713	50	2.1	412	4	US-09-925-065A-488378	Sequence 488378, A	C 786	49	2.1	453	12	US-10-301-480-634693	Sequence 634693, A
C 714	50	2.1	412	4	US-09-925-065A-488378	Sequence 488378, A	C 787	49	2.1	455	9	US-10-674-124A-23917	Sequence 23917, A
C 715	50	2.1	416	9	US-10-357-930-30924	Sequence 30924, A	C 788	49	2.1	467	6	US-10-027-632-284997	Sequence 284997, A
C 716	50	2.1	416	9	US-10-357-930-31074	Sequence 31074, A	C 789	49	2.1	467	6	US-10-027-632-284997	Sequence 284997, A
C 717	50	2.1	416	9	US-10-357-930-31074	Sequence 31074, A	C 790	49	2.1	468	6	US-10-027-632-284997	Sequence 284997, A
C 718	50	2.1	418	3	US-09-918-995-13198	Sequence 13198, A	C 791	49	2.1	468	6	US-10-027-632-284997	Sequence 284997, A
C 719	50	2.1	429	3	US-09-867-701-7436	Sequence 7436, App	C 792	49	2.1	468	7	US-10-027-632-284997	Sequence 284997, A
C 720	50	2.1	431	9	US-10-357-930-549	Sequence 549, App	C 793	49	2.1	468	7	US-10-027-632-284997	Sequence 284997, A
C 721	50	2.1	439	12	US-10-301-480-50076	Sequence 50076, A	C 794	49	2.1	470	4	US-09-925-065A-360145	Sequence 360145, A
C 722	50	2.1	439	12	US-10-301-480-50076	Sequence 50076, A	C 795	49	2.1	470	4	US-09-925-065A-360145	Sequence 360145, A
C 723	50	2.1	442	3	US-09-918-995-14858	Sequence 14858, A	C 796	49	2.1	470	5	US-09-925-065A-360145	Sequence 360145, A
C 724	50	2.1	443	9	US-10-357-930-5813	Sequence 5813, App	C 797	49	2.1	470	5	US-09-925-065A-360145	Sequence 360145, A
C 725	50	2.1	444	3	US-09-918-995-9073	Sequence 9073, App	C 798	49	2.1	495	12	US-10-301-480-312257	Sequence 312257, A
C 726	50	2.1	444	3	US-09-918-995-9073	Sequence 9073, App	C 799	49	2.1	495	12	US-10-301-480-312257	Sequence 312257, A
C 727	50	2.1	452	9	US-10-674-124A-852	Sequence 852, App	C 800	49	2.1	495	12	US-10-301-480-312257	Sequence 312257, A
C 728	50	2.1	454	3	US-10-357-930-57273	Sequence 57273, A	C 801	49	2.1	495	12	US-10-301-480-312257	Sequence 312257, A
C 729	50	2.1	458	3	US-09-918-995-26594	Sequence 26594, A	C 802	49	2.1	498	4	US-10-301-480-925667	Sequence 925667, A
C 730	50	2.1	459	4	US-09-925-065A-638504	Sequence 638504, A	C 803	49	2.1	498	4	US-09-925-065A-638504	Sequence 638504, A
C 731	50	2.1	459	4	US-09-925-065A-638504	Sequence 638504, A	C 804	49	2.1	498	4	US-09-925-065A-638504	Sequence 638504, A
C 732	50	2.1	460	4	US-09-925-065A-292771	Sequence 292771, A	C 805	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 733	50	2.1	460	5	US-09-925-065A-193825	Sequence 193825, A	C 806	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 734	50	2.1	462	6	US-10-027-632-193825	Sequence 193825, A	C 807	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 735	50	2.1	462	12	US-10-301-480-369641	Sequence 369641, A	C 808	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 736	50	2.1	462	12	US-10-301-480-369641	Sequence 369641, A	C 809	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 737	50	2.1	465	12	US-10-301-480-983050	Sequence 983050, A	C 810	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 738	50	2.1	465	6	US-09-920-300A-288	Sequence 288, App	C 811	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 739	50	2.1	465	6	US-10-033-528-288	Sequence 288, App	C 812	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 740	50	2.1	465	10	US-10-099-926-288	Sequence 288, App	C 813	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 741	50	2.1	471	9	US-10-961-587-288	Sequence 288, App	C 814	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 742	50	2.1	471	9	US-10-674-124A-9629	Sequence 9629, App	C 815	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 743	50	2.1	471	10	US-10-779-543-16692	Sequence 16692, A	C 816	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 744	50	2.1	484	4	US-09-925-065A-885611	Sequence 885611, A	C 817	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 745	50	2.1	484	4	US-09-925-065A-885611	Sequence 885611, A	C 818	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 746	50	2.1	488	4	US-09-925-065A-32786	Sequence 32786, A	C 819	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 747	50	2.1	488	5	US-09-925-065A-32786	Sequence 32786, A	C 820	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A
C 748	50	2.1	488	9	US-10-357-930-48010	Sequence 48010, A	C 820	49	2.1	498	5	US-09-925-065A-228205	Sequence 228205, A

C 821	48	2.0	201	10	US-10-995-561-46236	Sequence 46236, A	894	47	2.0	428	7	US-10-027-632-142769	Sequence 142769, A
C 822	48	2.0	201	10	US-10-995-561-47326	Sequence 47326, A	895	47	2.0	428	7	US-10-027-632-142770	Sequence 142770, A
C 823	48	2.0	201	10	US-10-995-561-63776	Sequence 63776, A	896	47	2.0	428	7	US-10-027-632-142771	Sequence 142771, A
C 824	48	2.0	201	10	US-10-995-561-65114	Sequence 65114, A	897	47	2.0	430	3	US-09-867-701-233	Sequence 233, App
C 825	48	2.0	201	10	US-10-995-561-75078	Sequence 75078, A	898	47	2.0	440	12	US-10-301-480-150888	Sequence 450888, A
C 826	48	2.0	201	15	US-11-124-368A-5432	Sequence 5432, A	899	47	2.0	440	12	US-10-301-480-1064297	Sequence 1064297, A
C 827	48	2.0	201	15	US-11-124-368A-5433	Sequence 5433, App	900	47	2.0	442	4	US-09-925-065A-381822	Sequence 381822, A
C 828	48	2.0	201	15	US-11-124-368A-5434	Sequence 5434, App	901	47	2.0	442	5	US-09-925-065A-181822	Sequence 181822, A
C 829	48	2.0	201	16	US-11-124-367A-11089	Sequence 10809, A	902	47	2.0	447	9	US-10-357-930-21139	Sequence 21139, A
C 830	48	2.0	201	16	US-11-124-367A-11229	Sequence 11229, A	903	47	2.0	447	9	US-10-357-930-23488	Sequence 23488, A
C 831	48	2.0	201	16	US-11-124-367A-18609	Sequence 18609, A	904	47	2.0	464	6	US-10-027-632-253506	Sequence 253506, A
C 832	48	2.0	201	16	US-11-124-367A-33390	Sequence 33390, A	905	47	2.0	464	6	US-10-027-632-253507	Sequence 253507, A
C 833	48	2.0	206	3	US-09-867-701-3477	Sequence 3477, A	906	47	2.0	464	7	US-10-027-632-253506	Sequence 253506, A
C 834	48	2.0	242	3	US-09-984-429-614	Sequence 614, App	907	47	2.0	464	7	US-10-301-480-88291	Sequence 88291, A
C 835	48	2.0	243	3	US-09-984-429-675	Sequence 675, App	908	47	2.0	464	12	US-10-301-480-88292	Sequence 88292, A
C 836	48	2.0	275	3	US-09-764-891-8380	Sequence 8380, App	909	47	2.0	464	12	US-10-301-480-88292	Sequence 88292, A
C 837	48	2.0	285	3	US-09-764-891-8387	Sequence 8387, App	910	47	2.0	464	12	US-10-301-480-701700	Sequence 701700, A
C 838	48	2.0	309	3	US-09-764-847-1475	Sequence 1475, App	911	47	2.0	464	12	US-10-301-480-701701	Sequence 701701, A
C 839	48	2.0	309	3	US-09-764-847-1476	Sequence 1476, App	912	47	2.0	473	4	US-09-925-065A-331292	Sequence 331292, A
C 840	48	2.0	309	6	US-10-092-154-1475	Sequence 1475, App	913	47	2.0	473	4	US-09-925-065A-331293	Sequence 331293, A
C 841	48	2.0	309	6	US-10-092-154-1476	Sequence 1476, App	914	47	2.0	473	5	US-09-925-065A-331292	Sequence 331292, A
C 842	48	2.0	359	6	US-10-027-632-288929	Sequence 288929, A	915	47	2.0	473	5	US-09-925-065A-331293	Sequence 331293, A
C 843	48	2.0	359	7	US-10-027-632-288929	Sequence 288929, A	916	47	2.0	478	9	US-10-357-930-331177	Sequence 321177, A
C 844	48	2.0	374	3	US-09-796-692-5136	Sequence 5136, App	917	47	2.0	480	3	US-09-918-995-26628	Sequence 26628, A
C 845	48	2.0	374	6	US-10-040-862-5136	Sequence 5136, App	918	47	2.0	480	3	US-09-918-995-12124	Sequence 12124, A
C 846	48	2.0	374	7	US-10-057-475B-5136	Sequence 5136, App	919	47	2.0	480	10	US-10-779-543-17707	Sequence 17707, A
C 847	48	2.0	374	9	US-10-764-324-5136	Sequence 5136, App	920	47	2.0	485	3	US-09-918-995-11848	Sequence 11848, A
C 848	48	2.0	374	9	US-10-764-324-5136	Sequence 5136, App	921	47	2.0	495	12	US-10-301-480-7920	Sequence 7920, App
C 849	48	2.0	389	9	US-10-674-124A-7537	Sequence 7537, App	922	47	2.0	495	12	US-10-301-480-405095	Sequence 405095, A
C 850	48	2.0	405	16	US-11-043-752-2215	Sequence 2215, App	923	47	2.0	495	12	US-10-301-480-405096	Sequence 405096, A
C 851	48	2.0	450	5	US-09-925-065A-946351	Sequence 946351, A	924	47	2.0	495	12	US-10-301-480-612504	Sequence 621250, A
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C 857	48	2.0	496	10	US-10-779-543-21199	Sequence 21199, A	930	46	1.9	201	8	US-10-741-601-28840	Sequence 28840, A
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C 864	47	2.0	201	10	US-10-995-561-25243	Sequence 25243, A	937	46	1.9	201	9	US-10-741-600-58924	Sequence 58924, A
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C 875	47	2.0	201	16	US-11-124-367A-32452	Sequence 32452, A	948	46	1.9	208	8	US-10-085-783A-46583	Sequence 46583, A
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C 886	47	2.0	391	10	US-09-803-719-2310	Sequence 2310, App	959	46	1.9	396	9	US-10-357-930-35094	Sequence 35094, A
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C 888	47	2.0	422	3	US-09-814-353-13401	Sequence 13401, A	961	46	1.9	408	9	US-10-674-124A-21478	Sequence 21478, A
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ALIGNMENTS

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RESULT 1
US-10-822-254-1
; Sequence 1, Application US/10822254
; Publication No. US2005003783A1
; GENERAL INFORMATION:
; APPLICANT: Taremi, S S
; APPLICANT: Xie, Gaolian
; APPLICANT: Hesson, Thomas E
; APPLICANT: Ducu, Jose S
; APPLICANT: Strickland, Corey
; APPLICANT: Windsor, William
; APPLICANT: Madison, Vincent
; APPLICANT: Zhang, Runtin
; APPLICANT: Reichert, Paul
; TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Metho
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: JB06017US01
; CURRENT APPLICATION NUMBER: US/10/822,254
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/461,787
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-822-254-1
Query Match 13.8%; Score 327; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.6e-158;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-10-822-254-5
; Sequence 5, Application US/10822254
; Publication No. US2005003783A1
; GENERAL INFORMATION:
; APPLICANT: Taremi, S S
; APPLICANT: Xie, Gaolian
; APPLICANT: Hesson, Thomas E
; APPLICANT: Ducu, Jose S
; APPLICANT: Strickland, Corey
; APPLICANT: Windsor, William
; APPLICANT: Madison, Vincent
; APPLICANT: Zhang, Runtin
; APPLICANT: Reichert, Paul
; TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Metho
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: JB06017US01
; CURRENT APPLICATION NUMBER: US/10/822,254
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/461,787
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-822-254-5
Query Match 11.6%; Score 276; DB 9; Length 327;
Best Local Similarity 99.7%; Pred. No. 5.3e-132;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 660 GACTCAGGTACATCTGTGATGAGAAC 686
Db 301 GACTCAGGTACATCTGTGATGAGAAC 327

RESULT 3
US-10-822-254-7
; Sequence 7, Application US/1082254
; Publication No. US20050037383A1
; GENERAL INFORMATION:
; APPLICANT: Taremi, S S
; APPLICANT: Xie, Gaolian
; APPLICANT: Hesson, Thomas E
; APPLICANT: Ducca, Jose S
; APPLICANT: Strickland, Corey
; APPLICANT: Windsor, William
; APPLICANT: Madison, Vincent
; APPLICANT: Zhang, Rumin
; APPLICANT: Reichert, Paul
; TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Methods
; FILE REFERENCE: JB06017US01
; CURRENT APPLICATION NUMBER: US/10/822,254
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/461,787
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-822-254-7

Query Match 11.6%; Score 276; DB 9; Length 327;
Best Local Similarity 9.7%; Pred. No. 5.3e-132;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 TCACGATTCAGCTTCGGAACAAGACCCCTGTTAGCCAAAGCCATGCTTTTGAAG 60
QY 420 TTATTAAAGTCTGTGTGTCACAAAAGACCTTACTATGAAAGAGTTCTTTTAT 479
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Db 301 GACTCAGGTACATCTGTGATGAGAAC 327

RESULT 4
US-10-822-254-9
; Sequence 9, Application US/1082254
; Publication No. US20050037383A1
; GENERAL INFORMATION:
; APPLICANT: Taremi, S S
; APPLICANT: Xie, Gaolian
; APPLICANT: Hesson, Thomas E
; APPLICANT: Ducca, Jose S
; APPLICANT: Strickland, Corey
; APPLICANT: Windsor, William
; APPLICANT: Madison, Vincent
; APPLICANT: Zhang, Rumin
; APPLICANT: Reichert, Paul
; TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Methods
; FILE REFERENCE: JB06017US01
; CURRENT APPLICATION NUMBER: US/10/822,254
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/461,787
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-822-254-9

Query Match 9.5%; Score 225; DB 9; Length 327;
Best Local Similarity 9.4%; Pred. No. 1.8e-105;
Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 360 TCACGATTCAGCTTCGGAACAAGACCCCTGTTAGCCAAAGCCATGCTTTTGAAG 419
Db 1 TCACGATTCAGCTTCGGAACAAGACCCCTGTTAGCCAAAGCCATGCTTTTGAAG 60
QY 420 TTATTAAAGTCTGTGTGTCACAAAAGACCTTACTATGAAAGAGTTCTTTTAT 479
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QY 660 GACTCAGGTACATCTGTGATGAGAAC 686
Db 301 GACTCAGGTACATCTGTGATGAGAAC 327

RESULT 5
US-10-895-393-16
; Sequence 16, Application US/10895393
; Publication No. US20050048549A1
; GENERAL INFORMATION:
; APPLICANT: CAO, Liangxian
; APPLICANT: MEHTA, Anuradha
; APPLICANT: MARSHKIN, Nikolai A.
; APPLICANT: PELISGRINI, Matthew C.
; APPLICANT: ROMEO, Charles M.
; APPLICANT: TRIFILIDS, Panayiota
; APPLICANT: TROTTA, Christopher R.
; TITLE OF INVENTION: Methods and Agents for Screening for Compounds Capable of Modulating

TITLE OF INVENTION: Expression
FILE REFERENCE: 19025.012
CURRENT APPLICATION NUMBER: US/10/895.393
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: PCT/US04/01643
PRIOR FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 60/441,637
PRIOR FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 296
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-895-393-16

Query Match 9.1%; Score 215; DB 10; Length 296;
Best Local Similarity 100.0%; Pred. No. 2.9e-100; Indels 0; Gaps 0;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 129 AGCACCCTGCTCCCGGATTTAGTGCCTGAGAGGCGCCAGTGCCTGCGCGAGAGTGG 188
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DB 181 AATGATCCCGAGGCGCCAGGCGTGTGCTTCGCG 215

RESULT 6
US-10-088-144
Sequence 144, Application US/10211088
Publication No. US20030104479A1
GENERAL INFORMATION:
APPLICANT: Bright, Gary R.
APPLICANT: Premkumar, D. David
APPLICANT: Chen, Yih-Tai
TITLE OF INVENTION: No. US20030104479A1e1 Fusion Proteins And Assays For Molecular B
FILE REFERENCE: 01-1022-US
CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/309,395
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/341,589
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn version 3.1
SEQ ID NO 144
LENGTH: 176
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence encoding binding domain
US-10-211-088-144

Query Match 7.4%; Score 176; DB 6; Length 176;
Best Local Similarity 100.0%; Pred. No. 5.4e-80; Indels 0; Gaps 0;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 ATGACTAAAGCATATATGATGAGAACCAACATATTTGATATTTGTCATATGATCTT 120
QY 555 CTAGAGATTTGTTTGGCGTGCAGAGCTTCTGTGTAAGACACAGAAATATA 610
DB 121 CTAGAGATTTGTTTGGCGTGCAGAGCTTCTGTGTAAGACACAGAAATATA 176

RESULT 7
US-10-007-926A-120
Sequence 120, Application US/10007926A
Publication No. US20030143539A1
GENERAL INFORMATION:
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: HOUTGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: FERT, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
FILE REFERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 120
LENGTH: 319
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 5' terminal sequence. mouse double minute 2, gene.
FEATURE:
OTHER INFORMATION: human homolog of, p53-binding protein (MDM2)
NAME/KEY: modified_base
LOCATION: (1)
OTHER INFORMATION: a, t, c or g
FEATURE:
NAME/KEY: modified_base
LOCATION: (278)
OTHER INFORMATION: a, t, c or g
US-10-007-926A-120

Query Match 7.0%; Score 167; DB 7; Length 319;
Best Local Similarity 100.0%; Pred. No. 2.7e-75; Indels 0; Gaps 0;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1773 ACTTATTTCCCTGCTGACCTGCTATTAAGAAATTATATTTCTAATATATTAACCC 1832
DB 2 ACTTATTTCCCTGCTGACCTGCTATTAAGAAATTATATTTCTAATATATTAACCC 61
QY 1833 TAGGAATTTAGACAACCTGAATTTATTCACATATATCAAAAGTGAGAAATGCCCTCAAT 1892
DB 62 TAGGAATTTAGACAACCTGAATTTATTCACATATATCAAAAGTGAGAAATGCCCTCAAT 121
QY 1893 CACATAGATTTCTTCTCTTATGATATATTAATGAACCTTATTTGGTAGTG 1939
DB 122 CACATAGATTTCTTCTCTTATGATATATTAATGAACCTTATTTGGTAGTG 168

RESULT 8
US-10-109-213-1
Sequence 1, Application US/10109213
Publication No. US20020168670A1
GENERAL INFORMATION:
APPLICANT: Becker, David J.
TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
FILE REFERENCE: IBIS0009
CURRENT APPLICATION NUMBER: US/10/109,213
CURRENT FILING DATE: 2002-03-27

```

; PRIOR APPLICATION NUMBER: US/09/200.355
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 199
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-109-213-1

Query Match
Best Local Similarity 77.9%; Pred. No. 2e-65;
Matches 155; Conservative 43; Mismatches 1; Indels 0; Gaps 0

QY 244 GAACTGGGGAGTCTTTAGAGGACCCCGACTCCAGCCGGAAAAACCCGGATGTGAGGA 303
DB 1 GAAACUGGGGAGUCUUGAGGAGACCCCGACUCCAAACGGAAAAACCCGGAGUGGAGGA 60

QY 304 GGAGCGAAATGTGCATATACCAACATGTCTGTACTTATGTGTGCTGTATACCACTCAC 363
DB 61 GGAGGGAATUGUGCAAUACCAACAUUCUGUACCUACUAGUGUGUGUAAACCAACCUACA 120

QY 364 AGATTCCAGCTTCGGAACAAGAGACCCCTGTGTAGACCAAAAGCATTCCTTTGAATTAT 423
DB 121 AGAUTCACAGCTTCGGAACAAGAGACCCCTGTGTAGACCAAAAGCATTCCTTTGAATTAT 180

QY 424 TAAAGTCTGTGTGTGTCACA 442
DB 181 UAAAGUCUGUGUGGACACA 199

RESULT 9
US-10-109-213-2
; Sequence 2, Application US/10109213
; Publication No. US20020168670A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
; FILE REFERENCE: IBIS0009
; CURRENT APPLICATION NUMBER: US/10/109,213
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/09/200,355
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 199
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-109-213-2

Query Match
Best Local Similarity 5.8%; Score 138; DB 6; Length 199;
Matches 102; Conservative 36; Mismatches 0; Indels 0; Gaps 0

QY 305 CAGGCAATGTGCATATACCAACATGTCTGTACTTACTGTAGTGTGCTGTATACCACTCAC 364
DB 62 CAGGCAATGTGCATATACCAACATGTCTGTACTTACTGTAGTGTGCTGTATACCACTCAC 121

QY 365 GATTCGAGCTTCGGAACAAGAGACCCCTGTGTAGACCAAAAGCATTCCTTTGAATTAT 424
DB 122 GATTCGAGCTTCGGAACAAGAGACCCCTGTGTAGACCAAAAGCATTCCTTTGAATTAT 181

QY 425 AAAGTCTGTGTGTGTCACA 442
DB 182 AAAGUCUGUGUGGACACA 199

RESULT 10
US-10-822-254-11
; Sequence 11, Application US/10822254
; Publication No. US20050037383A1
; GENERAL INFORMATION:

```

APPLICANT: Taremi, S S
 APPLICANT: Xie, Gaolian
 APPLICANT: Hesson, Thomas E
 APPLICANT: Ducca, Jose S
 APPLICANT: Strickland, Corey
 APPLICANT: Windsor, William
 APPLICANT: Madison, Vincent
 APPLICANT: Zhang, Rumlin
 APPLICANT: Reichert, Paul
 TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Meth
 FILE REFERENCE: JB06017US01
 CURRENT APPLICATION NUMBER: US/10/822,254
 CURRENT FILING DATE: 2004-04-09
 PRIOR APPLICATION NUMBER: US 60/461,787
 PRIOR FILING DATE: 2003-04-10
 PRIOR APPLICATION NUMBER: US 60/547,265
 PRIOR FILING DATE: 2004-02-24
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 11
 LENGTH: 327
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-822-254-11

Query Match 4.6%; Score 109; DB 9; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4e-45;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 578 AAGCTTCTGTGMAAGACAGAGAAATATATACCATGATCTACAGAACTTGTAAGT 637
 DB 219 AAGCTTCTGTGMAAGACAGAGAAATATATACCATGATCTACAGAACTTGTAAGT 278

QY 638 AGTCATCGACAGGAATCATCGACTCGATCATCTGTGAGTAGAAGC 686
 DB 279 AGTCATCGACAGGAATCATCGACTCGATCATCTGTGAGTAGAAGC 327

RESULT 11
 US-09-960-706-717
 Sequence 717, Application US/09960706
 Publication No. US20030134280A1
 GENERAL INFORMATION:
 APPLICANT: Mungen, William E.
 TITLE OF INVENTION: Identifying Drugs for and diagnosis of Benign Prostatic Hyperplae
 FILE REFERENCE: 44921-5029-01US
 CURRENT APPLICATION NUMBER: US/09/960,706
 CURRENT FILING DATE: 2001-09-24
 PRIOR APPLICATION NUMBER: 60/223,323
 PRIOR FILING DATE: 2000-08-07
 PRIOR APPLICATION NUMBER: 09/873,319
 PRIOR FILING DATE: 2001-06-05
 NUMBER OF SEQ ID NOS: 1124
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 717
 LENGTH: 385
 TYPE: DNA
 ORGANISM: Homo sapiens
 OTHER INFORMATION: Genbank Accession No. US20030134280A1 N20967
 US-09-960-706-717

Query Match 4.0%; Score 94; DB 3; Length 385;
 Best Local Similarity 100.0%; Pred. No. 2.6e-37;
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGGTTAGACGAGATGTCTCGATCTCTGACCTCGATCGCCACCTC 2333
 DB 13 GGGTTTACCGGTTAGACGAGATGTCTCGATCTCTGACCTCGATCGCCACCTC 72

2334 GGGTTTACCGGTTAGACGAGATGTCTCGATCTCTGACCTCGATCGCCACCTC 2367

Db 73 GGCTCCCAAGTGTGGATTACAGGATGAGC 106

RESULT 12

US-11-124-367A-27407/c
; Sequence 27407, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: C001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27407
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-27407

Query Match 3.8%; Score 91; DB 16; Length 201;

Best Local Similarity 100.0%; Pred. No. 9,1e-36;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2282 CCGTTTACCGAGATGTCGATCTCTGACCTCGTGCATCCGCCACTTCGGCTTCCC 2341

Db 100 CCGTTTACCGAGATGTCGATCTCTGACCTCGTGCATCCGCCACTTCGGCTTCCC 41

Qy 2342 AAAGTGTGGATTACAGGATGAGCCG 2372

Db 40 AAAGTGTGGATTACAGGATGAGCCG 10

RESULT 13

US-11-124-367A-27362/c
; Sequence 27362, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: C001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27362
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-27362

Query Match 3.7%; Score 88; DB 16; Length 201;

Best Local Similarity 100.0%; Pred. No. 3,3e-34;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2285 TGTTAGCCAGAGTGTCTGATCTCTGACCTGATTCGCCACCTCGGCTTCCCAA 2344

Db 100 TGTTAGCCAGAGTGTCTGATCTCTGACCTGATTCGCCACCTCGGCTTCCCAA 41

Qy 2345 GTGCTGGATTACAGGATGAGCCG 2372

Db 40 GTGCTGGATTACAGGATGAGCCG 13

RESULT 14

US-09-764-877-2621
; Sequence 2621, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2621
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2621

Query Match 3.7%; Score 88; DB 3; Length 309;

Best Local Similarity 100.0%; Pred. No. 3,4e-34;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2274 GGGTTTACCGTGTAGCCAGATGTCGATCTCTGACCTCGTGCATCCGCCACTTC 2333

Db 200 GGGTTTACCGTGTAGCCAGATGTCGATCTCTGACCTCGTGCATCCGCCACTTC 259

Qy 2334 GGCTCCCAAGTGTGGATTACAGGC 2361

Db 260 GGCTCCCAAGTGTGGATTACAGGC 287

RESULT 15

US-10-242-515-2621
; Sequence 2621, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031

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/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2621
/ LENGTH: 309
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-242-515-2621

Query Match
Best Local Similarity 100.0%; Score 88; DB 7; Length 309;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCCAGATGATCTCTGACCTCGATCCGCCACCTC 2333
DB 200 GGGTTTACCGTGTAGCCAGATGATCTCTGACCTCGATCCGCCACCTC 259
QY 2334 GGGCTCCCAAAGCTGCGGATTTACAGGC 2361
DB 260 GGGCTCCCAAAGCTGCGGATTTACAGGC 287

RESULT 16
US-11-124-367A-27363/C
/ Sequence 27363, Application US/11124367A
/ Publication No. US20060024700A1
/ GENERAL INFORMATION:
/ APPLICANT: Michele Cargill
/ APPLICANT: Hongjin Huang
/ TITLE OF INVENTION: Genetic Polymorphisms Associated with
/ FILE REFERENCE: CL001519.ORD
/ CURRENT APPLICATION NUMBER: US/11/124,367A
/ PRIOR FILING DATE: 2005-05-09
/ PRIOR APPLICATION NUMBER: US 60/568,846
/ PRIOR FILING DATE: 2004-05-07
/ PRIOR APPLICATION NUMBER: US 60/582,609
/ PRIOR FILING DATE: 2004-06-25
/ PRIOR APPLICATION NUMBER: US 60/599,554
/ PRIOR FILING DATE: 2004-08-09
/ NUMBER OF SEQ ID NOS: 34460
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 27363
/ LENGTH: 201
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-124-367A-27363

Query Match
Best Local Similarity 100.0%; Score 83; DB 16; Length 201;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGATGTTCTGATCTCTGACCTCGATCCGCCACCTCGGCTCCCAAAGTCT 2349
DB 100 GCCAGATGTTCTGATCTCTGACCTCGATCCGCCACCTCGGCTCCCAAAGTCT 41
QY 2350 GGGATTACAGGATGAGCCACCG 2372
DB 40 GGGATTACAGGATGAGCCACCG 18

RESULT 17
US-09-925-065A-472406/C
/ Sequence 472406, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
```

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/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 472406
/ LENGTH: 285
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-472406

Query Match
Best Local Similarity 100.0%; Score 82; DB 4; Length 285;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGATGATCTCTGACCTCGTATCCGCCACCTCGGCTC 2339
DB 231 CACCGTGTAGCCAGATGATCTCTGACCTCGTATCCGCCACCTCGGCTC 172
QY 2340 CCAAAGTCTGGGATTTACAGGC 2361
DB 171 CCAAAGTCTGGGATTTACAGGC 150

RESULT 18
US-09-925-065A-472407/C
/ Sequence 472407, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 472407
/ LENGTH: 285
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-472407

Query Match
Best Local Similarity 100.0%; Score 82; DB 4; Length 285;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGATGATCTCTGACCTCGTATCCGCCACCTCGGCTC 2339
DB 231 CACCGTGTAGCCAGATGATCTCTGACCTCGTATCCGCCACCTCGGCTC 172
QY 2340 CCAAAGTCTGGGATTTACAGGC 2361
DB 171 CCAAAGTCTGGGATTTACAGGC 150

RESULT 19
US-09-925-065A-472406/C
/ Sequence 472406, Application US/09925065A
```

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Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIORITY APPLICATION NUMBER: US 60/243,096
PRIORITY FILING DATE: 2000-10-24
PRIORITY APPLICATION NUMBER: US 60/252,147
PRIORITY FILING DATE: 2000-11-20
PRIORITY APPLICATION NUMBER: US 60/250,092
PRIORITY FILING DATE: 2000-11-30
PRIORITY APPLICATION NUMBER: US 60/261,766
PRIORITY FILING DATE: 2001-01-16
PRIORITY APPLICATION NUMBER: US 60/289,846
PRIORITY FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 472406
LENGTH: 285
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-472406

Query Match 3.5%; Score 82; DB 5; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.5e-31;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2280 CACCGTGTACCCAGATGCTCGATCTCTGACCTCGATCCGCCACCTGGCCTC 2339
|||
Db 231 CACCGTGTACCCAGATGCTCGATCTCTGACCTCGATCCGCCACCTGGCCTC 172

OY 2340 CCAAAGTCTGGATTTACAGC 2361
|||
Db 171 CCAAAGTCTGGATTTACAGC 150

RESULT 20
US-09-925-065A-472407/C
Sequence 472407, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIORITY APPLICATION NUMBER: US 60/243,096
PRIORITY FILING DATE: 2000-10-24
PRIORITY APPLICATION NUMBER: US 60/252,147
PRIORITY FILING DATE: 2000-11-20
PRIORITY APPLICATION NUMBER: US 60/250,092
PRIORITY FILING DATE: 2000-11-30
PRIORITY APPLICATION NUMBER: US 60/261,766
PRIORITY FILING DATE: 2001-01-16
PRIORITY APPLICATION NUMBER: US 60/289,846
PRIORITY FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 472407
LENGTH: 285
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-472407

Query Match 3.5%; Score 82; DB 5; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.5e-31;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2280 CACCGTGTACCCAGATGCTCGATCTCTGACCTCGATCCGCCACCTGGCCTC 2339
|||
Db 231 CACCGTGTACCCAGATGCTCGATCTCTGACCTCGATCCGCCACCTGGCCTC 172

OY 2340 CCAAAGTCTGGATTTACAGC 2361
|||
Db 171 CCAAAGTCTGGATTTACAGC 150


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Db      231 CACCGTGTGACGAGATGATCTCGATCTCTGATCCGTGATCCGCCACCTCGGCTC 172
QY      2340 CCAAGTGCTGGGATTACAGGC 2361
        |||||
        |||||
Db      171 CCAAGTGCTGGGATTACAGGC 150

RESULT 21
US-11-124-367A-27364/c
; Sequence 27364, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: C1001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27364
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-27364

Query Match      3.2%; Score 77; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 1,7e-28;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2286 ATGCTCTGATCTCTGATCTGATCTCGGACCTCGGCTCCCAAGTCTGGGATT 2355
        |||||
        |||||
Db      100 ATGCTCTGATCTCTGATCTGATCTCGGACCTCGGATCCGCCACCTCGGCTCCCAAGTCTGGGATT 41

QY      2356 ACAGGATGAGCCACCG 2372
        |||||
        |||||
Db      40 ACAGGATGAGCCACCG 24

RESULT 22
US-09-925-065A-567530
; Sequence 567530, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 567530
; LENGTH: 340
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-09-925-065A-567530

Query Match
Best Local Similarity 100.0%; Score 77; DB 4; Length 340;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGCTCTGATCTCTGACCTGCTGATCGCCACCTCGGCTCCCAAA 2344
DB 55 TGTAGCCAGATGCTCTGATCTCTGACCTGCTGATCGCCACCTCGGCTCCCAAA 114
QY 2345 GTGCTGGATTACAGGC 2361
DB 115 GTGCTGGATTACAGGC 131

RESULT 23
US-09-925-065A-567530
; Sequence 567530, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 567530
; LENGTH: 340
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-567530

Query Match
Best Local Similarity 3.2%; Score 77; DB 5; Length 340;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGCTCTGATCTCTGACCTGCTGATCGCCACCTCGGCTCCCAAA 2344
DB 55 TGTAGCCAGATGCTCTGATCTCTGACCTGCTGATCGCCACCTCGGCTCCCAAA 114
QY 2345 GTGCTGGATTACAGGC 2361
DB 115 GTGCTGGATTACAGGC 131

RESULT 24
US-10-674-124A-17487
; Sequence 17487, Application US/10674124A
; Publication No. US20040197979A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMAYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATTELLITE
; FILE REFERENCE: ORIN-003C1P
; CURRENT APPLICATION NUMBER: US/10/674,124A
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621

; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 17487
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: chr11.fa.07frz.71465096
; FEATURE:
; OTHER INFORMATION: Located on chromosome 11
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosome short arm and 5'-terminus of this base
; FEATURE:
; OTHER INFORMATION: sequence : 57058295
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 247203
US-10-674-124A-17487

Query Match
Best Local Similarity 3.2%; Score 77; DB 9; Length 427;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGATGCTCTGATCTCTGACCTGCTGATCGCCACCTCGGCTCCCAAA 2344
DB 255 TGTAGCCAGATGCTCTGATCTCTGACCTGCTGATCGCCACCTCGGCTCCCAAA 314
QY 2345 GTGCTGGATTACAGGC 2361
DB 315 GTGCTGGATTACAGGC 331

RESULT 25
US-09-925-065A-231416/c
; Sequence 231416, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231416
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-231416

Query Match
Best Local Similarity 3.2%; Score 76; DB 4; Length 461;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGATGCTCTGATCTCTGACCTGCTGATCGCCACCTCGGCTCCCAAG 2345
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Db      245 GTTAGCCAGATGTCTCGATCTCTGACCTCGATCCGCCCACTCGGCTCCCAAG 186
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Oy      2346 TGCTGGATTACAGGC 2361
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Db      185 TGCTGGATTACAGGC 170
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RESULT 26

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US-09-925-065A-231416/c
; Sequence 231416, Application US/09925065A
; Publication No. US2005028172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231416
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-231416
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Query Match      3.2%; Score 76; DB 5; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.1e-28;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      2286 GTTAGCCAGATGTCTCGATCTCTGACCTCGATCCGCCCACTCGGCTCCCAAG 2345
      |||
Db      245 GTTAGCCAGATGTCTCGATCTCTGACCTCGATCCGCCCACTCGGCTCCCAAG 186
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Oy      2346 TGCTGGATTACAGGC 2361
      |||
Db      185 TGCTGGATTACAGGC 170
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RESULT 27

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US-10-301-480-314882/c
; Sequence 314882, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 314882
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-314882
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Query Match      3.2%; Score 76; DB 12; Length 469;
Best Local Similarity 100.0%; Pred. No. 6.1e-28;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      2286 GTTAGCCAGATGTCTCGATCTCTGACCTCGATCCGCCCACTCGGCTCCCAAG 2345
      |||
Db      245 GTTAGCCAGATGTCTCGATCTCTGACCTCGATCCGCCCACTCGGCTCCCAAG 186
```

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Oy      2346 TGCTGGATTACAGGC 2361
      |||
Db      185 TGCTGGATTACAGGC 170
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RESULT 28

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US-10-301-480-928291/c
; Sequence 928291, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 928291
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-928291
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Query Match      3.2%; Score 76; DB 12; Length 469;
Best Local Similarity 100.0%; Pred. No. 6.1e-28;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      2286 GTTAGCCAGATGTCTCGATCTCTGACCTCGATCCGCCCACTCGGCTCCCAAG 2345
      |||
Db      245 GTTAGCCAGATGTCTCGATCTCTGACCTCGATCCGCCCACTCGGCTCCCAAG 186
```

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Oy      2346 TGCTGGATTACAGGC 2361
      |||
Db      185 TGCTGGATTACAGGC 170
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RESULT 29

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US-09-541-848-49/c
; Sequence 49, Application US/09541848
; Publication No. US20030119765A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, Jiandong
; APPLICANT: AGRAWAL, Sudhir
; APPLICANT: ZHANG, Ruiwen
; TITLE OF INVENTION: MD-M2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 29924/98057C
; CURRENT APPLICATION NUMBER: US/09/541,848
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 09/383,507
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/073,567
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 08/916,834
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentm Ver. 2.0
; SEQ ID NO 49
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; SEQ ID NO 1267
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1267

Query Match 3.0%; Score 72; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGATGCTCTGATCTCTGACCTGCTGATCCGCCACCTGGCCTCCCAAGTCT 2349
DB 217 GCCAGATGCTCTGATCTCTGACCTGCTGATCCGCCACCTGGCCTCCCAAGTCT 276

QY 2350 GGGATTACAGGC 2361
DB 277 GGGATTACAGGC 288

RESULT 34

US-10-092-154-1267
; Sequence 1267, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1267
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1267

Query Match 3.0%; Score 72; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 7.2e-26;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGATGCTCTGATCTCTGACCTGCTGATCCGCCACCTGGCCTCCCAAGTCT 2349
DB 217 GCCAGATGCTCTGATCTCTGACCTGCTGATCCGCCACCTGGCCTCCCAAGTCT 276

QY 2350 GGGATTACAGGC 2361
DB 277 GGGATTACAGGC 288

RESULT 35

US-10-074-024-601/c
; Sequence 601, Application US/10074024
; Publication No. US20030232975A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC001C1
; CURRENT APPLICATION NUMBER: US/10/074,024
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 879
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 601
; LENGTH: 181
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-074-024-601

Query Match 2.9%; Score 69; DB 7; Length 181;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGGTTTACCGTTTACCGAGATGCTCTGACCTGCT 2319
DB 129 TTTTAGTAGAGACAGGGTTTACCGTTTACCGAGATGCTCTGACCTGCT 70
QY 2320 GATCCGCC 2328
DB 69 GATCCGCC 61

RESULT 36

US-10-741-601-19428/c
; Sequence 19428, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19428
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-19428

Query Match 2.9%; Score 69; DB 8; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGGTTTACCGTTTACCGAGATGCTCTGACCTGCT 2319
DB 186 TTTTAGTAGAGACAGGGTTTACCGTTTACCGAGATGCTCTGACCTGCT 127

QY 2320 GATCCGCC 2328
DB 126 GATCCGCC 118

RESULT 37

US-10-741-600-53227/c
; Sequence 53227, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53227
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-53227

Query Match 2.9%; Score 69; DB 9; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGGTTTACCGTTTACCGAGATGCTCTGACCTGCT 2319
DB 186 TTTTAGTAGAGACAGGGTTTACCGTTTACCGAGATGCTCTGACCTGCT 127

QY 2320 GATCCGCC 2328
DB 126 GATCCGCC 118

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RESULT 38
US-09-764-847-1418/c
; Sequence 1418, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1418
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1418

Query Match
Best Local Similarity 100.0%; Score 69; DB 3; Length 293;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGAGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 2319
DB 115 TTTTAGTAGAGACAGGAGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 56
QY 2320 GATCCGCC 2328
DB 55 GATCCGCC 47

RESULT 39
US-09-764-891-7947
; Sequence 7947, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7947
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7947

Query Match
Best Local Similarity 100.0%; Score 69; DB 3; Length 293;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGAGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 2319
DB 179 TTTTAGTAGAGACAGGAGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 238
QY 2320 GATCCGCC 2328
DB 239 GATCCGCC 247

RESULT 40
US-09-764-891-8222
; Sequence 8222, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
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; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8222
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8222

Query Match
Best Local Similarity 100.0%; Score 69; DB 3; Length 293;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGAGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 2319
DB 179 TTTTAGTAGAGACAGGAGGTTTCACCGTGTAGCCAGAGATGTCGATCTCTGACCTCGT 238
QY 2320 GATCCGCC 2328
DB 239 GATCCGCC 247
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Search completed: August 4, 2006, 14:32:15
Job time : 2567 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 20:43:09 ; Search time 499 Seconds
(without alignments)
7528.771 Million cell updates/sec

Title: US-09-966-724B-2

Perfect score: 2372

Sequence: 1 GCACCGCGCAGAGCTTGCTG.....ATTACAGCATGACGACCG 2372

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Gapop 60.0 , Gapext 60.0

Searched: 2193277 seqs, 791917567 residues

Word size : 1

Total number of hits satisfying chosen parameters: 3365896

Minimum DB seq length: 5

Maximum DB seq length: 500

Post-processing: Listing first 1000 summaries

Database : Published Applications NA New:*

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3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEM_PUB_seq.*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEM_PUB_seq.*
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7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEM_PUB_seq.*
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9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEM_PUB_seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	166	7.0	437	US-11-266-748A-7936	Sequence 7936, App
2	157	6.6	364	US-11-266-748A-60150	Sequence 60150, A
3	55	2.3	428	US-11-266-748A-57794	Sequence 57794, A
4	50	2.1	50	US-10-511-937-283	Sequence 283, App
5	50	2.1	474	US-11-266-748A-60447	Sequence 60447, A
6	44	1.9	500	US-11-266-748A-21382	Sequence 21382, A
7	43	1.8	438	US-11-266-748A-50804	Sequence 50804, A
8	43	1.8	434	US-11-266-748A-21936	Sequence 21936, A
9	43	1.8	444	US-11-266-748A-31940	Sequence 31940, A
10	42	1.8	463	US-11-266-748A-23062	Sequence 23062, A
11	42	1.8	463	US-11-266-748A-46391	Sequence 46391, A
12	40	1.7	349	US-11-327-124A-215	Sequence 215, App
13	39	1.6	245	US-11-266-748A-217154	Sequence 217154, A
14	39	1.6	359	US-11-266-748A-414670	Sequence 414670, A
15	38	1.6	455	US-11-266-748A-61942	Sequence 61942, A
16	38	1.6	464	US-11-266-748A-61449	Sequence 61449, A
17	38	1.6	486	US-11-266-748A-21711	Sequence 21711, A
18	38	1.6	486	US-11-266-748A-23850	Sequence 23850, A
19	37	1.6	224	US-11-266-748A-170884	Sequence 170884, A
20	37	1.6	355	US-11-301-554-749	Sequence 749, App
21	37	1.6	425	US-11-266-748A-208969	Sequence 208969, A
22	37	1.6	437	US-11-266-748A-50353	Sequence 50353, A
23	37	1.6	461	US-11-266-748A-211874	Sequence 211874, A
24	37	1.6	461	US-11-266-748A-235428	Sequence 235428, A

C 25	36	1.5	50	6	US-10-554-711-12	Sequence 12, App1
C 26	36	1.5	50	6	US-10-554-711-17	Sequence 17, App1
C 27	36	1.5	50	6	US-10-554-711-24	Sequence 24, App1
C 28	36	1.5	50	6	US-10-554-711-26	Sequence 26, App1
C 29	36	1.5	50	6	US-10-554-711-29	Sequence 29, App1
C 30	36	1.5	50	6	US-10-554-711-27	Sequence 27, App1
C 31	36	1.5	50	6	US-10-554-711-30	Sequence 30, App1
C 32	36	1.5	213	8	US-11-266-748A-40751	Sequence 40751, A
C 33	36	1.5	335	8	US-11-266-748A-35463	Sequence 35463, A
C 34	36	1.5	335	8	US-11-266-748A-43802	Sequence 43802, A
C 35	36	1.5	448	8	US-11-266-748A-40654	Sequence 40654, A
C 36	36	1.5	462	8	US-11-266-748A-48475	Sequence 48475, A
C 37	36	1.5	474	8	US-11-266-748A-60828	Sequence 60828, A
C 38	35	1.5	50	6	US-10-554-711-13	Sequence 13, App1
C 39	35	1.5	50	6	US-10-554-711-25	Sequence 25, App1
C 40	35	1.5	50	6	US-10-554-711-32	Sequence 32, App1
C 41	35	1.5	50	6	US-10-554-711-33	Sequence 33, App1
C 42	35	1.5	432	7	US-11-195-344-1	Sequence 1, App1
C 43	35	1.5	432	7	US-11-195-344-205	Sequence 205, App
C 44	35	1.5	452	7	US-11-195-344-257	Sequence 257, App
C 45	35	1.5	454	8	US-11-266-748A-208180	Sequence 208180, A
C 46	34	1.4	241	8	US-11-266-748A-658	Sequence 658, App
C 47	34	1.4	403	6	US-10-488-619-441	Sequence 441, App
C 48	34	1.4	406	8	US-11-266-748A-60844	Sequence 60844, A
C 49	34	1.4	500	8	US-11-266-748A-182520	Sequence 182520, A
C 50	34	1.4	500	8	US-11-266-748A-243061	Sequence 243061, A
C 51	33	1.4	33	6	US-10-511-937-2350	Sequence 2350, App
C 52	33	1.4	259	8	US-11-266-748A-45464	Sequence 45464, A
C 53	33	1.4	281	8	US-11-266-748A-390684	Sequence 390684, A
C 54	33	1.4	401	8	US-11-266-748A-481402	Sequence 481402, A
C 55	33	1.4	444	8	US-11-266-748A-21894	Sequence 21894, A
C 56	33	1.4	444	8	US-11-266-748A-352411	Sequence 352411, A
C 57	33	1.4	466	8	US-11-266-748A-372197	Sequence 372197, A
C 58	33	1.4	466	8	US-11-266-748A-455276	Sequence 455276, A
C 59	33	1.4	467	8	US-11-266-748A-258804	Sequence 258804, A
C 60	33	1.4	467	8	US-11-266-748A-378659	Sequence 378659, A
C 61	33	1.4	467	8	US-11-266-748A-319321	Sequence 319321, A
C 62	33	1.4	491	8	US-11-266-748A-319555	Sequence 319555, A
C 63	33	1.4	491	8	US-11-266-748A-239494	Sequence 239494, A
C 64	33	1.4	291	8	US-11-266-748A-210345	Sequence 210345, A
C 65	32	1.3	363	8	US-11-266-748A-219570	Sequence 219570, A
C 66	32	1.3	363	8	US-11-266-748A-239499	Sequence 239499, A
C 67	32	1.3	371	6	US-10-533-365-67	Sequence 67, App1
C 68	32	1.3	427	8	US-11-266-748A-208464	Sequence 208464, A
C 69	32	1.3	427	8	US-11-266-748A-233625	Sequence 233625, A
C 70	32	1.3	444	8	US-11-266-748A-57844	Sequence 57844, A
C 71	32	1.3	453	8	US-11-266-748A-215396	Sequence 215396, A
C 72	32	1.3	454	8	US-11-266-748A-218625	Sequence 218625, A
C 73	32	1.3	456	8	US-11-266-748A-40897	Sequence 40897, A
C 74	32	1.3	456	8	US-11-266-748A-216622	Sequence 216622, A
C 75	32	1.3	461	8	US-11-266-748A-48548	Sequence 48548, A
C 76	32	1.3	462	6	US-10-473-173-180	Sequence 180, App
C 77	32	1.3	470	8	US-11-266-748A-21426	Sequence 21426, A
C 78	32	1.3	494	7	US-11-327-124A-16	Sequence 16, App1
C 79	32	1.3	498	8	US-11-266-748A-317267	Sequence 317267, A
C 80	32	1.3	498	8	US-11-266-748A-238575	Sequence 238575, A
C 81	32	1.3	499	8	US-11-266-748A-212638	Sequence 212638, A
C 82	32	1.3	499	8	US-11-266-748A-236022	Sequence 236022, A
C 83	32	1.3	499	8	US-11-266-748A-350940	Sequence 350940, A
C 84	31	1.3	246	8	US-11-266-748A-434319	Sequence 434319, A
C 85	31	1.3	295	8	US-11-266-748A-282201	Sequence 282201, A
C 86	31	1.3	295	8	US-11-266-748A-308841	Sequence 308841, A
C 87	31	1.3	295	8	US-11-266-748A-391453	Sequence 391453, A
C 88	31	1.3	295	8	US-11-266-748A-482171	Sequence 482171, A
C 89	31	1.3	295	8	US-11-266-748A-214906	Sequence 214906, A
C 90	31	1.3	380	8	US-11-266-748A-48852	Sequence 48852, A
C 91	31	1.3	459	8	US-11-301-554-884	Sequence 884, App
C 92	31	1.3	461	8	US-11-266-748A-215552	Sequence 215552, A
C 93	31	1.3	468	8	US-11-266-748A-211933	Sequence 211933, A
C 94	31	1.3	489	8	US-11-266-748A-53648	Sequence 53648, A
C 95	31	1.3	500	8	US-11-266-748A-218469	Sequence 218469, A
C 96	31	1.3	500	8	US-11-266-748A-239991	Sequence 239991, A
C 97	31	1.3	500	8	US-11-266-748A-239991	Sequence 239991, A

98	30	1.3	347	6	US-10-505-928-440	Sequence 440, App	c 171	27	1.1	413	8	US-11-266-748A-21229	Sequence 21229, A
99	30	1.3	384	8	US-11-266-748A-210849	Sequence 210849, A	c 172	27	1.1	419	8	US-11-266-748A-60690	Sequence 60690, A
100	30	1.3	391	8	US-11-301-554-173	Sequence 173, App	c 173	27	1.1	420	8	US-11-266-748A-217022	Sequence 217022, A
101	30	1.3	419	8	US-11-266-748A-60184	Sequence 60184, A	c 174	27	1.1	424	8	US-11-266-748A-218796	Sequence 218796, A
102	30	1.3	427	8	US-11-266-748A-77564	Sequence 77564, A	c 175	27	1.1	424	8	US-11-266-748A-218796	Sequence 218796, A
103	30	1.3	427	8	US-11-266-748A-109897	Sequence 109897, A	c 176	27	1.1	425	8	US-11-266-748A-212697	Sequence 212697, A
104	30	1.3	427	8	US-11-266-748A-130375	Sequence 130375, A	c 177	27	1.1	428	8	US-11-266-748A-60247	Sequence 60247, A
105	30	1.3	468	8	US-11-266-748A-36523	Sequence 36523, A	c 178	27	1.1	432	8	US-11-266-748A-52846	Sequence 52846, A
106	30	1.3	486	8	US-11-266-748A-37649	Sequence 37649, A	c 179	27	1.1	435	8	US-11-266-748A-21814	Sequence 21814, A
107	30	1.3	486	8	US-11-266-748A-40537	Sequence 40537, A	c 180	27	1.1	435	8	US-11-266-748A-236119	Sequence 236119, A
108	29	1.2	325	8	US-11-266-748A-40530	Sequence 50550, A	c 181	27	1.1	444	8	US-11-266-748A-58121	Sequence 58121, A
109	29	1.2	368	8	US-11-266-748A-211661	Sequence 211661, A	c 182	27	1.1	444	8	US-11-266-748A-219920	Sequence 219920, A
110	29	1.2	368	8	US-11-266-748A-235285	Sequence 235285, A	c 183	27	1.1	444	8	US-11-266-748A-237314	Sequence 237314, A
111	29	1.2	373	8	US-11-266-748A-214041	Sequence 214041, A	c 184	27	1.1	445	8	US-11-266-748A-59073	Sequence 59073, A
112	29	1.2	405	8	US-11-266-748A-302934	Sequence 302934, A	c 185	27	1.1	456	8	US-11-266-748A-175563	Sequence 175563, A
113	29	1.2	411	8	US-11-266-748A-81193	Sequence 81193, A	c 186	27	1.1	460	8	US-11-242-317-5	Sequence 5, App1
114	29	1.2	411	6	US-10-533-365-220	Sequence 134004, A	c 187	27	1.1	461	7	US-11-195-344-243	Sequence 243, App
115	29	1.2	414	6	US-10-533-365-220	Sequence 220, App	c 188	27	1.1	464	8	US-11-266-748A-60549	Sequence 60549, A
116	29	1.2	419	8	US-11-266-748A-212040	Sequence 212040, A	c 189	27	1.1	476	8	US-11-266-748A-212633	Sequence 212633, A
117	29	1.2	461	8	US-11-266-748A-58274	Sequence 58274, A	c 190	27	1.1	478	8	US-11-266-748A-49000	Sequence 49000, A
118	29	1.2	461	6	US-10-488-619-56	Sequence 56, App1	c 191	27	1.1	478	8	US-11-266-748A-209370	Sequence 209370, A
119	29	1.2	479	8	US-11-266-748A-217144	Sequence 217144, A	c 192	27	1.1	494	8	US-11-266-748A-46730	Sequence 46730, A
120	29	1.2	479	8	US-11-266-748A-238515	Sequence 238515, A	c 193	27	1.1	498	8	US-11-266-748A-87607	Sequence 87607, A
121	29	1.2	480	8	US-11-266-748A-89815	Sequence 89815, A	c 194	27	1.1	498	8	US-11-266-748A-140418	Sequence 140418, A
122	29	1.2	480	8	US-11-266-748A-142626	Sequence 14626, A	c 195	27	1.1	498	8	US-11-266-748A-378283	Sequence 378283, A
123	29	1.2	485	8	US-11-266-748A-46131	Sequence 46131, A	c 196	26	1.1	247	8	US-11-266-748A-461662	Sequence 461662, A
124	28	1.2	50	6	US-10-511-937-1606	Sequence 1606, App	c 197	26	1.1	247	8	US-11-266-748A-378283	Sequence 378283, A
125	28	1.2	50	6	US-10-511-937-1606	Sequence 34, App1	c 198	26	1.1	286	8	US-11-266-748A-3875	Sequence 3875, App
126	28	1.2	270	8	US-11-266-748A-6747	Sequence 6747, App	c 199	26	1.1	294	8	US-11-266-748A-268290	Sequence 268290, A
127	28	1.2	287	8	US-11-266-748A-373681	Sequence 373681, A	c 200	26	1.1	294	8	US-11-266-748A-328807	Sequence 328807, A
128	28	1.2	287	8	US-11-266-748A-457060	Sequence 457060, A	c 201	26	1.1	300	6	US-10-501-187-100	Sequence 100, App
129	28	1.2	382	8	US-11-266-748A-213802	Sequence 213802, A	c 202	26	1.1	312	8	US-11-266-748A-180924	Sequence 180924, A
130	28	1.2	382	8	US-11-266-748A-236642	Sequence 236642, A	c 203	26	1.1	315	8	US-11-266-748A-50126	Sequence 50126, A
131	28	1.2	389	8	US-11-266-748A-213068	Sequence 213068, A	c 204	26	1.1	315	8	US-11-266-748A-209585	Sequence 209585, A
132	28	1.2	389	8	US-11-266-748A-336279	Sequence 336279, A	c 205	26	1.1	327	8	US-11-266-748A-266719	Sequence 266719, A
133	28	1.2	390	8	US-11-266-748A-215127	Sequence 215127, A	c 206	26	1.1	327	8	US-11-266-748A-327736	Sequence 327736, A
134	28	1.2	404	8	US-11-266-748A-58419	Sequence 58419, A	c 207	26	1.1	346	8	US-11-266-748A-236571	Sequence 236571, A
135	28	1.2	415	8	US-11-266-748A-213974	Sequence 213974, A	c 208	26	1.1	346	8	US-11-266-748A-359346	Sequence 359346, A
136	28	1.2	421	8	US-11-266-748A-207818	Sequence 207818, A	c 209	26	1.1	360	8	US-11-266-748A-386983	Sequence 386983, A
137	28	1.2	421	8	US-11-266-748A-233233	Sequence 233233, A	c 210	26	1.1	360	8	US-11-266-748A-442725	Sequence 442725, A
138	28	1.2	422	8	US-11-266-748A-217737	Sequence 217737, A	c 211	26	1.1	361	8	US-11-266-748A-3948	Sequence 3948, A
139	28	1.2	424	8	US-11-266-748A-58256	Sequence 58256, A	c 212	26	1.1	383	8	US-11-266-748A-40876	Sequence 40876, A
140	28	1.2	442	8	US-11-266-748A-273829	Sequence 273829, A	c 213	26	1.1	383	8	US-11-266-748A-214760	Sequence 214760, A
141	28	1.2	442	8	US-11-266-748A-33436	Sequence 33436, A	c 214	26	1.1	383	8	US-11-266-748A-237232	Sequence 237232, A
142	28	1.2	450	8	US-11-266-748A-212640	Sequence 212640, A	c 215	26	1.1	386	8	US-11-266-748A-13230	Sequence 13230, A
143	28	1.2	450	8	US-11-266-748A-58829	Sequence 58829, A	c 216	26	1.1	391	8	US-11-266-748A-210466	Sequence 210466, A
144	28	1.2	476	8	US-11-266-748A-40829	Sequence 40829, A	c 217	26	1.1	391	8	US-11-266-748A-58065	Sequence 58065, A
145	28	1.2	486	8	US-11-266-748A-208047	Sequence 208047, A	c 218	26	1.1	412	8	US-11-266-748A-21549	Sequence 21549, A
146	28	1.2	486	8	US-11-266-748A-213159	Sequence 213159, A	c 219	26	1.1	412	8	US-11-266-748A-336501	Sequence 336501, A
147	28	1.2	486	8	US-11-266-748A-233404	Sequence 233404, A	c 220	26	1.1	428	8	US-11-266-748A-207499	Sequence 207499, A
148	28	1.2	491	8	US-11-301-554-1555	Sequence 1155, App	c 221	26	1.1	431	8	US-11-266-748A-60574	Sequence 60574, A
149	28	1.2	495	8	US-11-266-748A-53941	Sequence 53941, A	c 222	26	1.1	431	8	US-11-266-748A-207499	Sequence 207499, A
150	28	1.2	500	8	US-11-266-748A-50716	Sequence 50716, A	c 223	26	1.1	439	8	US-11-266-748A-31504	Sequence 31504, A
151	28	1.2	500	8	US-11-266-748A-210425	Sequence 210425, A	c 224	26	1.1	439	8	US-11-266-748A-237314	Sequence 237314, A
152	28	1.2	500	6	US-10-554-711-20	Sequence 20, App1	c 225	26	1.1	442	8	US-11-266-748A-102866	Sequence 102866, A
153	27	1.1	50	6	US-10-554-711-28	Sequence 414675, A	c 226	26	1.1	442	8	US-11-266-748A-338589	Sequence 338589, A
154	27	1.1	241	8	US-11-266-748A-414675	Sequence 212798, A	c 227	26	1.1	448	8	US-11-266-748A-15577	Sequence 15577, A
155	27	1.1	315	8	US-11-266-748A-212798	Sequence 236111, A	c 228	26	1.1	448	8	US-11-266-748A-463790	Sequence 463790, A
156	27	1.1	327	8	US-11-266-748A-3334	Sequence 3334, App	c 229	26	1.1	449	8	US-11-266-748A-231540	Sequence 231540, A
157	27	1.1	339	8	US-11-266-748A-52131	Sequence 52131, A	c 230	26	1.1	449	8	US-11-266-748A-31504	Sequence 31504, A
158	27	1.1	362	8	US-11-266-748A-26809	Sequence 26809, A	c 231	26	1.1	455	8	US-11-266-748A-315257	Sequence 315257, A
159	27	1.1	362	8	US-11-266-748A-32806	Sequence 32806, A	c 232	26	1.1	455	8	US-11-266-748A-237486	Sequence 237486, A
160	27	1.1	370	8	US-11-266-748A-60139	Sequence 60139, A	c 233	26	1.1	462	8	US-11-266-748A-219920	Sequence 219920, A
161	27	1.1	375	8	US-11-266-748A-50849	Sequence 50849, A	c 234	26	1.1	462	8	US-11-266-748A-463790	Sequence 463790, A
162	27	1.1	375	8	US-11-266-748A-207441	Sequence 207421, A	c 235	26	1.1	463	8	US-11-266-748A-274995	Sequence 274995, A
163	27	1.1	375	8	US-11-266-748A-213248	Sequence 213248, A	c 236	26	1.1	463	8	US-11-266-748A-110957	Sequence 110957, A
164	27	1.1	375	8	US-11-266-748A-233055	Sequence 233055, A	c 237	26	1.1	463	8	US-11-266-748A-55667	Sequence 55667, A
165	27	1.1	386	8	US-11-266-748A-215391	Sequence 215391, A	c 238	26	1.1	469	8	US-11-266-748A-209125	Sequence 209125, A
166	27	1.1	387	6	US-10-533-365-218	Sequence 66, App1	c 239	26	1.1	469	8	US-11-266-748A-37651	Sequence 37651, A
167	27	1.1	392	6	US-10-488-619-66	Sequence 57891, A	c 240	26	1.1	480	8	US-11-266-748A-40254	Sequence 40254, A
168	27	1.1	393	8	US-11-266-748A-57891	Sequence 15579, A	c 241	26	1.1	480	8	US-11-266-748A-40254	Sequence 40254, A
169	27	1.1	413	8	US-11-266-748A-15579	Sequence 15579, A	c 242	26	1.1	480	8	US-11-266-748A-40254	Sequence 40254, A
170	27	1.1	413	8	US-11-266-748A-15579	Sequence 15579, A	c 243	26	1.1	480	8	US-11-266-748A-40254	Sequence 40254, A

C 244	26	1.1	480	8	US-11-266-748A-214608	Sequence 214608, App	C 317	24	1.0	315	8	US-11-266-748A-11209	Sequence 11209, A
C 245	26	1.1	481	8	US-11-301-554-583	Sequence 583, App	C 318	24	1.0	354	8	US-11-266-748A-32890	Sequence 32890, A
C 246	26	1.1	483	8	US-11-266-748A-53226	Sequence 53226, A	C 319	24	1.0	354	8	US-11-266-748A-32890	Sequence 32890, A
C 247	26	1.1	485	8	US-11-266-748A-61092	Sequence 61092, A	C 320	24	1.0	359	8	US-11-266-748A-312752	Sequence 312752, A
C 248	26	1.1	488	8	US-11-266-748A-257204	Sequence 257204, A	C 321	24	1.0	359	8	US-11-266-748A-326084	Sequence 326084, A
C 249	26	1.1	488	8	US-11-266-748A-317721	Sequence 317721, A	C 322	24	1.0	366	8	US-11-266-748A-375648	Sequence 375648, A
C 250	26	1.1	492	8	US-11-266-748A-59023	Sequence 59023, A	C 323	24	1.0	366	8	US-11-266-748A-389587	Sequence 389587, A
C 251	25	1.1	50	6	US-10-554-711-18	Sequence 18, App1	C 324	24	1.0	366	8	US-11-266-748A-459027	Sequence 459027, A
C 252	25	1.1	305	8	US-11-266-748A-373558	Sequence 373558, A	C 325	24	1.0	368	8	US-11-266-748A-356439	Sequence 356439, A
C 253	25	1.1	305	8	US-11-266-748A-456937	Sequence 456937, A	C 326	24	1.0	368	8	US-11-266-748A-316956	Sequence 316956, A
C 254	25	1.1	309	8	US-11-266-748A-377566	Sequence 377566, A	C 327	24	1.0	369	8	US-11-266-748A-49389	Sequence 49389, A
C 255	25	1.1	309	8	US-11-266-748A-460945	Sequence 460945, A	C 328	24	1.0	386	8	US-11-266-748A-209067	Sequence 209067, A
C 256	25	1.1	336	8	US-11-266-748A-217030	Sequence 217030, A	C 329	24	1.0	386	8	US-11-266-748A-33850	Sequence 33850, A
C 257	25	1.1	352	8	US-11-266-748A-207996	Sequence 207996, A	C 330	24	1.0	388	8	US-11-266-748A-373716	Sequence 373716, A
C 258	25	1.1	352	8	US-11-266-748A-233364	Sequence 233364, A	C 331	24	1.0	388	8	US-11-266-748A-457055	Sequence 457055, A
C 259	25	1.1	364	8	US-11-266-748A-268758	Sequence 268758, A	C 332	24	1.0	388	8	US-11-266-748A-457055	Sequence 457055, A
C 260	25	1.1	364	8	US-11-266-748A-339275	Sequence 339275, A	C 333	24	1.0	390	8	US-11-266-748A-38687	Sequence 38687, A
C 261	25	1.1	371	8	US-11-266-748A-255259	Sequence 255259, A	C 334	24	1.0	393	6	US-10-511-937-553	Sequence 583, App
C 262	25	1.1	371	8	US-11-266-748A-315776	Sequence 315776, A	C 335	24	1.0	393	8	US-11-266-748A-40029	Sequence 40029, A
C 263	25	1.1	398	8	US-11-266-748A-35620	Sequence 35620, A	C 336	24	1.0	393	8	US-11-266-748A-212048	Sequence 212048, A
C 264	25	1.1	398	8	US-11-266-748A-40097	Sequence 40097, A	C 337	24	1.0	403	8	US-11-266-748A-59681	Sequence 59681, A
C 265	25	1.1	402	8	US-11-266-748A-40889	Sequence 40889, A	C 338	24	1.0	403	8	US-11-266-748A-48527	Sequence 48527, A
C 266	25	1.1	402	8	US-11-266-748A-269588	Sequence 269588, A	C 339	24	1.0	403	8	US-11-266-748A-48527	Sequence 48527, A
C 267	25	1.1	402	8	US-11-266-748A-330105	Sequence 330105, A	C 340	24	1.0	403	8	US-11-266-748A-41338	Sequence 41338, A
C 268	25	1.1	402	8	US-11-266-748A-354482	Sequence 354482, A	C 341	24	1.0	403	8	US-11-266-748A-215384	Sequence 215384, A
C 269	25	1.1	402	8	US-11-266-748A-437861	Sequence 437861, A	C 342	24	1.0	410	7	US-11-195-344-267	Sequence 237569, A
C 270	25	1.1	406	8	US-11-266-748A-172552	Sequence 172552, A	C 343	24	1.0	410	8	US-11-266-748A-211886	Sequence 267, App
C 271	25	1.1	410	8	US-11-266-748A-36090	Sequence 36090, A	C 344	24	1.0	410	8	US-11-266-748A-35434	Sequence 215866, A
C 272	25	1.1	411	8	US-11-266-748A-217712	Sequence 217712, A	C 345	24	1.0	413	8	US-11-266-748A-37722	Sequence 37722, A
C 273	25	1.1	412	6	US-10-473-173-202	Sequence 202, App	C 346	24	1.0	413	8	US-11-266-748A-30881	Sequence 20881, A
C 274	25	1.1	414	8	US-11-266-748A-14228	Sequence 14228, A	C 347	24	1.0	414	8	US-11-266-748A-233784	Sequence 233784, A
C 275	25	1.1	418	8	US-11-266-748A-210930	Sequence 210930, A	C 348	24	1.0	416	8	US-11-266-748A-265384	Sequence 265384, A
C 276	25	1.1	418	8	US-11-266-748A-234788	Sequence 234788, A	C 349	24	1.0	416	8	US-11-266-748A-272825	Sequence 272825, A
C 277	25	1.1	420	8	US-11-266-748A-217856	Sequence 217856, A	C 350	24	1.0	416	8	US-11-266-748A-28052	Sequence 28052, A
C 278	25	1.1	421	8	US-11-266-748A-207818	Sequence 207818, A	C 351	24	1.0	416	8	US-11-266-748A-28052	Sequence 28052, A
C 279	25	1.1	421	8	US-11-266-748A-233223	Sequence 233223, A	C 352	24	1.0	417	8	US-11-266-748A-333342	Sequence 333342, A
C 280	25	1.1	427	8	US-11-266-748A-60396	Sequence 60396, A	C 353	24	1.0	417	8	US-11-266-748A-60896	Sequence 60896, A
C 281	25	1.1	434	8	US-11-266-748A-13922	Sequence 13922, A	C 354	24	1.0	426	8	US-11-266-748A-427459	Sequence 427459, A
C 282	25	1.1	438	6	US-10-802-875-15	Sequence 15, App1	C 355	24	1.0	435	8	US-11-266-748A-10313	Sequence 10313, A
C 283	25	1.1	438	6	US-10-812-797-15	Sequence 15, App1	C 356	24	1.0	435	8	US-11-266-748A-156124	Sequence 156124, A
C 284	25	1.1	439	8	US-11-266-748A-26508	Sequence 26508, A	C 357	24	1.0	439	8	US-11-266-748A-57856	Sequence 57856, A
C 285	25	1.1	439	8	US-11-266-748A-280430	Sequence 280430, A	C 358	24	1.0	439	8	US-11-266-748A-208475	Sequence 208475, A
C 286	25	1.1	439	8	US-11-266-748A-327025	Sequence 327025, A	C 359	24	1.0	442	8	US-11-266-748A-212715	Sequence 212715, A
C 287	25	1.1	454	8	US-11-266-748A-61325	Sequence 61325, A	C 360	24	1.0	442	8	US-11-266-748A-216435	Sequence 216435, A
C 288	25	1.1	454	8	US-11-266-748A-218434	Sequence 218434, A	C 361	24	1.0	442	8	US-11-266-748A-236067	Sequence 236067, A
C 289	25	1.1	454	8	US-11-266-748A-319080	Sequence 319080, A	C 362	24	1.0	442	8	US-11-266-748A-237167	Sequence 237167, A
C 290	25	1.1	460	8	US-11-266-748A-61850	Sequence 61850, A	C 363	24	1.0	446	8	US-11-266-748A-61962	Sequence 61962, A
C 291	25	1.1	471	8	US-11-266-748A-428919	Sequence 428919, A	C 364	24	1.0	446	8	US-11-266-748A-220128	Sequence 220128, A
C 292	25	1.1	472	8	US-11-266-748A-208501	Sequence 208501, A	C 365	24	1.0	446	8	US-11-266-748A-339797	Sequence 339797, A
C 293	25	1.1	481	8	US-11-266-748A-233640	Sequence 233640, A	C 366	24	1.0	454	6	US-10-488-619-608	Sequence 608, App
C 294	25	1.1	481	8	US-11-266-748A-12285	Sequence 12285, A	C 367	24	1.0	455	8	US-11-266-748A-60597	Sequence 60597, A
C 295	25	1.1	499	8	US-11-266-748A-208770	Sequence 208770, A	C 368	24	1.0	457	8	US-11-266-748A-215260	Sequence 215260, A
C 296	25	1.1	500	8	US-11-266-748A-176746	Sequence 176746, A	C 369	24	1.0	461	8	US-11-266-748A-211845	Sequence 211845, A
C 297	24	1.0	44	7	US-11-320-440-35	Sequence 35, App1	C 370	24	1.0	461	8	US-11-266-748A-219111	Sequence 219111, A
C 298	24	1.0	50	6	US-10-554-711-31	Sequence 31, App1	C 371	24	1.0	463	8	US-11-266-748A-239351	Sequence 239351, A
C 299	24	1.0	50	6	US-11-266-748A-86962	Sequence 86962, A	C 372	24	1.0	469	8	US-11-266-748A-54081	Sequence 54081, A
C 300	24	1.0	132	8	US-11-266-748A-139773	Sequence 139773, A	C 373	24	1.0	469	8	US-11-266-748A-216763	Sequence 216763, A
C 301	24	1.0	134	8	US-11-266-748A-480210	Sequence 480210, A	C 374	24	1.0	473	8	US-11-266-748A-58875	Sequence 58875, A
C 302	24	1.0	134	8	US-11-266-748A-174239	Sequence 174239, A	C 375	24	1.0	475	8	US-11-266-748A-270974	Sequence 270974, A
C 303	24	1.0	142	8	US-11-266-748A-245972	Sequence 245972, A	C 376	24	1.0	475	8	US-11-266-748A-331491	Sequence 331491, A
C 304	24	1.0	161	8	US-11-266-748A-9507	Sequence 9507, App	C 377	24	1.0	479	8	US-11-266-748A-365710	Sequence 365710, A
C 305	24	1.0	161	8	US-11-266-748A-3507	Sequence 3507, App	C 378	24	1.0	479	8	US-11-266-748A-449089	Sequence 449089, A
C 306	24	1.0	175	8	US-11-266-748A-530	Sequence 530, App	C 379	24	1.0	481	8	US-11-266-748A-61447	Sequence 61447, A
C 307	24	1.0	197	8	US-11-266-748A-156892	Sequence 156892, A	C 380	24	1.0	484	8	US-11-266-748A-50263	Sequence 50263, A
C 308	24	1.0	211	8	US-11-266-748A-303706	Sequence 303706, A	C 381	24	1.0	484	8	US-11-266-748A-58439	Sequence 58439, A
C 309	24	1.0	238	8	US-11-266-748A-7811	Sequence 7811, App	C 382	24	1.0	496	8	US-11-266-748A-35661	Sequence 35661, A
C 310	24	1.0	246	8	US-11-266-748A-171099	Sequence 171099, A	C 383	24	1.0	497	8	US-11-266-748A-429915	Sequence 429915, A
C 311	24	1.0	246	8	US-11-266-748A-245260	Sequence 245260, A	C 384	24	1.0	500	8	US-11-266-748A-211962	Sequence 211962, A
C 312	24	1.0	278	8	US-11-266-748A-31915	Sequence 31915, A	C 385	24	1.0	500	8	US-11-266-748A-235493	Sequence 235493, A
C 313	24	1.0	278	8	US-11-266-748A-31915	Sequence 31915, A	C 386	24	1.0	23	6	US-10-511-937-1854	Sequence 1854, App
C 314	24	1.0	295	8	US-11-266-748A-378979	Sequence 378979, A	C 387	23	1.0	23	7	US-11-320-440-123	Sequence 123, App
C 315	24	1.0	295	8	US-11-266-748A-378979	Sequence 378979, A	C 388	23	1.0	212	8	US-11-266-748A-391857	Sequence 391857, A
C 316	24	1.0	295	8	US-11-266-748A-462358	Sequence 462358, A	C 389	23	1.0	212	8	US-11-266-748A-482575	Sequence 482575, A

390	23	1.0	267	7	US-11-195-344-245	Sequence 245, App	463	23	1.0	489	8	US-11-266-748A-208092	Sequence 208092,
391	23	1.0	300	8	US-11-266-748A-179736	Sequence 179736,	464	23	1.0	489	8	US-11-266-748A-234446	Sequence 233446,
392	23	1.0	330	8	US-11-266-748A-210257	Sequence 210257,	465	23	1.0	492	8	US-11-266-748A-40655	Sequence 40655, A
393	23	1.0	330	8	US-11-266-748A-234503	Sequence 234503,	466	23	1.0	494	8	US-11-266-748A-216594	Sequence 216594
394	23	1.0	332	8	US-11-266-748A-103943	Sequence 103943,	467	23	1.0	495	8	US-11-266-748A-16531	Sequence 16531, A
395	23	1.0	332	8	US-11-266-748A-156754	Sequence 156754,	468	23	1.0	499	7	US-11-327-124A-95	Sequence 95, App1
396	23	1.0	363	8	US-11-266-748A-208511	Sequence 208511,	469	23	1.0	500	8	US-11-266-748A-60541	Sequence 60541, A
397	23	1.0	363	8	US-11-266-748A-215102	Sequence 215102,	470	23	1.0	500	8	US-11-266-748A-207879	Sequence 207879
398	23	1.0	363	8	US-11-266-748A-237416	Sequence 237416,	471	23	1.0	500	8	US-11-266-748A-208052	Sequence 208052,
399	23	1.0	364	8	US-11-266-748A-50167	Sequence 50167, A	472	23	1.0	500	8	US-11-266-748A-208463	Sequence 208463,
400	23	1.0	374	8	US-11-266-748A-34252	Sequence 34252, A	473	23	1.0	500	8	US-11-266-748A-233269	Sequence 233269,
401	23	1.0	380	8	US-11-266-748A-59771	Sequence 59771, A	474	23	1.0	500	8	US-11-266-748A-233409	Sequence 233409,
402	23	1.0	381	8	US-11-266-748A-272697	Sequence 272697,	475	23	1.0	500	8	US-11-266-748A-233624	Sequence 233624,
403	23	1.0	381	8	US-11-266-748A-333214	Sequence 333214,	476	23	1.0	500	8	US-11-266-748A-419449	Sequence 419449,
404	23	1.0	386	8	US-11-301-554-1620	Sequence 1620, Ap	477	22	0.9	22	7	US-11-320-440-299	Sequence 299, App
405	23	1.0	393	8	US-11-266-748A-57906	Sequence 57906, A	478	22	0.9	60	7	US-11-320-440-167	Sequence 167, App
406	23	1.0	400	8	US-11-266-748A-59300	Sequence 59300, A	479	22	0.9	135	8	US-11-266-748A-375337	Sequence 375337,
407	23	1.0	400	8	US-11-266-748A-212986	Sequence 212986,	480	22	0.9	135	8	US-11-266-748A-458716	Sequence 458716,
408	23	1.0	400	8	US-11-266-748A-220108	Sequence 220108,	481	22	0.9	172	8	US-11-266-748A-302215	Sequence 302215,
409	23	1.0	400	8	US-11-266-748A-236231	Sequence 236231,	482	22	0.9	225	8	US-11-266-748A-272757	Sequence 272757,
410	23	1.0	407	8	US-11-266-748A-61956	Sequence 61956, A	483	22	0.9	225	8	US-11-266-748A-333274	Sequence 333274,
411	23	1.0	416	8	US-11-301-554-971	Sequence 971, App	484	22	0.9	260	8	US-11-301-554-1208	Sequence 1208, Ap
412	23	1.0	417	8	US-11-266-748A-360521	Sequence 360521,	485	22	0.9	265	8	US-11-266-748A-370073	Sequence 370073,
413	23	1.0	417	8	US-11-266-748A-443500	Sequence 443500,	486	22	0.9	265	8	US-11-266-748A-453452	Sequence 453452,
414	23	1.0	419	8	US-11-266-748A-60664	Sequence 60664, A	487	22	0.9	284	8	US-11-266-748A-21261	Sequence 21261,
415	23	1.0	419	8	US-11-266-748A-218587	Sequence 218587,	488	22	0.9	284	8	US-11-266-748A-235372	Sequence 235372,
416	23	1.0	425	8	US-11-266-748A-120605	Sequence 120605,	489	22	0.9	300	8	US-11-266-748A-102107	Sequence 102107,
417	23	1.0	427	8	US-11-266-748A-211069	Sequence 211069,	490	22	0.9	300	8	US-11-266-748A-154918	Sequence 154918,
418	23	1.0	429	8	US-11-266-748A-220153	Sequence 220153,	491	22	0.9	318	8	US-11-266-748A-613	Sequence 613, App
419	23	1.0	429	8	US-11-266-748A-239811	Sequence 239811,	492	22	0.9	336	8	US-11-266-748A-268902	Sequence 268902,
420	23	1.0	431	8	US-11-266-748A-217928	Sequence 217928,	493	22	0.9	336	8	US-11-266-748A-329419	Sequence 329419,
421	23	1.0	431	8	US-11-266-748A-238843	Sequence 238843,	494	22	0.9	355	8	US-11-266-748A-7890	Sequence 7890, Ap
422	23	1.0	437	8	US-11-266-748A-354318	Sequence 354318,	495	22	0.9	361	8	US-11-266-748A-167980	Sequence 167980,
423	23	1.0	437	8	US-11-266-748A-437597	Sequence 437597,	496	22	0.9	361	8	US-11-266-748A-244571	Sequence 244571,
424	23	1.0	438	8	US-11-266-748A-218338	Sequence 218338,	497	22	0.9	363	8	US-11-266-748A-48657	Sequence 48657, A
425	23	1.0	440	8	US-11-266-748A-53038	Sequence 53038,	498	22	0.9	365	8	US-11-266-748A-209002	Sequence 209002,
426	23	1.0	440	8	US-11-266-748A-216880	Sequence 216880,	499	22	0.9	371	8	US-11-266-748A-238819	Sequence 238819,
427	23	1.0	440	8	US-11-266-748A-238432	Sequence 238432,	500	22	0.9	371	8	US-11-266-748A-413510	Sequence 413510,
428	23	1.0	444	8	US-11-301-554-1607	Sequence 1607, Ap	501	22	0.9	381	8	US-11-266-748A-60593	Sequence 60593, A
429	23	1.0	450	8	US-11-266-748A-57914	Sequence 57914, A	502	22	0.9	389	8	US-11-266-748A-39554	Sequence 39554, A
430	23	1.0	451	8	US-11-266-748A-46898	Sequence 46898, A	503	22	0.9	397	8	US-11-266-748A-171009	Sequence 171009,
431	23	1.0	451	8	US-11-266-748A-209124	Sequence 209124,	504	22	0.9	405	8	US-11-266-748A-61347	Sequence 61347, A
432	23	1.0	451	8	US-11-266-748A-233877	Sequence 233877,	505	22	0.9	405	8	US-11-266-748A-218862	Sequence 218862,
433	23	1.0	451	8	US-11-266-748A-360272	Sequence 360272,	506	22	0.9	405	8	US-11-266-748A-237859	Sequence 237859,
434	23	1.0	451	8	US-11-266-748A-443651	Sequence 443651,	507	22	0.9	408	8	US-11-266-748A-369660	Sequence 369660,
435	23	1.0	452	8	US-11-266-748A-213717	Sequence 213717,	508	22	0.9	408	8	US-11-266-748A-453039	Sequence 453039,
436	23	1.0	454	8	US-11-266-748A-44582	Sequence 44582, A	509	22	0.9	411	8	US-11-266-748A-216947	Sequence 216947,
437	23	1.0	456	8	US-11-266-748A-60299	Sequence 60299, A	510	22	0.9	411	8	US-11-266-748A-238449	Sequence 238449,
438	23	1.0	466	8	US-11-266-748A-60462	Sequence 60462, A	511	22	0.9	412	8	US-11-266-748A-380640	Sequence 380640,
439	23	1.0	467	8	US-11-266-748A-217887	Sequence 217887,	512	22	0.9	412	8	US-11-266-748A-464019	Sequence 464019,
440	23	1.0	467	8	US-11-266-748A-238808	Sequence 238808,	513	22	0.9	414	8	US-11-266-748A-212041	Sequence 212041,
441	23	1.0	468	8	US-11-266-748A-59570	Sequence 59570, A	514	22	0.9	420	8	US-11-266-748A-254171	Sequence 254171,
442	23	1.0	469	6	US-10-473-173-361	Sequence 361, App	515	22	0.9	420	8	US-11-266-748A-314688	Sequence 314688,
443	23	1.0	470	8	US-11-266-748A-59873	Sequence 59873, A	516	22	0.9	428	8	US-11-266-748A-61350	Sequence 61350, A
444	23	1.0	470	8	US-11-266-748A-213428	Sequence 213428,	517	22	0.9	429	8	US-11-266-748A-378315	Sequence 378315,
445	23	1.0	470	8	US-11-266-748A-236469	Sequence 236469,	518	22	0.9	429	8	US-11-266-748A-461694	Sequence 461694,
446	23	1.0	471	8	US-11-266-748A-61484	Sequence 61484, A	519	22	0.9	434	8	US-11-266-748A-34911	Sequence 34911, A
447	23	1.0	474	8	US-11-266-748A-11285	Sequence 11285, A	520	22	0.9	436	8	US-11-266-748A-214830	Sequence 214830,
448	23	1.0	476	8	US-11-266-748A-212855	Sequence 212855,	521	22	0.9	436	8	US-11-266-748A-237270	Sequence 237270,
449	23	1.0	476	8	US-11-266-748A-61684	Sequence 61684, A	522	22	0.9	438	8	US-11-266-748A-212652	Sequence 212652,
450	23	1.0	477	8	US-11-266-748A-40467	Sequence 40467, A	523	22	0.9	438	8	US-11-266-748A-236034	Sequence 236034,
451	23	1.0	477	8	US-11-266-748A-58545	Sequence 58545, A	524	22	0.9	439	8	US-11-266-748A-49127	Sequence 49127, A
452	23	1.0	477	8	US-11-266-748A-213476	Sequence 213476,	525	22	0.9	441	8	US-11-266-748A-57819	Sequence 57819, A
453	23	1.0	480	8	US-11-266-748A-272042	Sequence 272042,	526	22	0.9	443	8	US-11-266-748A-208605	Sequence 208605,
454	23	1.0	480	8	US-11-266-748A-332559	Sequence 332559,	527	22	0.9	447	8	US-11-266-748A-33251	Sequence 33251, A
455	23	1.0	483	8	US-11-266-748A-59884	Sequence 59884, A	528	22	0.9	449	8	US-11-266-748A-267609	Sequence 267609,
456	23	1.0	483	8	US-11-266-748A-210893	Sequence 210893,	529	22	0.9	449	8	US-11-266-748A-328126	Sequence 328126,
457	23	1.0	483	8	US-11-266-748A-212889	Sequence 212889,	530	22	0.9	453	8	US-11-266-748A-12513	Sequence 12513, A
458	23	1.0	483	8	US-11-266-748A-215092	Sequence 215092,	531	22	0.9	458	8	US-11-266-748A-219446	Sequence 219446,
459	23	1.0	483	8	US-11-266-748A-236148	Sequence 236148,	532	22	0.9	459	8	US-11-266-748A-208989	Sequence 208989,
460	23	1.0	483	8	US-11-266-748A-237410	Sequence 237410,	533	22	0.9	462	8	US-11-266-748A-62059	Sequence 62059, A
461	23	1.0	485	8	US-11-266-748A-179215	Sequence 179215,	534	22	0.9	463	8	US-11-266-748A-60625	Sequence 60625, A
462	23	1.0	489	8	US-11-266-748A-40457	Sequence 40457, A	535	22	0.9	463	8	US-11-266-748A-218404	Sequence 218404,

C 536	22	0	9	464	8	US-11-266-748A-36655	Sequence 36655, A	C 609	21	0	9	367	8	US-11-301-554-1143	Sequence 1143, Ap
C 537	22	0	9	464	8	US-11-266-748A-215386	Sequence 215386,	C 610	21	0	9	368	8	US-11-301-554-1003	Sequence 1003, Ap
C 538	22	0	9	464	8	US-11-266-748A-237570	Sequence 237570,	C 611	21	0	9	368	8	US-11-301-554-1038	Sequence 1038, Ap
C 539	22	0	9	470	8	US-11-266-748A-208038	Sequence 208038,	C 612	21	0	9	368	8	US-11-301-554-1044	Sequence 1044, Ap
C 540	22	0	9	470	8	US-11-266-748A-233396	Sequence 233396,	C 613	21	0	9	368	8	US-11-301-554-1092	Sequence 1092, Ap
C 541	22	0	9	475	8	US-11-266-748A-40215	Sequence 40215, A	C 614	21	0	9	368	8	US-11-301-554-1164	Sequence 1164, Ap
C 542	22	0	9	475	8	US-11-266-748A-270609	Sequence 270609,	C 615	21	0	9	368	8	US-11-301-554-1584	Sequence 1584, Ap
C 543	22	0	9	475	8	US-11-266-748A-311126	Sequence 311126,	C 616	21	0	9	378	8	US-11-266-748A-7358	Sequence 7358, Ap
C 544	22	0	9	476	8	US-11-266-748A-298942	Sequence 298942,	C 617	21	0	9	378	8	US-11-266-748A-60305	Sequence 60305, A
C 545	22	0	9	478	8	US-11-266-748A-271233	Sequence 271233,	C 618	21	0	9	378	8	US-11-266-748A-61226	Sequence 61226, A
C 546	22	0	9	478	8	US-11-266-748A-311750	Sequence 311750,	C 619	21	0	9	378	8	US-11-266-748A-215128	Sequence 215128,
C 547	22	0	9	486	8	US-11-266-748A-40298	Sequence 40298, A	C 620	21	0	9	386	8	US-11-266-748A-208051	Sequence 208051,
C 548	22	0	9	486	8	US-11-266-748A-217217	Sequence 217217,	C 621	21	0	9	386	8	US-11-266-748A-233408	Sequence 233408,
C 549	22	0	9	488	8	US-11-266-748A-238560	Sequence 238560,	C 622	21	0	9	387	8	US-11-266-748A-37730	Sequence 37730, A
C 550	22	0	9	488	8	US-11-266-748A-218018	Sequence 218018,	C 623	21	0	9	387	8	US-11-266-748A-59696	Sequence 59696, A
C 551	22	0	9	491	8	US-11-266-748A-270226	Sequence 270226,	C 624	21	0	9	387	8	US-11-266-748A-208495	Sequence 208495,
C 552	22	0	9	491	8	US-11-266-748A-453605	Sequence 453605,	C 625	21	0	9	387	8	US-11-266-748A-40575	Sequence 40575, A
C 553	22	0	9	493	8	US-11-266-748A-53110	Sequence 53110, A	C 626	21	0	9	392	8	US-11-266-748A-53756	Sequence 53756, A
C 554	22	0	9	493	8	US-11-266-748A-209951	Sequence 209951,	C 627	21	0	9	392	8	US-11-266-748A-208651	Sequence 208651,
C 555	22	0	9	493	8	US-11-266-748A-213522	Sequence 213522,	C 628	21	0	9	398	8	US-11-266-748A-220339	Sequence 220339,
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C 557	22	0	9	493	8	US-11-266-748A-236507	Sequence 236507,	C 630	21	0	9	398	8	US-11-266-748A-239076	Sequence 239076,
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C 559	22	0	9	495	8	US-11-266-748A-214609	Sequence 214609,	C 632	21	0	9	399	8	US-11-266-748A-40695	Sequence 40695, A
C 560	22	0	9	495	8	US-11-266-748A-219534	Sequence 219534,	C 633	21	0	9	399	8	US-11-266-748A-213578	Sequence 213578,
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683	21	0.9	452	8	US-11-266-748A-215546	Sequence 215546, A	756	20	0.8	158	6	US-10-560-723-6	Sequence 6, Appl1
684	21	0.9	452	8	US-11-266-748A-237673	Sequence 237673, A	757	20	0.8	181	8	US-11-266-748A-413160	Sequence 413160, A
685	21	0.9	453	8	US-11-266-748A-61448	Sequence 61448, A	758	20	0.8	242	8	US-11-266-748A-52183	Sequence 52183, A
686	21	0.9	453	8	US-11-266-748A-208816	Sequence 208816, A	759	20	0.8	242	8	US-11-266-748A-210353	Sequence 210353, A
687	21	0.9	453	8	US-11-266-748A-208816	Sequence 208816, A	760	20	0.8	242	8	US-11-266-748A-234555	Sequence 224555, A
688	21	0.9	454	8	US-11-266-748A-215084	Sequence 215084, A	761	20	0.8	261	8	US-11-266-748A-392019	Sequence 392019, A
689	21	0.9	454	8	US-11-266-748A-237406	Sequence 237406, A	762	20	0.8	261	8	US-11-266-748A-482737	Sequence 482737, A
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691	21	0.9	455	8	US-11-266-748A-234607	Sequence 234607, A	764	20	0.8	281	8	US-11-266-748A-110035	Sequence 110035, A
692	21	0.9	456	8	US-11-266-748A-40742	Sequence 40742, A	765	20	0.8	284	8	US-11-266-748A-130697	Sequence 130697, A
693	21	0.9	456	8	US-11-266-748A-62020	Sequence 62020, A	766	20	0.8	284	8	US-11-266-748A-4139	Sequence 4139, Ap
694	21	0.9	456	8	US-11-266-748A-211887	Sequence 211887, A	767	20	0.8	288	6	US-10-526-905-7	Sequence 7, Appl1
695	21	0.9	456	8	US-11-266-748A-235435	Sequence 235435, A	768	20	0.8	309	8	US-11-266-748A-61532	Sequence 61532, A
696	21	0.9	456	8	US-11-266-748A-256213	Sequence 256213, A	769	20	0.8	318	8	US-11-266-748A-85708	Sequence 85708, A
697	21	0.9	456	8	US-11-266-748A-316730	Sequence 316730, A	770	20	0.8	318	8	US-11-266-748A-138519	Sequence 138519, A
698	21	0.9	456	7	US-11-195-344-17	Sequence 17, Appl	771	20	0.8	318	8	US-11-266-748A-363257	Sequence 363257, A
699	21	0.9	461	7	US-11-195-344-108	Sequence 108, Appl	772	20	0.8	318	8	US-11-266-748A-446636	Sequence 446636, A
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703	21	0.9	461	8	US-11-266-748A-234966	Sequence 234966, A	776	20	0.8	333	8	US-11-266-748A-27413	Sequence 207413, A
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712	21	0.9	470	8	US-11-266-748A-235074	Sequence 235074, A	785	20	0.8	363	8	US-11-266-748A-61094	Sequence 61094, A
713	21	0.9	473	8	US-11-266-748A-61739	Sequence 61739, A	786	20	0.8	367	8	US-11-266-748A-229439	Sequence 229439, A
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719	21	0.9	487	8	US-11-266-748A-217935	Sequence 217935, A	792	20	0.8	374	6	US-11-266-748A-233047	Sequence 239047, A
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722	21	0.9	493	7	US-11-195-344-214	Sequence 214, App	795	20	0.8	375	8	US-11-266-748A-137949	Sequence 137949, A
723	21	0.9	493	8	US-11-266-748A-213681	Sequence 213681, A	796	20	0.8	376	8	US-11-266-748A-377782	Sequence 377782, A
724	21	0.9	493	8	US-11-266-748A-236690	Sequence 236690, A	797	20	0.8	376	8	US-11-266-748A-461161	Sequence 461161, A
725	21	0.9	494	8	US-11-266-748A-60592	Sequence 60592, A	798	20	0.8	378	8	US-11-266-748A-215174	Sequence 215174, A
726	21	0.9	494	8	US-11-266-748A-239153	Sequence 239152, A	799	20	0.8	378	8	US-11-266-748A-413182	Sequence 413182, A
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729	21	0.9	496	8	US-11-266-748A-325915	Sequence 325915, A	802	20	0.8	389	8	US-11-266-748A-207727	Sequence 207727, A
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731	21	0.9	497	8	US-11-266-748A-257593	Sequence 257593, A	804	20	0.8	393	7	US-11-327-124A-62	Sequence 62, Appl1
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733	21	0.9	498	8	US-11-266-748A-62043	Sequence 62043, A	806	20	0.8	398	8	US-11-266-748A-431990	Sequence 431990, A
734	21	0.9	498	8	US-11-266-748A-213378	Sequence 213378, A	807	20	0.8	400	8	US-11-266-748A-17053	Sequence 17053, A
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739	21	0.9	499	8	US-11-266-748A-51338	Sequence 51338, A	812	20	0.8	403	8	US-11-266-748A-171421	Sequence 171421, A
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741	21	0.9	500	6	US-10-511-937-1277	Sequence 1277, Ap	814	20	0.8	404	8	US-11-266-748A-245334	Sequence 245334, A
742	21	0.9	500	6	US-10-511-937-2102	Sequence 2102, Ap	815	20	0.8	404	8	US-11-266-748A-35020	Sequence 35020, A
743	21	0.9	500	6	US-10-553-298-47	Sequence 27, Appl	816	20	0.8	411	8	US-11-266-748A-45659	Sequence 45659, A
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746	21	0.9	500	6	US-11-245-514-24	Sequence 24, Appl	819	20	0.8	414	8	US-11-266-748A-60310	Sequence 60310, A
747	21	0.9	500	6	US-11-245-514-24	Sequence 24, Appl	820	20	0.8	414	8	US-11-266-748A-218730	Sequence 218730, A
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749	21	0.9	500	6	US-11-245-514-24	Sequence 24, Appl	822	20	0.8	425	8	US-11-266-748A-214638	Sequence 214638, A
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751	21	0.9	500	6	US-11-245-514-24	Sequence 24, Appl	824	20	0.8	425	8	US-11-266-748A-362522	Sequence 445901, A
752	21	0.9	500	6	US-11-245-514-24	Sequence 24, Appl	825	20	0.8	425	8	US-11-266-748A-445901	Sequence 445901, A
753	21	0.9	500	6	US-11-266-748A-456023	Sequence 456023, A	826	20	0.8	427	6	US-10-488-619-986	Sequence 386, App
754	21	0.9	500	6	US-11-266-748A-426810	Sequence 426810, A	827	20	0.8	437	8	US-11-266-748A-53099	Sequence 53099, A

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C 830	20	0.8	437	8	US-11-266-748A-391218	Sequence 391218,	C 903	20	0.8	489	8	US-11-266-748A-458004	Sequence 458004,
C 831	20	0.8	437	8	US-11-266-748A-481936	Sequence 481936,	C 904	20	0.8	492	8	US-11-266-748A-60174	Sequence 60174, A
C 832	20	0.8	440	8	US-11-266-748A-355999	Sequence 355999,	C 905	20	0.8	492	8	US-11-266-748A-212861	Sequence 212861,
C 833	20	0.8	440	8	US-11-266-748A-449378	Sequence 449378,	C 906	20	0.8	492	8	US-11-266-748A-319589	Sequence 319589,
C 834	20	0.8	441	8	US-11-266-748A-296556	Sequence 296556,	C 907	20	0.8	492	8	US-11-266-748A-336154	Sequence 336154,
C 835	20	0.8	441	8	US-11-266-748A-362920	Sequence 362920,	C 908	20	0.8	492	8	US-11-266-748A-339513	Sequence 339513,
C 836	20	0.8	441	8	US-11-266-748A-446299	Sequence 446299,	C 909	20	0.8	494	8	US-11-266-748A-35588	Sequence 35588, A
C 837	20	0.8	443	8	US-11-266-748A-212655	Sequence 212655,	C 910	20	0.8	498	8	US-11-266-748A-207338	Sequence 207338,
C 838	20	0.8	443	8	US-11-266-748A-213882	Sequence 213882,	C 911	20	0.8	499	8	US-11-266-748A-61673	Sequence 61673, A
C 839	20	0.8	444	8	US-11-266-748A-428278	Sequence 428278,	C 912	20	0.8	500	7	US-11-266-748A-270941	Sequence 270941,
C 840	20	0.8	444	8	US-11-266-748A-61445	Sequence 61445, A	C 913	20	0.8	500	8	US-11-266-748A-331458	Sequence 331458,
C 841	20	0.8	445	8	US-11-266-748A-272294	Sequence 272294,	C 914	20	0.8	500	8	US-10-519-505-7	Sequence 519-505-7
C 842	20	0.8	445	8	US-11-266-748A-332811	Sequence 332811,	C 915	19	0.8	19	6	US-10-519-505-133	Sequence 519-505-133
C 843	20	0.8	446	8	US-11-266-748A-609929	Sequence 609929, A	C 916	19	0.8	19	6	US-11-255-980-15	Sequence 11-255-980-15
C 844	20	0.8	446	8	US-11-266-748A-212755	Sequence 212755,	C 917	19	0.8	158	8	US-11-266-748A-389946	Sequence 389946,
C 845	20	0.8	446	8	US-11-266-748A-236087	Sequence 236087,	C 918	19	0.8	158	8	US-11-266-748A-480664	Sequence 480664,
C 846	20	0.8	447	8	US-11-266-748A-57863	Sequence 57863, A	C 919	19	0.8	158	8	US-11-266-748A-307521	Sequence 307521,
C 847	20	0.8	449	8	US-11-266-748A-40567	Sequence 40567, A	C 920	19	0.8	161	8	US-11-266-748A-426711	Sequence 426711,
C 848	20	0.8	449	8	US-11-266-748A-218195	Sequence 218195,	C 921	19	0.8	174	8	US-11-266-748A-372317	Sequence 372317,
C 849	20	0.8	449	8	US-11-266-748A-238992	Sequence 238992,	C 922	19	0.8	196	8	US-11-266-748A-332754	Sequence 332754,
C 850	20	0.8	454	8	US-11-266-748A-60712	Sequence 60712, A	C 923	19	0.8	196	8	US-11-266-748A-373425	Sequence 373425,
C 851	20	0.8	456	8	US-11-266-748A-254834	Sequence 254834,	C 924	19	0.8	198	8	US-11-266-748A-456004	Sequence 456004,
C 852	20	0.8	456	8	US-11-266-748A-280429	Sequence 280429,	C 925	19	0.8	231	8	US-11-266-748A-377279	Sequence 377279,
C 853	20	0.8	456	8	US-11-266-748A-315351	Sequence 315351,	C 926	19	0.8	231	8	US-11-266-748A-460658	Sequence 460658,
C 854	20	0.8	456	8	US-11-266-748A-317024	Sequence 317024,	C 927	19	0.8	238	8	US-11-266-748A-100700	Sequence 100700,
C 855	20	0.8	457	8	US-11-266-748A-273416	Sequence 273416,	C 928	19	0.8	238	8	US-11-266-748A-153511	Sequence 153511,
C 856	20	0.8	457	8	US-11-266-748A-333933	Sequence 333933,	C 929	19	0.8	253	8	US-11-266-748A-302662	Sequence 302662,
C 857	20	0.8	459	8	US-11-266-748A-13005	Sequence 13005, A	C 930	19	0.8	253	8	US-11-266-748A-40703	Sequence 40703,
C 858	20	0.8	460	8	US-11-266-748A-52377	Sequence 52377, A	C 931	19	0.8	254	8	US-11-266-748A-372488	Sequence 372488,
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C 860	20	0.8	460	8	US-10-488-619-5216	Sequence 516, App	C 933	19	0.8	265	8	US-11-266-748A-267721	Sequence 267721,
C 861	20	0.8	461	6	US-11-266-748A-62022	Sequence 62022, A	C 934	19	0.8	265	8	US-11-266-748A-280662	Sequence 280662,
C 862	20	0.8	461	8	US-11-266-748A-215656	Sequence 215656,	C 935	19	0.8	265	8	US-11-266-748A-328238	Sequence 328238,
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C 865	20	0.8	462	8	US-11-266-748A-220276	Sequence 220276,	C 938	19	0.8	278	6	US-10-533-365-21	Sequence 10-533-365-21
C 866	20	0.8	462	8	US-11-266-748A-213153	Sequence 213153,	C 939	19	0.8	278	6	US-11-266-748A-173765	Sequence 173765,
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C 876	20	0.8	466	8	US-11-266-748A-333669	Sequence 333669,	C 949	19	0.8	292	8	US-11-266-748A-329133	Sequence 329133,
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C 882	20	0.8	470	8	US-11-266-748A-69076	Sequence 69076, A	C 955	19	0.8	311	8	US-11-266-748A-305554	Sequence 305554,
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c 992 19 0.8 394 8 US-11-266-748A-330802 Sequence 330802,
c 993 19 0.8 399 8 US-11-266-748A-273933 Sequence 273933,
c 994 19 0.8 400 8 US-11-266-748A-334450 Sequence 334450,
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c 997 19 0.8 408 8 US-11-266-748A-361995 Sequence 361995,
c 998 19 0.8 408 8 US-11-266-748A-445374 Sequence 445374,
c 999 19 0.8 413 7 US-11-327-124A-134 Sequence 134, App
1000 19 0.8 415 8 US-11-266-748A-218054 Sequence 218054,
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ALIGNMENTS

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RESULT 1
US-11-266-748A-7936
; Sequence 7936, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7936
; LENGTH: 437
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-7936
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Best Local Similarity 100.0%; Pred. No. 5.4e-57;
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Db 220 GATCAAAAGGACCTTGTACAGAGCCTTACAGAGAAACCTTCATCTTCAATTGGTT 279
Qy 771 TCTAGACCATCTACCTCATCTAGAGAGAGCAATTAGAGACAG 816
Db 280 TCTAGACCATCTACCTCATCTAGAGAGAGCAATTAGAGACAG 325
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RESULT 2
US-11-266-748A-60150
; Sequence 60150, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60150
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-60150
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Best Local Similarity 100.0%; Pred. No. 2.3e-53;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 372 GCTTCGGAACAAGAGACCTTGTGTAGACCAAGCATTTGCTTTGAAGTTATTTAAAGTCT 431
Db 61 GCTTCGGAACAAGAGACCTTGTGTAGACCAAGCATTTGCTTTGAAGTTATTTAAAGTCT 120
Qy 432 GTTGTGCAAAAAGACACTTATATCTATGAAAGAG 468
Db 121 GTTGTGCAAAAAGACACTTATATCTATGAAAGAG 157
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RESULT 3
US-11-266-748A-57794
; Sequence 57794, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 57794
LENGTH: 428
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-57794
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Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
US-10-511-937-283
; Sequence 283, Application US/10511937
; Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
PRIOR FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 283
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-511-937-283
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Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1   GACAACCAATTCAAATGATTTGCTACTTATTTCCCTAGTTGACCTGT 50
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RESULT 5
US-11-266-748A-60447
; Sequence 60447, Application US/11266748A
; Publication No. US2006013463A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 60447
LENGTH: 474
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-60447
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Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
US-11-266-748A-213882/c
; Sequence 213882, Application US/11266748A
; Publication No. US2006013463A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 213882
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-213882

Query Match          1.9%; Score 44; DB 8; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      332 GGGTTTACCGTGTAGCCAGATGCTCTCATCTCTGACCTC 289

RESULT 7
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; Sequence 50804, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50804
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (375)..(383)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
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; LOCATION: (385)..(402)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (404)..(429)
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; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-50804

Query Match          1.8%; Score 43; DB 8; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      52 TGATCCGCCCACTCGGCTCCCAAGTGTGGATTACAGGC 94

RESULT 8
US-11-266-748A-219366/C
; Sequence 219366, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 219366
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-219366

Query Match          1.8%; Score 43; DB 8; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2330 CTTGGGCTCCCAAGTGTGGATTACAGCATGAGCCACCG 2372
Db      143 CTTGGGCTCCCAAGTGTGGATTACAGCATGAGCCACCG 101

RESULT 9
US-11-266-748A-239401
; Sequence 239401, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
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; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 239401
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-239401

Query Match
Best Local Similarity 1.8%; Score 43; DB 8; Length 444;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2330 CCTCGACCTCCCAAGTGTGGAGATTACGCGATGAGCCAGC 2372
DB 302 CCTCGACCTCCCAAGTGTGGAGATTACGCGATGAGCCAGC 344

RESULT 10
US-11-266-748A-380602
; Sequence 380602, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 380602
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-380602

Query Match
Best Local Similarity 1.8%; Score 42; DB 8; Length 463;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2275 GGTTCACCGTGTAGCCAGATGCTCTGATCTCTGACCT 2316
DB 453 GGTTCACCGTGTAGCCAGATGCTCTGATCTCTGACCT 2316
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```

DB 11 GGTTCACCGTGTAGCCAGATGCTCTGATCTCTGACCT 52

RESULT 11
US-11-266-748A-463981/c
; Sequence 463981, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 463981
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-463981

Query Match
Best Local Similarity 1.8%; Score 42; DB 8; Length 463;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2275 GGTTCACCGTGTAGCCAGATGCTCTGATCTCTGACCT 2316
DB 453 GGTTCACCGTGTAGCCAGATGCTCTGATCTCTGACCT 412

RESULT 12
US-11-327-124A-215
; Sequence 215, Application US/11327124A
; Publication No. US20060166242A1
; GENERAL INFORMATION:
; APPLICANT: Fennell, Craig
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: MARKERS OF PRE-TERM LABOR
; FILE REFERENCE: 14096.1004USU1
; CURRENT APPLICATION NUMBER: US/11/327,124A
; PRIOR FILING DATE: 2006-01-06
; PRIOR APPLICATION NUMBER: US 60/641,875
; PRIOR FILING DATE: 2005-01-06
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 215
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-327-124A-215

Query Match
Best Local Similarity 1.7%; Score 40; DB 7; Length 349;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2285 TGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 2324
Db 54 TGTAGCCAGAGTGTCTCGATCTCTGACCTCGTATCC 93

RESULT 13
US-11-266-748A-217154
; Sequence 217154, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 217154
; LENGTH: 245
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-217154

Query Match 1.6%; Score 39; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2334 GGCCTCCCAAGTGTGGATTACGAGCATGAGCCACCG 2372
Db 74 GGCCTCCCAAGTGTGGATTACGAGCATGAGCCACCG 112

RESULT 14
US-11-266-748A-414670
; Sequence 414670, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 414670
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-61942

Query Match 1.6%; Score 38; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2293 AGGATGCTCTGATCTCTGACCTCGTATCCGCCACCG 2331
Db 314 AGGATGCTCTGATCTCTGACCTCGTATCCGCCACCG 352

RESULT 15
US-11-266-748A-61942/c
; Sequence 61942, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61942
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-61942
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Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2335 GCCTCCCAAGTGTGGATTACAGGCATGAGCCACC 2372
Db 270 GCCTCCCAAGTGTGGATTACAGGCATGAGCCACC 233

RESULT 16
US-11-266-748A-61449
; Sequence 61449, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61449
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-61449

Query Match 1.6%; Score 38; DB 8; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2335 GCCTCCCAAGTGTGGATTACAGGCATGAGCCACC 2372
Db 243 GCCTCCCAAGTGTGGATTACAGGCATGAGCCACC 280

RESULT 17
US-11-266-748A-217171
; Sequence 217171, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 217171
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-217171

Query Match 1.6%; Score 38; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2334 GCCTCCCAAGTGTGGATTACAGGCATGAGCCACC 2371
Db 339 GCCTCCCAAGTGTGGATTACAGGCATGAGCCACC 376

RESULT 18
US-11-266-748A-238530/c
; Sequence 238530, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 238530
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-238530

Query Match 1.6%; Score 38; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2334 GCCTCCCAAGTGTGGATTACAGGCATGAGCCACC 2371
Db 148 GCCTCCCAAGTGTGGATTACAGGCATGAGCCACC 111

RESULT 19

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US-11-266-748A-170884/c
; Sequence 170884, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 170884
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-170884

Query Match      1.6%; Score 37; DB 8; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
US-11-266-748A-170884/c
; Sequence 208969, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 208969
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-170884/c

Query Match      1.6%; Score 37; DB 8; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ NAME/KEY: misc feature
/ LOCATION: (24) ..(24)
/ OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-208969
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Query Match          1.6%; Score 37; DB 8; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      2325 GCCCAGCTGGGCTCCCAAGTCTGGATTACAGGC 2361
Db      392 GCCCAGCTGGGCTCCCAAGTCTGGATTACAGGC 356
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RESULT 22
US-11-266-748A-50353/C
/ Sequence 50353, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcriptome Microarray Technology and
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ PRIOR FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 50353
/ LENGTH: 437
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
US-11-266-748A-50353
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Query Match          1.6%; Score 37; DB 8; Length 437;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      2335 GCCTCCCAAGTCTGGATTACAGGCATGAGCCACC 2371
Db      344 GCCTCCCAAGTCTGGATTACAGGCATGAGCCACC 308
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RESULT 23
US-11-266-748A-211874
/ Sequence 211874, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcriptome Microarray Technology and
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ CURRENT FILING DATE: 2005-11-03
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/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 211874
/ LENGTH: 461
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
US-11-266-748A-211874
```

```
Query Match          1.6%; Score 37; DB 8; Length 461;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2325 GCCCAGCTGGGCTCCCAAGTCTGGATTACAGGC 2361
Db      69 GCCCAGCTGGGCTCCCAAGTCTGGATTACAGGC 105
```

```
RESULT 24
US-11-266-748A-235428/C
/ Sequence 235428, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcriptome Microarray Technology and
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ PRIOR FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 235428
/ LENGTH: 461
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
US-11-266-748A-235428
```

```
Query Match          1.6%; Score 37; DB 8; Length 461;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2325 GCCCACTGGGCGCTCCAAAGTGTGGATTACAGGC 2361
DB 393 GCCCACTGGGCGCTCCAAAGTGTGGATTACAGGC 357

RESULT 25
US-10-554-711-12/c
; Sequence 12, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-12

Query Match 1.5%; Score 36; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGGTGTAGCCAGAGATGTCGATCTC 2309
DB 36 GGGTTTACCGGTGTAGCCAGAGATGTCGATCTC 1

RESULT 26
US-10-554-711-17/c
; Sequence 17, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-17

Query Match 1.5%; Score 36; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGGTGTAGCCAGAGATGTCGATCTC 2309
DB 36 GGGTTTACCGGTGTAGCCAGAGATGTCGATCTC 1

RESULT 27
US-10-554-711-24/c
; Sequence 24, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-24

Query Match 1.5%; Score 36; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGGTGTAGCCAGAGATGTCGATCTC 2309
DB 36 GGGTTTACCGGTGTAGCCAGAGATGTCGATCTC 1

RESULT 28
US-10-554-711-26/c
; Sequence 26, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-26

Query Match 1.5%; Score 36; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGGTGTAGCCAGAGATGTCGATCTC 2309
DB 36 GGGTTTACCGGTGTAGCCAGAGATGTCGATCTC 1

RESULT 29
US-10-554-711-27/c
; Sequence 27, Application US/10554711
; Publication No. US20060115806A1

```

; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; PRIOR FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-27

Query Match
Best Local Similarity 1.5%; Score 36; DB 6; Length 50;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 2309
DB 36 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 1

RESULT 30
US-10-554-711-29/c
; Sequence 29, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; PRIOR FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-29

Query Match
Best Local Similarity 1.5%; Score 36; DB 6; Length 50;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 2309
DB 36 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 1

RESULT 31
US-10-554-711-30/c
; Sequence 30, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
```

```

; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; PRIOR FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-30

Query Match
Best Local Similarity 1.5%; Score 36; DB 6; Length 50;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 2309
DB 36 GGGTTTCAACCGTGTAGCCAGGATGTCCTCGATCTC 1

RESULT 32
US-11-266-748A-40751
; Sequence 40751, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40751
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-40751

Query Match
Best Local Similarity 1.5%; Score 36; DB 8; Length 213;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGGATGTCCTCGATCTCGACTCGTG 2320
DB 6 TGTAGCCAGGATGTCCTCGATCTCGACTCGTG 1

RESULT 33
US-11-266-748A-354643
```

```
; Sequence 354643, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03

Query Match      1.5%; Score 36; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 8.2e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2337 CTCCCAAGTCTGGATTACAGGATGAGCCACCG 2372
Db      1 CTCCCAAGTCTGGATTACAGGATGAGCCACCG 36

RESULT 34
US-11-266-748A-438022/c
; Sequence 438022, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
```

```
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 438022
; LENGTH: 335
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-438022

Query Match      1.5%; Score 36; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 8.2e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2337 CTCCCAAGTCTGGATTACAGGATGAGCCACCG 2372
Db      335 CTCCCAAGTCTGGATTACAGGATGAGCCACCG 300

RESULT 35
US-11-266-748A-40654
; Sequence 40654, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40654
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-40654

Query Match      1.5%; Score 36; DB 8; Length 448;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2326 CCACCTCGGCTCCCAAGTCTGGATTACAGGC 2361
Db      179 CCACCTCGGCTCCCAAGTCTGGATTACAGGC 214

RESULT 36
US-11-266-748A-48475/c
```

```

; Sequence 48475, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 48475
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-48475

Query Match          1.5%; Score 36; DB 8; Length 462;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2325 GCCCAGCTGGGCTCCCAAGTGCTGGGATTACAGG 2360
Db      387 GCCCAGCTGGGCTCCCAAGTGCTGGGATTACAGG 352

RESULT 37
US-11-266-748A-60828/c
; Sequence 60828, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18

```

```

; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 60828
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (363)..(363)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (440)..(440)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (453)..(453)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (461)..(461)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (474)..(474)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-60828

Query Match          1.5%; Score 36; DB 8; Length 474;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2325 GCCCAGCTGGGCTCCCAAGTGCTGGGATTACAGG 2360
Db      201 GCCCAGCTGGGCTCCCAAGTGCTGGGATTACAGG 166

RESULT 38
US-10-554-711-13/c
; Sequence 13, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-554-711-13

```

```

Query Match          1.5%; Score 35; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2294 GGATGCTCGATCTCTGACCTGTAATCCGCC 2328
Db      36 GGATGCTCGATCTCTGACCTGTAATCCGCC 2

RESULT 39
US-10-554-711-25/c

```

```

; Sequence 25, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-25

```

```

Query Match      1.5%; Score 35; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2294 GGATGCTTCGATCTCCTGACCTCGTGTGATCCGCC 2328
Db      36 GGATGCTTCGATCTCCTGACCTCGTGTGATCCGCC 2

```

```

RESULT 40
US-10-554-711-32/C
; Sequence 32, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-32

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Query Match      1.5%; Score 35; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2274 GGGTTTCACCGGTGAGCCAGGATGCTCGATCT 2308
Db      35 GGGTTTCACCGGTGAGCCAGGATGCTCGATCT 1

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Search completed: August 4, 2006, 20:56:33
Job time : 501 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2006, 13:41:44 ; Search time 11265 Seconds
(without alignments)
11774.581 Million cell updates/sec

Title: US-09-966-724B-2
Perfect score: 2372
Sequence: 1 GCACCGCGCAGAGCTTGCTG.....ATTACAGCATGAGCCACCG 2372

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 2795965780 residues

Word size : 1

Total number of hits satisfying chosen parameters: 36196904

Minimum DB seq length: 5
Maximum DB seq length: 500

Post-processing: listing first 1000 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss81:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	16.2	400	8	CNA09877 170004182
2	377	15.9	377	7	BF155177 QV0-BT084
3	367	15.5	482	10	R80343 R80343
4	320	13.5	427	1	AA214617 zt88h09.s
5	289	12.2	300	4	BK482386 DKFZp686H
6	234	9.9	486	7	AM070956 xa31h03.x
7	231	9.7	393	1	AL704062 DKFZp686N
8	219	9.2	476	7	BE676440 CT000980
9	211	8.9	365	8	CT000980 CT000980
10	200	8.4	399	10	H79860 yu78f12.r1
11	199	8.4	414	7	BF089387 PM2-HT092
12	193	8.1	421	7	BF3050973 QV1-HT041
13	167	7.0	319	10	H13638 y107c11.r1
14	167	7.0	469	7	BE935243 MR0-MT012
15	166	7.0	415	1	AI281316 qk39d01.x
16	166	7.0	421	1	AI336475 qo61d06.x
17	166	7.0	423	1	AA937920 of72e04.s
18	166	7.0	423	1	AI346140 qp43e08.x
19	166	7.0	437	1	AI274906 q149e03.x

C 20	148	6.2	148	7	AM999946 MR0-BN007
C 21	140	5.9	335	1	AI339173 G899a02.x
C 22	138	5.8	233	2	BF746144 RC1-RP025
C 23	129	5.4	253	7	BF336925 CM2-CT500
C 24	125	5.3	345	7	BE765314 IL2-NT010
C 25	119	5.0	227	7	BF081983 PM1-AN009
C 26	115	4.8	415	1	AI246037 qk44h12.x
C 27	108	4.6	366	1	AA568852 mm27a12.s
C 28	106	4.5	456	10	R80235 y196d02.s1
C 29	98	4.1	489	12	CC000590 UP-479-4N
C 30	94	4.0	385	10	N20967 yk57c04.s1
C 31	94	4.0	437	7	BE019522 bd57c10.y
C 32	92	3.9	147	2	BF949018 MR3-NN022
C 33	92	3.9	147	2	BF949018 MR3-NN022
C 34	88	3.7	151	10	FP35659 HSPD32490.H
C 35	88	3.7	298	2	BG956827 IL3-CT067
C 36	88	3.7	303	10	DM419606 HHAGE0193
C 37	88	3.7	389	11	AQ094950 HS 3028.A
C 38	88	3.7	454	11	AO153405 HS_2234.B
C 39	88	3.7	474	1	AL048925 DKFZp434K
C 40	87	3.7	330	3	BQ351361 QV0-HT036
C 41	87	3.7	433	2	BM127662 1e98b10.y
C 42	87	3.7	439	10	N27353 yw52e08.s1
C 43	87	3.7	440	2	BM127350 1e98b10.x
C 44	87	3.7	440	2	BM127350 1e98b10.x
C 45	87	3.7	465	9	DA257128 DA257128
C 46	87	3.7	479	9	DA517190 DA517190
C 47	87	3.7	497	5	CK906249 1e98b10.y
C 48	83	3.5	319	2	BG546523 602574272
C 49	83	3.5	187	4	BK955194 DKFZp781A
C 50	81	3.4	354	10	T47739 yb16904.s1
C 51	81	3.4	354	10	DM466069 HHAGE0073
C 52	80	3.4	422	11	CA434763 UI-H-D10-
C 53	80	3.3	276	10	AQ058627 CIT-HSP-2
C 54	78	3.3	355	2	DM428120 HHAGE0278
C 55	78	3.3	408	11	BG152682 naf58h12.
C 56	78	3.3	435	7	AE02826 RPTC11-58
C 57	78	3.3	438	3	BE042649 ho2a410.x
C 58	78	3.3	452	2	BUN52584 i076d08.x
C 59	77	3.2	210	1	BF911530 IL0-UT010
C 60	77	3.2	262	1	AA593359 nm07905.s
C 61	77	3.2	293	1	AA365165 EST75866
C 62	77	3.2	315	1	AA558227 n134e07.s
C 63	77	3.2	388	14	AA557854 n164e02.s
C 64	77	3.2	389	11	AG197480 Pan t1c0g1
C 65	77	3.2	398	11	AI312149 ta79b12.x
C 66	77	3.2	412	1	AQ058468 RPTC-11-4
C 67	77	3.2	485	9	AA810037 od11g04.s
C 68	76	3.2	385	1	DB061436 DB061436
C 69	76	3.2	454	4	AJ346318 SHR-00001
C 70	75	3.2	308	2	BK645662 DKFZp781J
C 71	75	3.2	377	11	BI060016 IL3-UT011
C 72	74	3.1	410	10	AQ005848 CIT-HSP-2
C 73	74	3.1	486	10	DM419014 HHAGE0017
C 74	74	3.1	326	1	H29303 ym60a07.s1
C 75	72	3.0	263	3	AA480772 ne86d10.s
C 76	72	3.0	263	3	BM692874 UI-E-CK1-
C 77	72	3.0	318	8	BM671457 UI-E-CK1-
C 78	72	3.0	417	8	CV421900 RC4-HT093
C 79	71	3.0	128	1	AI313166 qk81f06.x
C 80	71	3.0	140	1	AA687987 nt55f03.s
C 81	71	3.0	392	2	AA604326 no83g12.s
C 82	71	3.0	452	11	BF958161 RC5-NN106
C 83	70	3.0	297	10	AQ512849 HS 5144.B
C 84	70	3.0	324	11	DM421384 HHAGE0211
C 85	70	3.0	305	11	DM417557 HHAGE0182
C 86	70	3.0	375	1	AQ040371 CIT-HSP-2
C 87	70	3.0	377	9	AI251021 qk49h06.x
C 88	70	3.0	379	2	DR033662 5000BCT03
C 89	69	2.9	244	4	BG004281 RC6-GN007
C 90	69	2.9	257	4	BK491664 DKFZp781O
C 91	69	2.9	297	10	BG989387 MR2-HT116
C 92	69	2.9	303	1	DM421619 HHAGE0213
					AI216799 qm31h07.x

C 93	69	2.9	337	2	BF888015	BF888015 QV3-TN016	C 166	64	2.7	440	7	AW962713	AW962713 EST374786
C 94	69	2.9	390	10	DM430222	DM430222 HHAGE0029	C 167	64	2.7	455	11	AZ755765	AZ755765 ev05h02.r
C 95	69	2.9	431	10	N55273	N55273 Y24A6604.s1	C 168	64	2.7	471	9	DB146705	DB146705
C 96	69	2.9	432	5	CD676551	CD676551 h002d09.y	C 169	64	2.7	483	11	AQ798614	AQ798614 HS_2238.B
C 97	69	2.9	472	8	CV402640	CV402640 RC0-BN023	C 170	64	2.7	495	11	AQ264829	AQ264829 CTBT-EI-
C 98	69	2.9	482	9	DA309759	DA309759 DA309759	C 171	63	2.7	150	2	BQ494854	BQ494854 602540860
C 99	68	2.9	183	2	BF869171	BF869171 IL5-ET011	C 172	63	2.7	297	3	BQ277822	BQ277822 AGENCOURT
C 100	68	2.9	203	2	BG959152	BG959152 PM4-CT080	C 173	63	2.7	271	10	DM421639	DM421639 HHAGE0213
C 101	68	2.9	220	1	AA336362	AA336362 EST41153	C 174	63	2.7	327	7	BE243593	BE243593 RCS-CT059
C 102	68	2.9	240	1	AA378821	AA378821 EST911724	C 175	63	2.7	388	2	BF756894	BF756894 DB254923
C 103	68	2.9	240	1	AA378822	AA378822 EST911725	C 176	63	2.7	459	7	DB254923	DB254923
C 104	68	2.9	304	1	AL434706	AL434706 CT09E09.x	C 177	63	2.7	481	7	AW966181	AW966181
C 105	68	2.9	328	3	BU940536	BU940536 AGENCOURT	C 178	63	2.7	495	11	AQ631096	AQ631096
C 106	68	2.9	345	7	BE063133	BE063133 CM2-BT026	C 179	62	2.6	247	7	DB314361	DB314361
C 107	68	2.9	346	11	AQ057469	AQ057469 CIT-HSP-2	C 180	62	2.6	314	11	AQ373185	AQ373185
C 108	68	2.9	353	4	BK486268	BK486268 DKFZP6860	C 181	62	2.6	318	14	AG195739	AG195739 Pan trogl
C 109	68	2.9	361	11	AQ618132	AQ618132 HS_5168.B	C 182	62	2.6	347	7	AA346575	AA346575 EST52751
C 110	68	2.9	365	11	AQ134844	AQ134844 HS_3053_A	C 183	62	2.6	353	7	AW938400	AW938400
C 111	68	2.9	390	2	BQ354008	BQ354008 CM1-HT087	C 184	62	2.6	360	4	EX491893	EX491893
C 112	68	2.9	400	2	BG980008	BG980008 PM3-CN010	C 185	62	2.6	384	1	AA554319	AA554319
C 113	68	2.9	407	9	DB275663	DB275663 DB275663	C 186	62	2.6	408	3	BU953774	BU953774
C 114	68	2.9	414	4	BK486484	BK486484 DKFZP686A	C 187	62	2.6	422	3	BQ330072	BQ330072
C 115	68	2.9	415	2	BF767457	BF767457 CM1-CN006	C 188	62	2.6	474	11	AQ630172	AQ630172
C 116	68	2.9	436	3	BM831927	BM831927 K-EST0106	C 189	62	2.6	477	11	AQ432719	AQ432719
C 117	68	2.9	445	11	AQ108678	AQ108678 CIT-HSP-2	C 190	62	2.6	494	11	AQ588120	AQ588120
C 118	68	2.9	455	3	BQ082740	BQ082740 K-EST0144	C 191	61	2.6	247	1	AA744650	AA744650
C 119	68	2.9	466	2	BF8844783	BF8844783 RC5-HT0103	C 192	61	2.6	253	10	F00290	F00290
C 120	68	2.9	473	2	BF854162	BF854162 MR2-EN009	C 193	61	2.6	269	9	AA593267	AA593267 m08c09.s
C 121	68	2.9	481	4	BK506031	BK506031 DKFZP686N	C 194	61	2.6	390	5	CD722773	CD722773 o113h09.y
C 122	67	2.8	255	7	AW954446	AW954446 EST366516	C 195	61	2.6	434	9	DB296503	DB296503
C 123	67	2.8	313	10	DM415408	DM415408 HHAGE0161	C 196	61	2.6	434	9	AA629932	AA629932 ae64a05.s
C 124	67	2.8	459	11	B14696	B14696 342114.TV.C	C 197	60	2.5	252	1	AA185811	AA185811
C 125	67	2.8	484	1	AT339440	AT339440 CT02909.x	C 198	60	2.5	304	1	AU185811	AU185811
C 126	66	2.8	394	11	AQ044082	AQ044082 CIT-HSP-2	C 199	60	2.5	309	8	CM272355	CM272355
C 127	66	2.8	412	7	BE044986	BE044986 hnz5d03.x	C 200	60	2.5	314	4	CD103782	CD103782
C 128	66	2.8	414	9	DB343255	DB343255 DB343255	C 201	60	2.5	343	14	AG197866	AG197866
C 129	66	2.8	423	5	CD242224	CD242224 AGENCOURT	C 202	60	2.5	354	1	AA084715	AA084715
C 130	66	2.8	463	1	AT1141675	AT1141675 ct08c06.x	C 203	60	2.5	373	11	AV703682	AV703682
C 131	65	2.7	170	11	B57010	B57010 CIT-HSP-200	C 204	60	2.5	390	11	AQ386889	AQ386889
C 132	65	2.7	241	10	DM439608	DM439608 HHAGE0383	C 205	60	2.5	403	1	AA587662	AA587662
C 133	65	2.7	298	2	BF858756	BF858756 RC5-F7019	C 206	60	2.5	405	1	AT860020	AT860020
C 134	65	2.7	321	7	AW804281	AW804281 QV0-UM009	C 207	60	2.5	407	11	AQ206933	AQ206933
C 135	65	2.7	344	1	AA837058	AA837058 od18c04.s	C 208	60	2.5	416	1	AA827981	AA827981 od70d10.s
C 136	65	2.7	383	7	AW954447	AW954447 EST366517	C 209	60	2.5	420	1	AL709504	AL709504
C 137	65	2.7	410	1	AA161083	AA161083 zc62g12.s	C 210	60	2.5	450	1	AA581903	AA581903
C 138	65	2.7	413	2	BM313771	BM313771 ih06d04.x	C 211	60	2.5	456	2	AA311624	AA311624
C 139	65	2.7	425	2	BG292263	BG292263 602386711	C 212	60	2.5	462	7	AA469989	AA469989
C 140	65	2.7	433	4	BK509522	BK509522 DKFZP686N	C 213	60	2.5	470	11	AQ372508	AQ372508
C 141	65	2.7	438	11	AQ547205	AQ547205 RPCI-11-3	C 214	60	2.5	487	1	AT734098	AT734098
C 142	65	2.7	443	9	N66945	N66945 z848d11.s1	C 215	60	2.5	488	9	DB342571	DB342571
C 143	65	2.7	441	9	DB321305	DB321305 DB321305	C 216	59	2.5	170	10	DM456209	DM456209
C 144	65	2.7	454	1	AT299050	AT299050 qm14d12.x	C 217	59	2.5	207	10	BF850953	BF850953
C 145	65	2.7	456	11	AQ938658	AQ938658 NL1-CP9C	C 218	59	2.5	235	2	DR980073	DR980073
C 146	65	2.7	458	1	AA583808	AA583808 nm1h10.s	C 219	59	2.5	276	7	BE973738	BE973738
C 147	65	2.7	464	10	T55236	T55236 yH47b02.s1	C 220	59	2.5	283	10	DM426195	DM426195
C 148	65	2.7	478	2	BF875257	BF875257 QV3-ET009	C 221	59	2.5	294	10	DM422638	DM422638
C 149	65	2.7	485	10	H73389	H73389 yJ04h05.r1	C 222	59	2.5	313	3	BU954898	BU954898
C 150	65	2.7	487	11	AQ485557	AQ485557 RPCI-11-2	C 223	59	2.5	316	1	AT358501	AT358501
C 151	65	2.7	490	7	AM504669	AM504669 UI-HF-BN0	C 224	59	2.5	364	10	DY067428	DY067428
C 152	65	2.7	496	7	AM272758	AM272758 xu22f01.x	C 225	59	2.5	366	10	DY154827	DY154827 000802BAP
C 153	65	2.7	500	9	DN949487	DN949487 1r70a06.k	C 226	59	2.5	392	2	DB321502	DB321502
C 154	64	2.7	225	1	AA332624	AA332624 EST36596	C 227	59	2.5	409	7	AM193609	AM193609 xml8c02.x
C 155	64	2.7	226	2	BT101084	BT101084 MR2-EN009	C 228	59	2.5	412	7	AL699049	AL699049
C 156	64	2.7	305	3	BM677090	BM677090 UI-E-E01-	C 229	59	2.5	416	7	BE207545	BE207545 ba75a03.x
C 157	64	2.7	306	7	AM474160	AM474160 yJ11f12.x	C 230	59	2.5	484	2	BF724572	BF724572
C 158	64	2.7	324	3	BM721439	BM721439 UI-E-E01-	C 231	58	2.4	150	3	BQ311958	BQ311958
C 159	64	2.7	349	11	AQ104631	AQ104631 HS_3049_B	C 232	58	2.4	195	10	DM450956	DM450956
C 160	64	2.7	366	9	DA084230	DA084230 DA084230	C 233	58	2.4	217	3	BQ358234	BQ358234
C 161	64	2.7	372	11	AQ481144	AQ481144 RPCI-11-2	C 234	58	2.4	236	10	DM441895	DM441895
C 162	64	2.7	391	11	AV732611	AV732611 AV732611	C 235	58	2.4	256	9	DM441897	DM441897
C 163	64	2.7	399	11	AQ220113	AQ220113 HS_3248.B	C 236	58	2.4	263	10	F16274	F16274
C 164	64	2.7	412	1	AA613232	AA613232 nol9e05.s	C 237	58	2.4	264	10	DM4332914	DM4332914
C 165	64	2.7	421	5	CD686865	CD686865 EST3386.h	C 238	58	2.4	264	10	DM4332914	DM4332914

C 229	58	2.4	300	10	DM420646	DM420646 HHAGE0203	312	57	2.4	399	1	A1446638	A1446638 C11B09.x
C 240	58	2.4	310	7	BF217299	BF217299 601885644	313	57	2.4	402	1	AA437161	AA437161 zv61D10.x
C 241	58	2.4	325	1	AA569193	AA569193 nm30e07.s	314	57	2.4	403	11	A0030471	A0030471 HS_2183_A
C 242	58	2.4	341	10	DM408799	DM408799 HHAGE0095	315	57	2.4	408	2	BC272300	BC272300 nah67a09--
C 243	58	2.4	352	1	AA640034	AA640034 mp39g04.s	316	57	2.4	408	2	BM784814	BM784814 K-EST0063
C 244	58	2.4	355	2	BC993458	BC993458 CM3-HT117	317	57	2.4	408	3	BQ358368	BQ358368 RC0-HT093
C 245	58	2.4	359	1	AA346454	AA346454 EST5610	318	57	2.4	410	2	BF926380	BF926380 RC6-NT015
C 246	58	2.4	359	2	BI018146	BI018146 CM1-MT024	319	57	2.4	417	7	AV732919	AV732919 AV732919
C 247	58	2.4	371	5	H69640	H69640 YF91F07.r.1	320	57	2.4	420	7	BE832569	BE832569 CM3-MT011
C 248	58	2.4	371	10	CK000820	CK000820 AGENCOURT	321	57	2.4	431	3	BM766764	BM766764 K-EST0048
C 249	58	2.4	374	1	AA714632	AA714632 nx91a01.s	322	57	2.4	437	1	AA670468	AA670468 e937D08.s
C 250	58	2.4	378	11	AA056586	AA056586 C1T-HSP-2	323	57	2.4	437	11	AA0685482	AA0685482 HS_5528_B
C 251	58	2.4	380	2	BF802384	BF802384 CM0-CI009	324	57	2.4	438	1	AA134347	AA134347 zo23f09.s
C 252	58	2.4	387	11	BS8274	BS8274 C1T-HSP-201	325	57	2.4	442	4	EX952239	EX952239 DKFZP781C
C 253	58	2.4	393	11	AA129757	AA129757 HS_2253_A	326	57	2.4	443	1	A1291124	A1291124 CM15612.x
C 254	58	2.4	394	2	BI439766	BI439766 ic17f01.x	327	57	2.4	449	2	BC236735	BC236735 na147f01.
C 255	58	2.4	407	11	AA044609	AA044609 C1T-HSP-2	328	57	2.4	449	10	R97934	R97934 Y660H09.s1
C 256	58	2.4	408	11	AA052575	AA052575 HS_5207_A	329	57	2.4	449	13	C2453628	C2453628 MCF735G19
C 257	58	2.4	423	1	AA079688	AA079688 zm21b04.s	330	57	2.4	450	4	CA950254	CA950254 1r89b10.x
C 258	58	2.4	434	1	AA001029	AA001029 ze46b12.x	331	57	2.4	451	2	BF832548	BF832548 PM3-HT090
C 259	58	2.4	436	1	AI016000	AI016000 ou95g03.x	332	57	2.4	452	5	CD369526	CD369526 UI-H-FTI-
C 260	58	2.4	441	1	AI674873	AI674873 wc77f09.x	333	57	2.4	453	4	EX952224	EX952224 DKFZP781A
C 261	58	2.4	445	7	BE072475	BE072475 QV3-BT053	334	57	2.4	455	4	BM821684	BM821684 K-EST0090
C 262	58	2.4	445	11	AA0224580	AA0224580 HS_2012_A	335	57	2.4	457	7	AA467340	AA467340 he09e09.x
C 263	58	2.4	451	7	AA070037	AA070037 xt28c12.x	336	57	2.4	457	9	DB300351	DB300351 DB300351
C 264	58	2.4	460	2	BI019428	BI019428 CM3-MT019	337	57	2.4	458	5	CK429370	CK429370 o135g02.y
C 265	58	2.4	469	7	AA081048	AA081048 xc39g08.x	338	57	2.4	458	11	B99780	B99780 C1T-HSP-228
C 266	58	2.4	476	9	DB362271	DB362271 DB362271	339	57	2.4	461	1	AA513293	AA513293 nm8505.s
C 267	58	2.4	483	3	BU581466	BU581466 in37b11.y	340	57	2.4	461	11	AA0188539	AA0188539 HS_3228_B
C 268	58	2.4	485	1	AA601253	AA601253 no14h05.s	341	57	2.4	462	9	DA320912	DA320912 DA320912
C 269	58	2.4	486	11	BQ427185	BQ427185 C1E1-B1-	342	57	2.4	466	9	DB215542	DB215542 DB215542
C 270	58	2.4	488	1	BQ478120	BQ478120 ik81a01.x	343	57	2.4	466	11	AA041292	AA041292 RPT-11-1
C 271	58	2.4	490	9	DB375094	DB375094 DB375094	344	57	2.4	467	3	BU570301	BU570301 AGENCOURT
C 272	58	2.4	500	11	B37212	B37212 HS-1043-A1-	345	57	2.4	472	2	BF825390	BF825390 wh94a08.x
C 273	58	2.4	135	2	BI029483	BI029483 IL5-MT026	346	57	2.4	472	2	BF825390	BF825390 RC4-HN003
C 274	57	2.4	138	10	N45188	N45188 YV25H02.r.1	347	57	2.4	476	2	BF831846	BF831846 PM3-HT090
C 275	57	2.4	175	3	BQ337417	BQ337417 CM3-MT034	348	57	2.4	478	1	AA173374	AA173374 zp32d02.x
C 276	57	2.4	194	7	AA0849378	AA0849378 IL3-CT021	349	57	2.4	481	1	A1291268	A1291268 EST180368
C 277	57	2.4	194	7	AA0849378	AA0849378 IL3-CT021	350	57	2.4	481	1	AA309254	AA309254 EST180368
C 278	57	2.4	201	10	DM449760	DM449760 HHAGE0474	351	57	2.4	485	5	CD724032	CD724032 o129e06.y
C 279	57	2.4	220	2	AA093004	AA093004 QV0-NN114	352	57	2.4	487	3	BM831357	BM831357 K-EST0105
C 280	57	2.4	230	2	BF942942	BF942942 QV0-NN114	353	57	2.4	487	3	BM831357	BM831357 K-EST0105
C 281	57	2.4	261	2	BF988583	BF988583 CM3-GN010	354	57	2.4	490	9	DB208237	DB208237 DB208237
C 282	57	2.4	269	2	BI019457	BI019457 CM3-MT019	355	57	2.4	491	3	BM988774	BM988774 UI-H-DIO-
C 283	57	2.4	272	4	BK479592	BK479592 DKFZP686B	356	57	2.4	491	3	BP418287	BP418287 BP418287
C 284	57	2.4	274	10	F32894	F32894 HSPD5590 H	357	57	2.4	492	7	BB872393	BB872393 601448655
C 285	57	2.4	282	7	AA236342	AA236342 xm73c09.x	358	57	2.4	494	1	AU147696	AU147696 AU147696
C 286	57	2.4	285	2	BI030892	BI030892 IL5-MT026	359	57	2.4	166	11	A2516814	A2516814 ABRL5PALH
C 287	57	2.4	292	4	BK501252	BK501252 DKFZP779M	360	57	2.4	166	11	A2516814	A2516814 ABRL5PALH
C 288	57	2.4	295	7	BE167863	BE167863 CM2-HT051	361	57	2.4	226	3	BQ335219	BQ335219 IL5-MT026
C 289	57	2.4	301	8	CR772766	CR772766 DKFZP468D	362	57	2.4	316	11	B34242	B34242 H39713
C 290	57	2.4	303	2	BI029244	BI029244 IL5-MT026	363	57	2.4	322	10	H39713	H39713 y052h07.r.1
C 291	57	2.4	305	11	AA0631069	AA0631069 RPT-11-4	364	57	2.4	325	10	H44095	H44095 y073d03.r.1
C 292	57	2.4	320	2	BF896589	BF896589 QV1-MT022	365	57	2.4	328	3	BQ342707	BQ342707 CM2-NN114
C 293	57	2.4	321	7	AA440976	AA440976 he06f06.x	366	57	2.4	340	7	AA2646959	AA2646959 XG5d411.x
C 294	57	2.4	322	3	BO346538	BO346538 RC6-NT015	367	57	2.4	353	5	CD767839	CD767839 AGENCOURT
C 295	57	2.4	342	4	CA946468	CA946468 ni106f01.x	368	57	2.4	355	14	DU638728	DU638728 C1E1-HI
C 296	57	2.4	347	5	CD369571	CD369571 UI-H-FTI-	369	57	2.4	401	1	AA503473	AA503473 ng21h12.s
C 297	57	2.4	350	1	AA863453	AA863453 oh43a08.s	370	57	2.4	409	11	AA0216392	AA0216392 HS_2189_A
C 298	57	2.4	353	2	BF899983	BF899983 CM3-MT019	371	57	2.4	410	12	CG891563	CG891563 YGME244K3
C 299	57	2.4	357	2	BI086493	BI086493 602849765	372	57	2.4	423	11	B70666	B70666 C1T-HSP-206
C 300	57	2.4	357	2	BE933711	BE933711 QV4-HT089	373	57	2.4	427	7	AA512667	AA512667 xm02c05.x
C 301	57	2.4	359	7	BE933711	BE933711 QV4-HT089	374	57	2.4	428	10	R54885	R54885 y174g04.r.1
C 302	57	2.4	361	10	DM464911	DM464911 HHAGE0061	375	57	2.4	437	10	T91187	T91187 yd50d11.s1
C 303	57	2.4	362	1	AI537556	AI537556 CP10A09.x	376	57	2.4	445	11	AA0521948	AA0521948 HS_5063_B
C 304	57	2.4	363	4	CA434669	CA434669 UI-H-DIO-	377	57	2.4	452	1	AA773584	AA773584 abv61d08.s
C 305	57	2.4	368	7	AV764526	AV764526 AV764526	378	57	2.4	455	7	AV742337	AV742337 AV742337
C 306	57	2.4	373	7	AA794809	AA794809 RC6-UM001	379	57	2.4	460	8	CV319379	CV319379 CM2-NN114
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C 309	57	2.4	396	2	BI027138	BI027138 QV1-MT013	382	57	2.4	467	7	AV742309	AV742309 AV742309
C 310	57	2.4	397	2	BI019410	BI019410 CM3-MT019	383	57	2.4	474	1	AA584458	AA584458 nm05g09.s
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C 386	56	2.4	479	3	BP387566	459	55	2.3	330	10	R38154
C 387	56	2.4	479	11	AQ225492	C 460	55	2.3	332	4	CB308854
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C 389	56	2.4	497	11	B56584	462	55	2.3	335	1	AA678436
C 390	55	2.3	107	2	BF874937	463	55	2.3	336	9	DB299114
C 391	55	2.3	164	7	DM457213	464	55	2.3	336	11	AZ319869
C 392	55	2.3	174	10	AM834106	465	55	2.3	337	1	A1284669
C 393	55	2.3	185	10	DM453655	466	55	2.3	338	10	T07451
C 394	55	2.3	188	10	DM453224	467	55	2.3	339	10	F26152
C 395	55	2.3	192	11	AQ419192	468	55	2.3	339	11	B45091
C 396	55	2.3	195	10	DM450918	469	55	2.3	340	10	DM409176
C 397	55	2.3	197	2	BF872215	470	55	2.3	342	1	AA376763
C 398	55	2.3	197	2	BF872217	471	55	2.3	343	3	BU726254
C 399	55	2.3	206	7	AV740060	472	55	2.3	344	11	AZ319531
C 400	55	2.3	212	10	DM447603	473	55	2.3	345	9	AM519248
C 401	55	2.3	220	1	A1536555	474	55	2.3	345	9	DB372995
C 402	55	2.3	222	7	AV738722	475	55	2.3	346	2	BF769371
C 403	55	2.3	222	10	DM445354	476	55	2.3	346	3	BU564460
C 404	55	2.3	226	1	AA160954	477	55	2.3	351	2	B1044658
C 405	55	2.3	226	7	BE142249	478	55	2.3	352	4	BK485943
C 406	55	2.3	230	10	DM442711	479	55	2.3	352	11	AO628938
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C 408	55	2.3	238	11	AA493852	481	55	2.3	354	10	DM466089
C 409	55	2.3	241	11	BH010820	482	55	2.3	355	11	AOQ27777
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C 411	55	2.3	244	11	BH010819	484	55	2.3	355	11	AOQ13393
C 412	55	2.3	245	7	BE172686	485	55	2.3	357	11	AA586562
C 413	55	2.3	246	4	BK475938	486	55	2.3	357	11	B48798
C 414	55	2.3	250	2	B1016461	487	55	2.3	357	7	BF091721
C 415	55	2.3	251	3	BU736283	488	55	2.3	359	3	BQ082389
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C 420	55	2.3	272	8	CN270383	493	55	2.3	364	11	AQ585080
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C 427	55	2.3	290	10	DM423986	500	55	2.3	375	1	A1053672
C 428	55	2.3	292	9	DB306239	501	55	2.3	377	7	AV760937
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C 433	55	2.3	295	10	DM422350	506	55	2.3	383	2	BF771291
C 434	55	2.3	301	10	DM420342	507	55	2.3	383	7	AM769399
C 435	55	2.3	302	3	BQ372743	508	55	2.3	384	1	A1446182
C 436	55	2.3	302	11	AQ066068	509	55	2.3	385	3	BM710678
C 437	55	2.3	305	3	BQ441427	510	55	2.3	389	1	A1266576
C 438	55	2.3	306	1	AA332991	511	55	2.3	392	11	AQ205664
C 439	55	2.3	307	10	AA559290	512	55	2.3	395	7	BE834614
C 440	55	2.3	307	10	DM417194	513	55	2.3	395	1	AA810370
C 441	55	2.3	308	1	AA605274	514	55	2.3	396	11	AO893103
C 442	55	2.3	308	4	BK507755	515	55	2.3	396	11	AA252263
C 443	55	2.3	309	8	CN411432	516	55	2.3	398	4	BK494090
C 444	55	2.3	310	1	AA653964	517	55	2.3	398	14	AG198961
C 445	55	2.3	310	10	DM416528	518	55	2.3	399	1	AA101626
C 446	55	2.3	310	14	AG191703	519	55	2.3	400	3	BO315479
C 447	55	2.3	311	4	BO429929	520	55	2.3	401	1	AA574110
C 448	55	2.3	311	4	CB228842	521	55	2.3	401	4	BK374494
C 449	55	2.3	314	1	AA806602	522	55	2.3	401	9	DB374494
C 450	55	2.3	314	2	B1012428	523	55	2.3	402	1	AA348311
C 451	55	2.3	318	1	A1349874	524	55	2.3	403	1	AA302963
C 452	55	2.3	318	7	AM474152	525	55	2.3	404	1	AA233519
C 453	55	2.3	320	1	AA365694	526	55	2.3	404	7	AV729449
C 454	55	2.3	320	3	BU535916	527	55	2.3	404	10	N71724
C 455	55	2.3	320	3	BU565821	528	55	2.3	404	11	AOQ52661
C 456	55	2.3	322	10	DM412850	529	55	2.3	407	1	A1610159
C 457	55	2.3	323	4	CB230995	530	55	2.3	408	11	AO463801

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534	5	2.3	411	1	AI023082	AI023082	C	607	55	2.3	474	9	DA524257
535	5	2.3	412	11	AO381154	AO381154	C	608	55	2.3	475	11	AQ322667
536	5	2.3	413	1	AA598494	AA598494	C	609	55	2.3	476	11	AQ460418
537	5	2.3	414	10	F36273	F36273	C	610	55	2.3	478	4	BX494077
538	5	2.3	414	11	AQ201960	AQ201960	C	611	55	2.3	478	8	CN427732
539	5	2.3	415	7	BE049139	BE049139	C	612	55	2.3	478	11	B15716
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543	5	2.3	417	1	AU048124	AU048124	C	616	55	2.3	480	10	AA215474
544	5	2.3	420	2	BI044664	BI044664	C	617	55	2.3	481	11	B59125
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546	5	2.3	425	1	AA021133	AA021133	C	619	55	2.3	483	2	BG939415
547	5	2.3	427	9	DB360700	DB360700	C	620	55	2.3	485	7	BE464596
548	5	2.3	427	10	N26137	N26137	C	621	55	2.3	487	3	BQ776396
549	5	2.3	427	11	AQ060704	AQ060704	C	622	55	2.3	487	10	H64884
550	5	2.3	428	11	B94683	B94683	C	623	55	2.3	487	10	N59782
551	5	2.3	428	7	BM353142	BM353142	C	624	55	2.3	489	1	A1188327
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553	5	2.3	428	7	BE155879	BE155879	C	626	55	2.3	490	9	DA791977
554	5	2.3	430	10	RE7504	RE7504	C	627	55	2.3	491	3	BQ694140
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556	5	2.3	431	3	BU430249	BU430249	C	629	55	2.3	492	3	BM993628
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559	5	2.3	433	1	AA740993	AA740993	C	632	55	2.3	493	1	AL707211
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561	5	2.3	437	7	AM270270	AM270270	C	634	55	2.3	494	11	AQ675979
562	5	2.3	437	1	AA680211	AA680211	C	635	55	2.3	495	10	H64858
563	5	2.3	438	1	AI925812	AI925812	C	636	55	2.3	495	7	AM576391
564	5	2.3	438	1	AA613421	AA613421	C	637	55	2.3	497	8	CN411482
565	5	2.3	438	10	HS9797	HS9797	C	638	55	2.3	49		

677	54	2.3	362	1	AA668594	AA668594 ac44h06.s	C 750	54	2.3	475	4	C18699	C18699 C18699 Huma
C 678	54	2.3	365	10	T69648	T69648 yc4c07.r1	C 751	54	2.3	476	11	AO552314	AO552314 RPT-11-3
C 679	54	2.3	369	9	AV647080	AV647080 AV647080	C 752	54	2.3	480	11	AO547395	AO547395 RPT-11-4
680	54	2.3	369	9	DB373898	DB373898 DB373898	C 753	54	2.3	483	11	AA223258	AA223258 zc08b04.s
681	54	2.3	369	11	AQ043567	AQ043567 CIT-HSP-2	C 754	54	2.3	484	11	AZ916651	AZ916651 up-3b7-BB
682	54	2.3	370	7	BF476591	BF476591 naa57b12.	C 755	54	2.3	484	10	N25042	N25042 yw40D05.s1
C 683	54	2.3	372	2	BF827410	BF827410 RC3-HN002	C 756	54	2.3	485	10	N25965	N25965 yx87h06.s1
684	54	2.3	374	9	DB373537	DB373537 DB373537	C 757	54	2.3	493	7	AM833903	AM833903 QVO-TT000
C 685	54	2.3	377	11	AO58459	AO58459 HS-3085.B	C 758	54	2.3	495	8	CR557033	CR557033 DKF2P459A
686	54	2.3	385	10	R02223	R02223 yb06G07.s1	C 759	54	2.3	500	3	BM994083	BM994083 UI-H-DT0-
687	54	2.3	386	7	AM504326	AM504326 UI-HF-BN0	C 760	53	2.2	135	10	DM460741	DM460741 HHAGE0574
688	54	2.3	387	9	DB378639	DB378639 DB378639	C 761	53	2.2	138	2	BI053776	BI053776 CM3-GN033
C 689	54	2.3	389	11	AQ0505005	AQ0505005 RPT-11-2	C 762	53	2.2	177	2	BF848555	BF848555 IL5-BN08
690	54	2.3	390	10	TS4503	TS4503 yb06G07.s1	C 763	53	2.2	179	10	DM454711	DM454711 HHAGE0514
C 691	54	2.3	393	9	DB376634	DB376634 DB376634	C 764	53	2.2	200	7	AM502694	AM502694 UI-HF-BR0
C 692	54	2.3	398	2	BF780054	BF780054 MR4-DT007	C 765	53	2.2	247	1	AA594701	AA594701 nc01G11.s
693	54	2.3	398	9	DB373538	DB373538 DB373538	C 766	53	2.2	252	3	BU736279	BU736279 UI-E-DX0-
694	54	2.3	399	11	AQ755575	AQ755575 HS-2210.B	C 767	53	2.2	254	1	AA910118	AA910118 oe28f11.s
C 695	54	2.3	401	2	BF839225	BF839225 MR1-HT106	C 768	53	2.2	259	10	DM434273	DM434273 HHAGE0330
C 696	54	2.3	401	2	BF839325	BF839325 MR1-HT106	C 769	53	2.2	280	10	DM427007	DM427007 HHAGE0267
697	54	2.3	404	1	A1827259	A1827259 w109h12.x	C 770	53	2.2	287	1	AU100425	AU100425 am93f09.s
698	54	2.3	404	10	H04758	H04758 yj51d01.s1	C 771	53	2.2	300	1	AU100425	AU100425
699	54	2.3	406	1	A1493634	A1493634 CH3907.x	C 772	53	2.2	301	5	CD689775	CD689775 EST6298.h
C 700	54	2.3	406	2	BF875930	BF875930 CM0-ET016	C 773	53	2.2	326	10	R83585	R83585 yP16a06.r1
701	54	2.3	410	1	AA113861	AA113861 zn65h04.s	C 774	53	2.2	328	1	A1446464	A1446464 tJ19f02.x
C 702	54	2.3	410	1	AA579249	AA579249 nf28e01.s	C 775	53	2.2	331	1	AA856969	AA856969 oe03e09.s
703	54	2.3	410	9	DB341290	DB341290 DB341290	C 776	53	2.2	358	1	AA635433	AA635433 nc72b01.s
704	54	2.3	411	1	AA218727	AA218727 zq97g08.s	C 777	53	2.2	358	1	AU156018	AU156018 AU156018
C 705	54	2.3	411	7	BE139567	BE139567 xt20b06.x	C 778	53	2.2	373	11	AZ755935	AZ755935 ew04b11.x
706	54	2.3	411	11	AQ371385	AQ371385 HS-5043.A	C 779	53	2.2	374	11	B37346	B37346 HS-1043-A2-
C 707	54	2.3	412	1	AV651452	AV651452 AV651452	C 780	53	2.2	377	11	AQ102230	AQ102230 HS-3029.A
708	54	2.3	412	10	R82210	R82210 yj17g08.s1	C 781	53	2.2	379	11	AQ199759	AQ199759 RPT11-47
C 710	54	2.3	414	1	AA533138	AA533138 nj46h04.s	C 782	53	2.2	385	1	BO358965	BO358965 PM0-HT131
711	54	2.3	415	1	A1934307	A1934307 w001c06.x	C 783	53	2.2	389	1	AA151807	AA151807 zG81b01.x
C 712	54	2.3	416	10	R71624	R71624 y153b05.s1	C 784	53	2.2	391	1	AA151807	AA151807 zL39g02.x
713	54	2.3	417	1	AA67819	AA67819 EST78964	C 785	53	2.2	392	8	CR559619	CR559619 DKF2P459A
C 714	54	2.3	422	1	A1720141	A1720141 as78b08.x	C 786	53	2.2	403	11	AQ146678	AQ146678 HS-2242.A
715	54	2.3	422	7	AM407220	AM407220 UI-HF-BN0	C 787	53	2.2	404	10	T15407	T15407 IB1095 Infa
716	54	2.3	424	10	T94866	T94866 ye32e03.s1	C 788	53	2.2	405	9	DA085752	DA085752 DA085752
717	54	2.3	426	1	A1921673	A1921673 w028f02.x	C 789	53	2.2	408	9	DA819736	DA819736 DA819736
C 718	54	2.3	426	7	AM172727	AM172727 xJ02f07.x	C 790	53	2.2	416	11	B31253	B31253 HS-1007-A2-
719	54	2.3	426	9	DB324377	DB324377 DB324377	C 791	53	2.2	417	9	DB251574	DB251574 DB251574
C 720	54	2.3	428	11	C2462377	C2462377 MCF752e21	C 792	53	2.2	420	1	AA508091	AA508091 ng93c05.s
721	54	2.3	429	5	CF138927	CF138927 UI-HF-BN0	C 793	53	2.2	420	10	T71998	T71998 ye07e06.r1
C 722	54	2.3	430	11	AQ0583324	AQ0583324 RPT-11-4	C 794	53	2.2	423	11	AQ231927	AQ231927 HS-3243.B
723	54	2.3	430	11	AQ0583324	AQ0583324 RPT-11-4	C 795	53	2.2	423	11	AQ231927	AQ231927 HS-3243.B
C 724	54	2.3	435	11	AQ020131	AQ020131 CIT-HSP-2	C 796	53	2.2	424	11	AQ264587	AQ264587 CITBT-EI-
725	54	2.3	436	10	TS5329	TS5329 ya88b05.s1	C 797	53	2.2	430	9	BF893985	BF893985 QV1-MT016
726	54	2.3	437	5	CF138927	CF138927 UI-HF-BN0	C 798	53	2.2	439	7	AM469462	AM469462 hc84g01.x
C 727	54	2.3	437	7	AV759362	AV759362 AV759362	C 799	53	2.2	443	9	DB196263	DB196263 DB196263
728	54	2.3	437	9	DB379680	DB379680 DB379680	C 800	53	2.2	454	11	AQ547510	AQ547510 RPT-11-4
C 729	54	2.3	437	10	R35972	R35972 yH91b04.s1	C 801	53	2.2	458	4	BY508242	BY508242 DKF2P686H
730	54	2.3	440	5	CF137334	CF137334 UI-HF-BN0	C 802	53	2.2	464	11	AQ589864	AQ589864 HS-5336.B
C 731	54	2.3	442	2	BM512395	BM512395 IL5-GN003	C 803	53	2.2	476	5	CF709816	CF709816 CCADN72TF
732	54	2.3	442	2	BM512395	BM512395 IL5-GN003	C 804	53	2.2	477	9	DB372844	DB372844 DB372844
C 733	54	2.3	446	11	AQ0082746	AQ0082746 RPT11-54	C 805	53	2.2	486	11	AQ138184	AQ138184 HS-3074.B
734	54	2.3	448	14	CR972883	CR972883 Homo sapi	C 806	53	2.2	496	5	CF143355	CF143355 UI-HF-BR0
735	54	2.3	449	11	AQ062661	AQ062661 CIT-HSP-2	C 807	53	2.2	498	11	AQ0599623	AQ0599623 HS-5361.A
736	54	2.3	450	10	N30585	N30585 yw66g01.s1	C 808	53	2.2	131	2	BE995364	BE995364 CM0-HT125
737	54	2.3	451	10	A1742771	A1742771 wg64a10.x	C 809	52	2.2	217	2	BF743890	BF743890 PM3-BT083
738	54	2.3	455	10	W80462	W80462 zH82f07.s1	C 810	52	2.2	226	1	AA304782	AA304782 EST175771
739	54	2.3	457	10	R34721	R34721 yG43f05.s1	C 811	52	2.2	232	2	BI049324	BI049324 MRL-GN017
740	54	2.3	458	2	BF869358	BF869358 IL5-ET011	C 812	52	2.2	270	11	AQ0099538	AQ0099538 CIT-HSP-2
C 741	54	2.3	459	3	BU579746	BU579746 Im90C01.x	C 813	52	2.2	299	11	AQ588919	AQ588919 CITBT-B1-
742	54	2.3	463	4	BM636553	BM636553 K-EST0112	C 814	52	2.2	303	14	AG025853	AG025853 Homo sapi
C 743	54	2.3	463	4	BM636553	BM636553 K-EST0112	C 815	52	2.2	305	10	DM417621	DM417621 HHAGE0183
744	54	2.3	466	1	AA186870	AA186870 DKF2P781B	C 816	52	2.2	312	4	BO330163	BO330163 QVO-ET003
C 745	54	2.3	466	4	BM636553	BM636553 K-EST0112	C 817	52	2.2	316	3	BO330163	BO330163 QVO-ET003
746	54	2.3	471	10	R71121	R71121 y153b05.r1	C 818	52	2.2	324	2	BI031724	BI031724 IL5-MT026
C 747	54	2.3	471	10	R71121	R71121 y153b05.r1	C 819	52	2.2	330	1	AA487995	AA487995 ab12a09.x
748	54	2.3	473	4	BK645847	BK645847 DKF2P781J	C 821	52	2.2	331	7	AM875935	AM875935 QV2-PT001
749	54	2.3	475	2	BF773306	BF773306 CM3-IT004	C 822	52	2.2	333	10	DM410653	DM410653 HHAGE0113

C 823	52	2.2	335	10	DM410248	DM410248 HHAGE0109	C 896	51	2.2	290	10	DM423745	DM423745 HHAGE0234
C 824	52	2.2	336	11	AA632529	AA632529 NP81F03.s	C 897	51	2.2	294	7	BE934616	BE934616 RCO-HT093
C 825	52	2.2	338	11	AA0552753	AA0552753 RPTC-11-4	C 898	51	2.2	294	10	DM422364	DM422364 HHAGE0220
C 826	52	2.2	345	10	DM467527	DM467527 HHAGE0087	C 899	51	2.2	299	10	DM420725	DM420725 HHAGE0204
C 827	52	2.2	350	10	AA259245	AA259245 nc34902.s	C 900	51	2.2	304	7	AA973802	AA973802 EST185903
C 828	52	2.2	353	10	DM466288	DM466288 HHAGE0075	C 901	51	2.2	304	10	DM418229	DM418229 HHAGE0189
C 829	52	2.2	354	1	AA055613	AA055613 z176e05.s	C 902	51	2.2	308	9	DB350043	DB350043 DB350043
C 830	52	2.2	356	1	AA678843	AA678843 ah01e05.s	C 903	51	2.2	309	7	BE165312	BE165312 AGENC0072
C 831	52	2.2	366	3	AA938105	AA938105 c109h09.s	C 904	51	2.2	312	7	BE165312	BE165312 AGENC0072
C 832	52	2.2	368	3	BO353426	BO353426 RCO-HT093	C 905	51	2.2	314	1	AA771811	AA771811 a134f08.s
C 833	52	2.2	368	11	AA520456	AA520456 RPTC-11-1	C 906	51	2.2	316	4	BX507630	BX507630 DKEFP686C
C 834	52	2.2	376	1	AA764285	AA764285 AV764285	C 907	51	2.2	316	11	B39802	B39802 HS-1050-B1
C 835	52	2.2	383	1	AA487884	AA487884 ab12a09.s	C 908	51	2.2	320	1	AL705555	AL705555 DKEFP686C
C 836	52	2.2	386	10	TO3722	TO3722 1B795 Infan	C 909	51	2.2	322	1	AL700837	AL700837 DKEFP686C
C 837	52	2.2	386	11	B31865	B31865 HS-1012-B1-	C 910	51	2.2	323	1	AA501122	AA501122 ng18e05.s
C 838	52	2.2	392	10	H74004	H74004 y813d08.r1	C 911	51	2.2	324	1	AA079515	AA079515 zmg97c01.s
C 839	52	2.2	393	2	B1049547	B1049547 IL5-GN024	C 912	51	2.2	326	1	AI886176	AI886176 wm16902.x
C 840	52	2.2	406	2	BF897810	BF897810 QV1-MT022	C 913	51	2.2	328	2	BG056088	BG056088 naf87c02.x
C 841	52	2.2	407	1	AA542991	AA542991 n155a06.s	C 914	51	2.2	328	10	N43757	N43757 y118e03.r1
C 842	52	2.2	410	4	BX503320	BX503320 DKEFP2779D	C 915	51	2.2	337	2	BE153216	BE153216 nah27e02
C 843	52	2.2	414	2	BF880328	BF880328 QV3-ET017	C 916	51	2.2	338	11	AO111265	AO111265 C1T-HSP-2
C 844	52	2.2	420	7	BB892923	BB892923 BB892923	C 917	51	2.2	339	11	B99975	B99975 C1T-HSP-228
C 845	52	2.2	432	1	AI871722	AI871722 wm51f03.x	C 918	51	2.2	339	1	AI474388	AI474388 th19e11.x
C 846	52	2.2	433	5	CD689013	CD689013 EST5535.h	C 919	51	2.2	339	10	DM409400	DM409400 HHAGE0101
C 847	52	2.2	437	3	BO353303	BO353303 RCO-HT093	C 920	51	2.2	340	10	DM409032	DM409032 HHAGE0097
C 848	52	2.2	448	10	R91994	R91994 yP96a02.r1	C 921	51	2.2	342	1	AA847984	AA847984 od72a12.s
C 849	52	2.2	449	11	AO184635	AO184635 HS_2212_A	C 922	51	2.2	342	1	AI367975	AI367975 qv93f10.x
C 850	52	2.2	452	1	AA134367	AA134367 z024a09.s	C 923	51	2.2	346	10	DM467397	DM467397 HHAGE0086
C 851	52	2.2	453	1	AA126035	AA126035 zmw76d02.s	C 924	51	2.2	347	2	BG150677	BG150677 nah97b09.
C 852	52	2.2	454	11	AO016037	AO016037 C1T-HSP-2	C 925	51	2.2	348	7	AW274349	AW274349 xw74g09.x
C 853	52	2.2	459	1	AA126051	AA126051 zmw76a03.s	C 926	51	2.2	349	2	BC491882	BC491882 602535977
C 854	52	2.2	463	1	AL700093	AL700093 DKEFP686E	C 927	51	2.2	349	3	BO963522	BO963522 AGENC0082
C 855	52	2.2	479	9	DE214012	DE214012 DB214012	C 928	51	2.2	349	10	DM466972	DM466972 HHAGE0082
C 856	52	2.2	488	3	BO353742	BO353742 RCO-HT093	C 929	51	2.2	351	7	AV760571	AV760571 AV760571
C 857	52	2.2	491	4	CB856940	CB856940 NISC na04	C 930	51	2.2	351	10	TO6828	TO6828 EST04717.Fe
C 858	52	2.2	500	3	BP397912	BP397912 BP397912	C 931	51	2.2	360	1	AT301700	AT301700 C136G08.x
C 859	51	2.2	106	7	BE748217	BE748217 601571432	C 932	51	2.2	362	8	CMB363902	CMB363902 170006003
C 860	51	2.2	117	3	BO343448	BO343448 IL3-NT010	C 933	51	2.2	362	11	AO245201	AO245201 HS_2057_B
C 861	51	2.2	123	7	BE157292	BE157292 RQ4-HT037	C 934	51	2.2	364	1	AA378623	AA378623 EST191342
C 862	51	2.2	160	2	BF874655	BF874655 MCI-ET014	C 935	51	2.2	364	1	AA533725	AA533725 nj92d04.s
C 863	51	2.2	188	10	DM453709	DM453709 HHAGE0504	C 936	51	2.2	364	11	AO425900	AO425900 C1TBI-B1-
C 864	51	2.2	191	7	BE068791	BE068791 MR0-BT037	C 937	51	2.2	368	7	AM273218	AM273218 xrt35e08.x
C 865	51	2.2	191	7	BE068791	BE068791 MR0-BT037	C 938	51	2.2	369	2	BE915806	BE915806 IL3-UT011
C 866	51	2.2	202	3	BO380292	BO380292 CM4-UT001	C 939	51	2.2	370	11	B85287	B85287 RPTC11-1414
C 867	51	2.2	205	7	AA676769	AA676769 he25b09.x	C 940	51	2.2	375	7	AM303196	AM303196 xrt89h02.x
C 868	51	2.2	218	11	AO633750	AO633750 RPTC-11-4	C 941	51	2.2	377	10	F29702	F29702 HSPD19728.H
C 869	51	2.2	219	1	DM446001	DM446001 HHAGE0437	C 942	51	2.2	378	5	CD559049	CD559049 AGENC0087
C 870	51	2.2	224	1	AA361344	AA361344 EST70608	C 943	51	2.2	379	7	AM301350	AM301350 x875g06.x
C 871	51	2.2	224	3	BO330240	BO330240 RCG-ET006	C 944	51	2.2	380	5	CD519406	CD519406 AGENC0087
C 872	51	2.2	225	10	DM444548	DM444548 HHAGE0422	C 945	51	2.2	381	1	AA450199	AA450199 z442f12.r
C 873	51	2.2	229	1	AA515435	AA515435 ng66e05.s	C 946	51	2.2	381	7	AM377709	AM377709 IL5-HT020
C 874	51	2.2	237	1	BO350736	BO350736 MRL-C7073	C 947	51	2.2	381	11	AO096088	AO096088 HS_3030.A
C 875	51	2.2	247	3	BO352900	BO352900 RCG-HT084	C 948	51	2.2	382	4	BX479992	BX479992 DKEFP686B
C 876	51	2.2	255	11	AO508267	AO508267 RPTC-11-3	C 949	51	2.2	383	7	AV753615	AV753615 AV753615
C 877	51	2.2	256	1	AA175207	AA175207 ac79d03.s	C 950	51	2.2	383	11	AO480855	AO480855 RPTC11-2
C 878	51	2.2	257	3	BO336826	BO336826 CM3-MT011	C 951	51	2.2	384	11	AO010095	AO010095 HS_2263_A
C 879	51	2.2	265	1	AA847952	AA847952 od72b02.s	C 952	51	2.2	384	11	B37215	B37215 HS-1043-A1-
C 880	51	2.2	267	10	DM431896	DM431896 HHAGE0306	C 953	51	2.2	384	11	AO205724	AO205724 HS_3236.B
C 881	51	2.2	268	1	AA279427	AA279427 z885e04.s	C 954	51	2.2	385	1	AL048616	AL048616 DKEFP654J
C 882	51	2.2	269	7	AM873325	AM873325 hm04d02.x	C 955	51	2.2	387	11	AO072030	AO072030 HS_3020.A
C 883	51	2.2	270	10	P34558	P34558 HSPD29484.H	C 956	51	2.2	392	11	B37555	B37555 HS-1044-AZ-
C 884	51	2.2	275	10	DM428660	DM428660 HHAGE0283	C 957	51	2.2	393	7	BE883619	BE883619 MRL-FN000
C 885	51	2.2	275	11	AO261617	AO261617 C1TBI-B1-	C 958	51	2.2	393	11	AO240790	AO240790 C1T-HSP-2
C 886	51	2.2	276	10	DM428362	DM428362 HHAGE0280	C 959	51	2.2	394	1	AA401657	AA401657 z65d11.s
C 887	51	2.2	276	10	DM428375	DM428375 HHAGE0281	C 960	51	2.2	394	2	BE101316	BE101316 PM3-ET015
C 888	51	2.2	277	1	AA916039	AA916039 cg30a06.s	C 961	51	2.2	395	1	AA393286	AA393286 ct74e06.r
C 889	51	2.2	279	1	AA934680	AA934680 co08b12.s	C 962	51	2.2	396	1	AL601253	AL601253 DKEFP313J
C 890	51	2.2	281	1	AA357552	AA357552 EST16294	C 963	51	2.2	396	1	AO585337	AO585337 RPTC-11-4
C 891	51	2.2	282	10	DM426277	DM426277 HHAGE0260	C 964	51	2.2	397	8	CV385031	CV385031 QV1-AN005
C 892	51	2.2	286	10	DM426502	DM426502 HHAGE0262	C 965	51	2.2	398	1	AA372481	AA372481 EST84406
C 893	51	2.2	282	10	AA348859	AA348859 EST55403	C 966	51	2.2	401	11	AO313069	AO313069 RPTC11-11
C 894	51	2.2	286	2	BF830141	BF830141 PM2-HN008	C 967	51	2.2	404	1	AT744826	AT744826 ct15e08.x
C 895	51	2.2	290	7	AM063143	AM063143 TN0288.KR	C 968	51	2.2	404	4	CB296692	CB296692 12B22059_

699 51 2.2 409 10 H38858 H38858 yp48g08.s1
970 51 2.2 410 3 BQ373602 BQ373602 RCO-FT007
971 51 2.2 413 7 BA476017 u683b09.x
972 51 2.2 414 9 DB357596 DB357596 DB357596
973 51 2.2 415 1 AA252763 AA252763 z627d01.8
974 51 2.2 415 2 BG007574 RC2-GN026 BG007574 RC2-GN026
975 51 2.2 415 7 BE771854 CM3-FT009 BE771854 CM3-FT009
976 51 2.2 416 7 AV727786 AV727786 AV727786
977 51 2.2 417 4 CB137537 CB137537 K-EST0190
978 51 2.2 418 2 BC491641 BC491641 602535977
979 51 2.2 419 11 AQ490798 AQ490798 RPT-11-2
980 51 2.2 423 1 AY760920 AY760920 RP41_91E1
981 51 2.2 424 10 T28550 T28550 EST48019.Hu
982 51 2.2 427 5 CD511277 CD511277 AGENCOURT
983 51 2.2 428 8 B1019449 B1019449 CM3-MT019
984 51 2.2 430 8 CR739611 CR739611 CR739611
985 51 2.2 431 1 A1921649 wo28c05.x A1921649 wo28c05.x
986 51 2.2 432 1 AA765580 aa03912.B AA765580 aa03912.B
987 51 2.2 433 9 DB298038 DB298038 DB298038
988 51 2.2 435 1 AA723372 AA723372 ag88h03.r
989 51 2.2 435 9 DB300895 DB300895 DB300895
990 51 2.2 435 10 DR421737 DR421737 nav02m03.
991 51 2.2 437 10 T90474 T90474 yd43h09.s1
992 51 2.2 437 11 B51709 B51709 CIT978SK-A-
993 51 2.2 438 3 BQ429710 BQ429710 AGENCOURT
994 51 2.2 438 11 A0223268 A0223268 HS_2010_B
995 51 2.2 438 11 A0226823 A0226823 HS_2016_B
996 51 2.2 438 11 A0628177 A0628177 CITB1-ET-
997 51 2.2 439 1 AV709707 AV709707 AV709707
998 51 2.2 439 8 CR766123 CR766123 DKFZp459E
999 51 2.2 439 10 R40625 R40625 yf72g10.s1
1000 51 2.2 440 3 BQ373603 BQ373603 RCO-FT007

ALIGNMENTS

RESULT 1
CN409877 400 bp mRNA linear EST 16-MAY-2004
LOCUS 17000418214393 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN409877
ACCESSION CN409877.1 GI:47397001
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Pang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowksi,J and Stanton,L.W.
TITLE Transcriptional characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 400 Std Error: 0.00.
Location/Qualifiers

FEATURES

source
1..400
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"

/note="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hbs cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

Query Match 16.2%; Score 384; DB 8; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.4e-171;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

408 TTGCTTTGAAGTTATTAAGTCTGTGGCGCAAAAACACCTTACTATTGAAGAG 467
17 TTGCTTTGAAGTTATTAAGTCTGTGGCGCAAAAACACCTTACTATTGAAGAG 76
468 GTTCTTTTATCTGGCGCATATATATATATATATATATATATATATATATATAT 527
77 GTTCTTTTATCTGGCGCATATATATATATATATATATATATATATATATATAT 136
528 CATATGTATATATTTGTTCAAAATGATCTTCTAGAGATTTGTTGGCGTCCAGCTTCT 587
137 CATATGTATATATTTGTTCAAAATGATCTTCTAGAGATTTGTTGGCGTCCAGCTTCT 196
588 GTGAAGAGCAACGAAATATATATATATATATATATATATATATATATATATAT 647
197 GTGAAGAGCAACGAAATATATATATATATATATATATATATATATATATATAT 256
648 CAGGAATCATCGGCTCAGGATCATCTGTAGTGAAGAAAGTGCACCTTGAAGTGGG 707
257 CAGGAATCATCGGCTCAGGATCATCTGTAGTGAAGAAAGTGCACCTTGAAGTGGG 316
708 AGTATCAAAAGACCTTGTACAAAGCTTCAGGAAGAAAGCTTCATCTTCAATTGG 767
317 AGTATCAAAAGACCTTGTACAAAGCTTCAGGAAGAAAGCTTCATCTTCAATTGG 376
768 GTTCTTTGACCATCTACCTCATCT 791
377 GTTCTTTGACCATCTACCTCATCT 400

RESULT 2
BF151177 377 bp mRNA linear EST 30-OCT-2000
LOCUS QVO-BT0847-250900-410-907 BT0847 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF151177
ACCESSION BF151177.1 GI:11050360
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 377)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsumura,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.G.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-QVO-BT0847-250

DEFINITION ztr8h09.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:682817 3'
similar to gb:M92424 MDM2 PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA214617
VERSION AA214617.1 GI:1813254
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 427)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
AUTHORS Email: cgaps-rt@mail.nih.gov
TITLE This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
COMMENT Seq primer: -41m3 fwd. Et from Amersham
High quality sequence stop: 412.
FEATURES
Source
Location/Qualifiers
1..427
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5586137"
/db_xref="taxon:9606"
/clone="IMAGE:682817"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_1fb="NCI CGAP GCBI"
/note="Vector: pT73D-Pac1; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was prepared from human tonsillar cells
enriched for germinal center B cells by flow sorting
(CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr.
David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA
synthesis was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAGAGGAGCGGCGCTCACTTTTCTTTTCTT-3'
] Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 13.5%; Score 320; DB 1; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.6e-140;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY CCCCCTGAAGAACTGGGGAGTCTTGAGGACCCCGACTCCAAGCGCAAAACCCCGG 293
DB CCCCCTGAAGAACTGGGGAGTCTTGAGGACCCCGACTCCAAGCGCAAAACCCCGG 167
QY ATGTGAGGAGCAAGCAATGTGCAATGCTGTACTGACTGATGTGTCTGTA 353
DB ATGTGAGGAGCAAGCAATGTGCAATGCTGTACTGACTGATGTGTCTGTA 227
QY ACCACCTCAGATTCAGCTTCGGAACAAGAGCCCTGTGTAACCAAGCATTTGCTT 413
DB ACCACCTCAGATTCAGCTTCGGAACAAGAGCCCTGTGTAACCAAGCATTTGCTT 287
QY TTGAAGTATTAAAGTCTGGTGGACAAAAGACCTTATACATATGAAAGAGTTCTT 473
DB TTGAAGTATTAAAGTCTGGTGGACAAAAGACCTTATACATATGAAAGAGTTCTT 347
QY TTTTATCTTGGCCAGTATATATGACTAAGCATTTATGATGAGAAGCAACATATT 533
DB TTTTATCTTGGCCAGTATATATGACTAAGCATTTATGATGAGAAGCAACATATT 407
QY 534 GTAATATTGTCGAATGATCT 553
DB 408 GTAATATTGTCGAATGATCT 427

RESULT 5
BX482386 300 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686H06230.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFZp686H06230.5', mRNA sequence.
ACCESSION BX482386
VERSION BX482386.1 GI:31942229
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 300)
Koehler, K., Beyer, A., Mewes, H. W., Weil, B., Amld, C., Osanger, A.,
Fodor, G., Han, M. and Wiemann, S.
EST (Koehler, K., Beyer, A., Mewes, H. W., Weil, B., Amld, C., et al.)
Unpublished (2003)
JOURNAL Contact: MIPS
COMMENT MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Heinrich-
Heine-University, Duesseldorf/Germany) within the cDNA sequencing
consortium of the German Genome Project. No al sequence available.
This clone (DKFZp686H06230) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
Source
Location/Qualifiers
1..300
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686H06230"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1fb="686 (synonym: hlcc3)"
/note="Vector: pT73Bx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN
Query Match 12.2%; Score 289; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 9.8e-126;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY CCATGATCTACAGGAACCTTGTAAGTCAATCAGCAGGAATCTCGAATCAGTACAT 672
DB CCATGATCTACAGGAACCTTGTAAGTCAATCAGCAGGAATCTCGAATCAGTACAT 71
QY CTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGATGATCAAAAGACCTTTTACAG 732
DB CTGTGAGTGAAGACAGGTGTCACTTGAAGTGGAGATGATCAAAAGACCTTTTACAG 131
QY AGCTTCAGGAAGAAACCTTCATCTTCAACATTTGTTCTAGACATCTACCTCATCTA 792
DB AGCTTCAGGAAGAAACCTTCATCTTCAACATTTGTTCTAGACATCTACCTCATCTA 191
QY GAAGAGAGCAATTAAGTGAAGACAGAAAGAAATTCAGATGAATTAATCTGGTGAAGACAAA 852
DB GAAGAGAGCAATTAAGTGAAGACAGAAAGAAATTCAGATGAATTAATCTGGTGAAGACAAA 251
QY 853 GAAAACGCCACAATCTGATATGTAATTTCCCTTTCTTTGATGAAGCCT 901
DB 252 GAAAACGCCACAATCTGATATGTAATTTCCCTTTCTTTGATGAAGCCT 300
RESULT 6
AM070956 486 bp mRNA linear EST 20-OCT-2000
LOCUS AM070956
DEFINITION xaj1h03.x1 NCI CGAP Br18 Homo sapiens cDNA clone IMAGE:2568437 3'

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominae; Homo. 1 (bases 1 to 476)
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
TITLE	Unpublished (1997)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	Email: cgapbs-remail.nih.gov Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMLL, send email to: info@image.lml.gov Seq primer: -40UP from Glbco High quality sequence stop: 436.
FEATURES	Location/Qualifiers
SOURCE	1..476 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3296115" /tissue_type="B-cell, chronic lymphocytic leukemia" /lab_host="DH10B" /clone_lib="NCI CGAP CL11" /note="Vector: pTRITD-Pact, Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCCGCATGTGTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTRIT3 vector. Library is normalized, and was constructed by Bento Soares and M.Patima Bonaldo."
ORIGIN	
Query Match	9.2%; Score 219; DB 7; Length 476;
Best Local Similarity	99.4%; Pred. No.2.1e-92;
Matches 319; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Oy	CCCCGTGAAGAAGAACTGGGAGCTTTGAGGGACCCCAGATTCAGAGCCGAAAAAACC
Dd	108 CCCCCTGAAGAAACTGGGAGCTTTGAGGGACCCCAGATTCAGAGCCGAAAAAACC
Oy	294 ATGTGAGAGCAGGCAATGTGCATAACCATGTGTGTAAGCTGATGTGTCTGTA
Dd	168 ATGTGTAAGAGCAGGCAATGTGCATAACCATGTGTGTAAGCTGATGTGTCTGTA
Oy	354 ACCACTCACAGATTCAGCTTCGGAACAAGAGACCCGTGTTAGCCAAAGCATTTGTT
Dd	228 ACCACTCACAGATTCAGCTTCGGAACAAGAGACCCGTGTTAGCCAAAGCATTTGTT
Oy	414 TTGAAGTATTAAAGTCTGTGGTGCACAAAAGACCTTTATCATAGAAAGAGGTTCTT
Dd	288 TTGAAGTATTAAAGTCTGTGGTGCACAAAAGACCTTTATCATAGAAAGAGGTTCTT
Oy	474 TTTTATCTTGGCAGATATATTATGACTAAACGATATATGATGAGAACCAACATATT
Dd	348 TTTTATCTTGGCAGATATATTATGACTAAACGATATATGATGAGAACCAACATATT
Oy	534 GTATATGTTCATATGATCTT 554
Dd	408 GTATATGTTCATATGATCTT 428
RESULT 9	
CT000980	CT000980 265 bp mRNA linear EST 28-JUN-2005

DEFINITION	CT000980 RZPD no.9016 Homo sapiens cDNA clone RZDPp9016H2223 5', mRNA sequence.
ACCESSION	CT000980
VERSION	CT000980.1 GI:68294863
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 265) Hell.O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D. and Korn,B.
TITLE	Human T-lymphocytes library
JOURNAL	Unpublished (2005)
COMMENT	Contact: Inge Arlart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Email: www.rzpd.de RZPD; RZDPp9016H2223. RZPDLIB; (Human T-Lymphocytes) RZPD LIB No. 9016 http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact: Inge Arlart RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel.: +49 30 32639 100 Fax: +49 30 32639 111 www.rzpd.de This clone is available from RZPD; http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZDPp9016H2223 contact RZPD (product-support@rzpd.de) for further information. Primer name: qe3_4 , Primer sequence: CGGATACAAATTCAACAGC. Location/Qualifiers 1..265 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="RZDPp9016H2223" /tissue_type="T-Lymphocytes" /dev_stage="adult" /lab_host="DH10B" /note="Vector: pOE80LSN_cloned; Site_1: SalI; Site_2: NotI; Vector: http://www.rzpd.de/info/vectors/pOE80LSN_cloned_pic.shtml ; 1st strand cDNA was prepared from mRNA obtained from human T-Lymphocytes with a NotI - oligo(dT) primer [5' GACTAGTTCTTGATCGGAGCGCCGCTTTTTTTTTTTT 3'] . Double-stranded cDNA was ligated to SalI adaptors, digested with NotI and cloned into the NotI and SalI sites of the pOE80LSN_cloned vector"
FEATURES	source
Query Match	8.9%; Score 211; DB 8; Length 265;
Best Local Similarity	100.0%; Pred. No. 1.4e-88;
Matches 211; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
ORIGIN	
Db	441 CAAAAGA CACTTATCTATGTGAAGAGGTTT TTTTATCTTGCGCAGTATATTATGACT 500 5 CAAAAGA CACTTATCTATGTGAAGAGGTTT TTTTATCTTGCGCAGTATATTATGACT 64
Oy	501 AAAGCAT TATATGATGAGAACCAACAATAT TGTAATTGTTCAATGATCTTC TAGA 560 Db 65 AAAGCAT TATATGATGAGAACCAACAACA TATGTAATTGTTCAATGATCTTC TAGA 124
Oy	561 GATTGGT TTGGCGGCCCAAGCTCTCTGTG AAGAAGCACAGAAATATATACATGATC 620 Db 125 GATTGGT TTGGCGGCCCAAGCTCTCTGTG AAGAAGCACAGAAATATATACATGATC 184
Oy	621 TACAGAA ACTGGTAGTGCATCATCAGAGG 651 Db 185 TACAGAA ACTGGTAGTGCATCATCAGAGG 215

RESULT	10
LOCUS	H79860
DEFINITION	yv78f12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:339951 5' similar to gbl[M87921] HUMANCD120 Human carcinoma cell-derived Alu RNA transcript, (tRNA); gb:M92424 MDM2 PROTEIN (HUMAN) ; mRNA sequence.
ACCESSION	H79860
VERSION	H79860.1 GI:1057949
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 399) Hillier,L., Clark,N., Dubugue,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterson,R., Williamson,A., Woldmann,P. and Wilson,R.
REFERENCE	The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
TITLE	High quality sequence strops: 332
JOURNAL	Source: IMAGE Consortium, LLNL
COMMENT	This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: M13Rp1 High quality sequence stop: 332.
FEATURES	Location/Qualifiers 1..399 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:3788904" /db_xref="taxon:9606" /clone="IMAGE:239951" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares fetal liver spleen INFLS" /note="Organ: Liver and Spleen; Vector: pTR73 (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACGGAGAAATTAATTAAAGATCTTTTTTTTTTTTTT 3'] , double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia) , digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTR73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN	
Query Match	8.4%; Score 200; DB 10; Length 399;
Best Local Similarity	100.0%; Prid. No. 2,4e-83;
Matches 200; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1800 TTAGAAGATTATATATTTCTTAACATATAAACCCTAGGAATTGTAGCAACTGGAATTTAT 1859
Dd	15 TTAGAGAAATTAATATTTCTTACATATAAACCCCTAGGAATTGTAGCAACTGGAATTTAT 74
OY	1860 TCACATATATCAAAAGTGAGAAAATGCCTCAATTCACTAGCATTAAGTTTCCTCTTAGATAA 1919
Dd	75 TCACATATATCAAAAGTGAGAAAATGCCTCAATTCACTAGCATTAAGTTTCCTCTTAGATAA 134
OY	1920 TTGACCACTTTGGTAGTGAATGTGAATTAATCTTACATATAATTTGACTTGGATATATGAGC 1979
Dd	135 TTGACCACTTTGGTAGTGAATGTGAATTAATCTTACATATAATTTGACTTGAATATATGAGC 194

QY	1980	TCATCCTTTACCACTCC	1999	
DB	195	TCATCCTTTACCACTCC	214	
RESULT 11				
LOCUS	BF089387			
DEFINITION	PM2-HT0927-050900-003-c12 HT0927 Homo sapiens cDNA, mRNA sequence.	414 bp	mRNA	EST 19-OCT-2000
ACCESSION	BF089387			
VERSION	BF089387.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 414) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordi,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.			
TITLE	Sequence sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
PUBMED	10737800			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01505-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICP Human Cancer Genome Project. This entry can be found in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?fl=&t2=PM2-HT0927-050900-003-C12&t3=2000-09-05&t4=1) Seq primer: puc 18 forward High quality sequence start: 19 High quality sequence stop: 414. Location/Qualifiers 1. 414 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_id="HT0927" /note="Organ: head, neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
FEATURES				
SOURCE				
ORIGIN				
Query Match	8.4%	Score 199;	DB 7;	Length 414;
Best Local Similarity	100.0%;	Pred. No. 7.2e-83;		
Matches 199;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	235	CCCGTGAAGAACTGGGGAGTCTTGAGGAGACCCCGACTCCAAAGCGGAAACCCCGA	294	
DB	59	CCCGTGAAGAACTGGGGAGTCTTGAGGAGACCCCGACTCCAAAGCGGAAACCCCGA	118	
QY	295	TGGTGAAGAGCAGGCAATGTGCAATACCAACAATGTCTGACTACTGATGCGCTGTAA	354	
DB	119	TGGTGAAGAGCAGGCAATGTGCAATACCAACAATGTCTGACTACTGATGCGCTGTAA	178	
QY	355	CCACCTTCACGATTCACGCTTCGGAACAAGACCTGTGTTAGACCAAGCCATTGCTTT	414	

Db	179	CCACCTCAGCATTCGACGCTTCGGACACAGACCCCTGTTACACCAAGCCATTCGTTT	238
QY	415	TGAAGTATTAAAGTCGT	433
Db	239	TGAAGTATTAAAGTCGT	257
RESULT 12			
LOCUS	BF350973		
DEFINITION	QV1-HT0412-290400-178-d04 HT0412 Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BF350973		
VERSION	BF350973.1	GI:11310047	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homi		
REFERENCE	1 (bases 1 to 221)		
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.P., Matsumura,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
PUBMED	10737800		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL. (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&ct=QV1-HT0412-290400-178-d04&ct3=2000-04-29&ct4=1) Seq primer: puc 18 forward. Location/Qualifiers 1. .221 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_id="HT0412" /note="Organ: head neck; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORS875 PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
ORIGIN			
Query Match	8.1%;	Score 193;	DB 7; Length 221;
Best Local Similarity	100.0%;	Pred. No. 5.3e-80;	
Matches 193;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1165	AGAGGATACAGATTCATTGGAAGAGATCCGAAATTCCTAGCTGACATTGGAAT	1224
Db	29	MAAGGATACAGATTCATTGGAAGAGATCCGAAATTCCTAGCTGACATTGGAAT	88
QY	1225	GCACTTCATGCAATGAAATGAAATCCCCCTTCATCATCATTTGCAACAGATGTTGGGCC	1284
Db	89	GCACCTTCATGCAATGAAATGAAATCCCCCTTCATCATCATTTGCAACAGATGTTGGGCC	148
QY	1285	TTTCGTGAGATTCGCTTCTGTAAGATTAAGGGAAGATTAAGGGGAATTCCTGTGAGAAAG	1344

Db		149	TTCGTGGAATTTGGCTTCCGTGAAGATAAAGGAAAGTAAGGGGAAATCTCGAGAAG	208
Oy		1345	CCAAACTGAAAA	1357
Db		209	CCAAACTGAAAA	221
RESULT_13				
LOCUS	H13638	319 bp	mRNA	linear
DEFINITION	H13638			EST 27-JUN-1995
ACCESSION	H13638			
VERSION	H13638			
KEYWORDS	H13638			
SOURCE	H13638			
ORGANISM	H13638			
REFERENCE	H13638			
AUTHORS	H13638			
TITLE	H13638			
JOURNAL	H13638			
COMMENT	H13638			
FEATURES	H13638			
source	H13638			
ORIGIN	H13638			
Query Match	H13638			
Best Local Similarity	H13638			
Matches	H13638			
Oy	1773	ACTATTTCCTCCTAGTGACCTGTCATTAAGAAGATTATATTTCTAACTATAATACC	18322	
Db	2	ACTATTTCCTCCTAGTGACCTGTCATTAAGAAGATTATATTTCTAACTATAATACC	61	

QY 1833 TAGGATTTAGACACCTGAAATTTATTCATATATCAAGTGAAGAAATGCCCAATT 1892
 DB 62 TAGGATTTAGACACCTGAAATTTATTCATATATCAAGTGAAGAAATGCCCAATT 121
 QY 1893 CACATAGATTTCTTCTCTTATGATATTAATGACCTACTTGGTGTGG 1939
 DB 122 CACATAGATTTCTTCTCTTATGATATTAATGACCTACTTGGTGTGG 168

RESULT 14
 BE935243/c 469 bp mRNA linear EST 02-OCT-2000
 LOCUS MRO-MT0124-250800-201-d08 MT0124 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BE935243
 ACCESSION BE935243
 VERSION BE935243.1 GI:10461319
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo
 1 (bases 1 to 469)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800

TITLE Contact: Simpson A.J.G.
 JOURNAL Laboratory of Cancer Genetics
 PUBMED Ludwig Institute for Cancer Research
 COMMENT Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL.
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2=MRO-MT0124-250
 800-201-d08&ct3=2000-08-25&ct4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 2
 High quality sequence stop: 469.
 Location/Qualifiers
 1..469
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="MT0124"
 /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN
 Query Match 7.0%; Score 167; DB 7; Length 469;
 Best Local Similarity 98.9%; Pred. No. 1.2e-67;
 Matches 367; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1518 ATTATTTATGACACCAAGAGATGTGAAGATTGAAAGGAGAAACCAAGACAAA 1577
 DB 469 ATTATTTATGACACCAAGAGATGTGAAGATTGAAAGGAGAAACCAAGACTAA 410
 QY 1578 GAAGAGAGTGTGGAATCTAGTTGCCCTTAATGCCATTGAACCTGTGTGATTGTGCA 1637

DB 409 GAAGAGAGTGTGGAATCTAGTTGCCCTTAATGCCATTGAACCTGTGTGATTGTGCA 350
 QY 1538 GGTGACCTTAAATGGTTGATTTGCATGCGAAACAGACATCTTATGGCTGCTTT 1697
 DB 349 GGTGACCTTAAATGGTTGATTTGCATGCGAAACAGACATCTTATGGCTGCTTT 290
 QY 1698 ACATGTGCAAGAAGCTTAAAGAAAGATTAAGCCCGCCAGATGTAGCAACCAATT 1757
 DB 289 ACATGTGCAAGAAGCTTAAAGAAAGATTAAGCCCGCCAGATGTAGCAACCAATT 230
 QY 1758 CAATGATGTGTCTACTTATTTCCCTAGTTGACCTGTCTATTAAGAAATTAATATT 1817
 DB 229 CAATGATGTGTCTACTTATTTCCCTAGTTGACCTGTCTATTAAGAAATTAATATT 170
 QY 1818 CTAACTATATTAACCTTAGAATTTAGCAACCTGAAATTTATTCATATATCAAGTGA 1877
 DB 169 CTAACTATATTAACCTTAGAATTTAGCAACCTGAAATTTATTCATATATCAAGTGA 110
 QY 1878 GAAATGCCCTC 1888
 DB 109 GAAATGCCCTC 99

RESULT 15
 LOCUS A1281316/c 415 bp mRNA linear EST 28-JAN-1999
 DEFINITION g459d01.x1 NCI CGAP C08 Homo sapiens cDNA clone IMAGE:1873249 3'
 similar to gb:M92424 MDM2 PROTEIN (HUMAN)), mRNA sequence.
 ACCESSION A1281316
 VERSION A1281316.1 GI:3919549
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo
 1 (bases 1 to 415)

REFERENCE NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lemon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/bdrip/image/image.html
 Insert Length: 1313 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 409.
 Location/Qualifiers
 1..415

FEATURES
 source
 1..415
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:1873249"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP C08"
 /note="Organ: colon; Vector: pT7T3D-Pact; 1st strand cDNA
 was prepared from colon adenocarcinoma, and was then
 primed with a Not I oligo(dt) primer. Double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested
 with Not I and cloned into the Not I and Eco RI sites of
 the modified pT7T3 vector. Library is normalized. Library
 was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 7.0%; Score 166; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 3.8e-67;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACGGTGTCACTTGAAGTGGAGT 710
|||||
DB 278 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACGGTGTCACTTGAAGTGGAGT 219
|||||

QY 711 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTACATTTGGTT 770
|||||
DB 218 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTACATTTGGTT 159
|||||

QY 771 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 816
|||||
DB 158 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 113
|||||

RESULT 16 421 bp mRNA linear EST 13-FEB-1999
A1336475/c
LOCUS go61d06.x1 NCI CGAP Co8 Homo sapiens CDNA clone IMAGE:1913003 3'
DEFINITION similar to gb:M92424 MDM2 PROTEIN (HUMAN);, mRNA sequence.
ACCESSION A1336475
VERSION A1336475.1 GI:4073402
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 421)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnlnl.gov/bbrp/image/image.html
Insert Length: 1356 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 396.
Location/Qualifiers
1. .421
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1913003"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_1lb="NCI CGAP Co8"
/note="Organ: colon; Vector: pT73D-PacI; 1st strand cDNA
was prepared from colon adenocarcinoma, and was then
primed with a Not I - oligo(dT) primer. Double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 7.0%; Score 166; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 3.8e-67;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACGGTGTCACTTGAAGTGGAGT 710
|||||
DB 282 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACGGTGTCACTTGAAGTGGAGT 223
|||||

QY 711 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTACATTTGGTT 770
|||||
DB 222 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTACATTTGGTT 163
|||||

QY 771 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 816
|||||
DB 162 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 117
|||||

RESULT 17 423 bp mRNA linear EST 30-APR-1998
AA937920/c
LOCUS oF72e04.s1 NCI CGAP Co8 Homo sapiens CDNA clone IMAGE:1435902 3'
DEFINITION similar to gb:M92424 MDM2 PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AA937920
VERSION AA937920.1 GI:3096031
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 423)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnlnl.gov/bbrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 396.
Location/Qualifiers
1. .423
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1435902"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_1lb="NCI CGAP Co8"
/note="Organ: colon; Vector: pT73D-PacI; 1st strand cDNA
was prepared from colon adenocarcinoma, and was then
primed with a Not I - oligo(dT) primer. Double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 7.0%; Score 166; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.8e-67;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACGGTGTCACTTGAAGTGGAGT 710
|||||
DB 278 GATCATCGGACTCAGGTACATCTGTGAGTGAGAAACGGTGTCACTTGAAGTGGAGT 219
|||||

QY 711 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTACATTTGGTT 770
|||||
DB 218 GATCAAAAGACCTTGTACAGAGCTTCAAGAAAGAAACCTTCATCTTACATTTGGTT 159
|||||

QY 771 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 816
|||||
DB 158 TCTAGACCATCTACCTCATCTTAGAAGAGCAATTAGTAGACAG 113
|||||

RESULT 18
AI346140/c 423 bp mRNA linear EST 30-DEC-1998
LOCUS
DEFINITION gp43608.x1 NCI CGAP C08 Homo sapiens cDNA clone IMAGE:1925798 3'
ACCESSION AI346140
VERSION similar to gb:M92424 MDM2 PROTEIN (HUMAN) ;, mRNA sequence.
KEYWORDS
SOURCE EST. AI346140.1 GI:4083346
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 423)
NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bdrp/image/image.html
Seq primer: -40UP from Glibco
High quality sequence stop: 407.
Location/Qualifiers
1. 423
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1925798"
/issue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_1lb="NCI CGAP C08"
/note="Organ: colon; Vector: pT73D-Pact; 1st strand cDNA
was prepared from colon adenocarcinoma, and was then
primed with a Not I - oligo(dt) primer. Double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 7.0%; Score 166; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 3.8e-67;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 651 GAATCATCGGACCTGATACATCTGTGAGGAGACGAGTCACTTGAAGTGGAGT 710
DB 278 GAATCATCGGACCTGATACATCTGTGAGGAGACGAGTCACTTGAAGTGGAGT 219
QY 711 GATCAAAAGGACCTTGTACAAGAGCTTCAGGAAGAGAACTTCATCTTCACTTTGGTT 770
DB 218 GATCAAAAGGACCTTGTACAAGAGCTTCAGGAAGAGAACTTCATCTTCACTTTGGTT 159
QY 771 TCTAGACCATCTACCTCATCTAGAGAGAGCAATTAGTAGACAG 816
DB 158 TCTAGACCATCTACCTCATCTAGAGAGAGCAATTAGTAGACAG 113

RESULT 19
AI274906/c 437 bp mRNA linear EST 29-JAN-1999
LOCUS
DEFINITION q149603.x1 NCI CGAP C08 Homo sapiens cDNA clone IMAGE:1875628 3'
ACCESSION similar to gb:M92424 MDM2 PROTEIN (HUMAN) ;, mRNA sequence.
AI274906

VERSION AI274906.1 GI:3897180
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 437)
NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bdrp/image/image.html
Insert Length: 1368 Std Error: 0.00
Seq primer: -40UP from Glibco
High quality sequence stop: 405.
Location/Qualifiers
1. 437
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1875628"
/issue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_1lb="NCI CGAP C08"
/note="Organ: colon; Vector: pT73D-Pact; 1st strand cDNA
was prepared from colon adenocarcinoma, and was then
primed with a Not I - oligo(dt) primer. Double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 7.0%; Score 166; DB 1; Length 437;
Best Local Similarity 100.0%; Pred. No. 3.8e-67;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 651 GAATCATCGGACCTGATACATCTGTGAGGAGACGAGTCACTTGAAGTGGAGT 710
DB 278 GAATCATCGGACCTGATACATCTGTGAGGAGACGAGTCACTTGAAGTGGAGT 219
QY 711 GATCAAAAGGACCTTGTACAAGAGCTTCAGGAAGAGAACTTCATCTTCACTTTGGTT 770
DB 218 GATCAAAAGGACCTTGTACAAGAGCTTCAGGAAGAGAACTTCATCTTCACTTTGGTT 159
QY 771 TCTAGACCATCTACCTCATCTAGAGAGAGCAATTAGTAGACAG 816
DB 158 TCTAGACCATCTACCTCATCTAGAGAGAGCAATTAGTAGACAG 113

RESULT 20
AW999946/c 148 bp mRNA linear EST 05-JUN-2000
LOCUS
DEFINITION MRO-BN0070-180400-014-C06 BN0070 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW999946
VERSION AW999946.1 GI:8260180
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 148)

AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED
10737800

COMMENT
Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=MR0-BN0070-180400-014-c06&tl=2000-04-18&tl=1)
Seq primer: puc 18 forward
High quality sequence stop: 148.

FEATURES
source
1. 148
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_11b="BN0070"
/note="Organ: breast normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 6.2%; Score 148; DB 7; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-58;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 849 CAAAGAAACGCGCAAAATCTGATGATATTCCTTCTTGATGAAGCCCTGGCTCG 908
DB 148 CAAAGAAACGCGCAAAATCTGATGATATTCCTTCTTGATGAAGCCCTGGCTCG 89
QY 909 TGTGTATTAAGGAGATATGTTGTGAAGAAGCAGTAGCATCTACAGGAGCCCA 968
DB 88 TGTGTATTAAGGAGATATGTTGTGAAGAAGCAGTAGCATCTACAGGAGCCCA 29
QY 969 TCGAATCCGATTTGATGCTGTGTTAA 996
DB 28 TCGAATCCGATTTGATGCTGTGTTAA 1

RESULT 21
AI339173 335 bp mRNA linear EST 29-DEC-1998
AI339173
LOCUS
DEFINITION
q999a02.x1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1946186 3', similar to gb:M92424 MDW2 PROTEIN (HUMAN), mRNA sequence.
ACCESSION
AI339173
VERSION
AI339173.1 GI:4076100
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 335)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
Unpublished (1997)

COMMENT
Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emsert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILIN at:
www.bio.lnl.gov/btrp/image/image.html

FEATURES
source
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 335
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1946186"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_11b="NCI CGAP GC4"
/note="Vector: pTT3D-Pac1; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 5.9%; Score 140; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-55;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 234 CCCCCTGAAGGAACCTGGGAGCTTGTAGGAGACCCCGACTCCAGCGGAACCCCGG 293
DB 108 CCCCCTGAAGGAACCTGGGAGCTTGTAGGAGACCCCGACTCCAGCGGAACCCCGG 167
QY 294 ATGTGAGGAGCAGCGCAATGTGCATATACCAATGTGTGTAAGTGTGCTGTGA 353
DB 168 ATGTGAGGAGCAGCGCAATGTGCATATACCAATGTGTGTAAGTGTGCTGTGA 227
QY 354 ACCACTTCAAGATTCACG 373
DB 228 ACCACTTCAAGATTCACG 247

RESULT 22
BF746144/c 233 bp mRNA linear EST 10-JAN-2001
BF746144
LOCUS
DEFINITION
RCL-BT0254-071100-118-c09 BT0254 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF746144
VERSION
BF746144.1 GI:12072820
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 233)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

PUBMED
COMMENT

10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RCl&t2=RCl-BT0254-071100-118-c09&t3=2000-11-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 107
High quality sequence stop: 233.
Location/Qualifiers

FEATURES
source

1. .233
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="BT0254"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 5.8%; Score 138; DB 2; Length 233;
Best Local Similarity 100.0%; Pred.No. 8.4e-54;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1586 TGTGATCTAGTTGCCCTTATGCACTTGAACCTTGATTTGTCAGAGTGAC 1645
|||||
DB 233 TGTGATCTAGTTGCCCTTATGCACTTGAACCTTGATTTGTCAGAGTGAC 174
|||||
QY 1646 TAAAAATGTTGATTTGTCATGCAAAACAGACATCTTATGCTTTACATGTGC 1705
|||||
DB 173 TAAAAATGTTGATTTGTCATGCAAAACAGACATCTTATGCTTTACATGTGC 114
|||||
QY 1706 AAAAGAGCTAAAGAAAG 1723
|||||
DB 113 AAAAGAGCTAAAGAAAG 96
|||||

RESULT 23

BF336925/c 253 bp mRNA linear EST 22-NOV-2000
LOCUS BF336925
DEFINITION CM2-CT5001-270900-403-b04 CT5001 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF336925
VERSION BF336925.1 GI:11307673
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 (bases 1 to 253)
Dias Neto, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.G.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.

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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t2=CM2-CT5001-270900-403-b04&t3=2000-09-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 253.
Location/Qualifiers

FEATURES
source

1. .253
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="CT5001"
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 5.4%; Score 129; DB 7; Length 253;
Best Local Similarity 100.0%; Pred.No. 1.6e-49;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1651 ATGTTGATTTGTCATGCAAAACAGACATCTTATGCGCTTACATGCAAGA 1710
|||||
DB 238 ATGTTGATTTGTCATGCAAAACAGACATCTTATGCGCTTACATGCAAGA 179
|||||
QY 1711 AGCTAAAGAAAGAAATTAAGCCCTGCGCATGTATGACACCAATTCATGTTGC 1770
|||||
DB 178 AGCTAAAGAAAGAAATTAAGCCCTGCGCATGTATGACACCAATTCATGTTGC 119
|||||
QY 1771 TAACCTATT 1779
|||||
DB 118 TAACCTATT 110
|||||

RESULT 24

BE765314 345 bp mRNA linear EST 19-SEP-2000
LOCUS BE765314
DEFINITION IL2-NT0102-280700-115-H11 NT0102 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE765314
VERSION BE765314.1 GI:10195238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1 (bases 1 to 345)
Dias Neto, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.G.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SF, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=et2=PM1-AN0094-070
900-003-c08et3=2000-09-07&et4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 344.
Location/Qualifiers
source
1. 345
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0102"
/note="Organ: nervous tumor; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 5.3%; Score 125; DB 7; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.3e-47;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 470 TCTTTTTCCTGGCAGTATATATGACTAAAGATATATGAGAGAGAAACA 529
DB 170 TCTTTTTCCTGGCAGTATATATGACTAAAGATATATGAGAGAGAAACA 229
QY 530 TATGTATATGTTCAATGATCTTCTAGAGATTGTTGGCGTCCAAAGCTTCTGT 589
DB 230 TATGTATATGTTCAATGATCTTCTAGAGATTGTTGGCGTCCAAAGCTTCTGT 289
QY 590 GAAAGGACACAGAAATATATATCCATGATCTACAGAACTTGATGTCATC 645
DB 290 GAAAGGACACAGAAATATATATCCATGATCTACAGAACTTGATGTCATC 345

RESULT 25
BF081983 227 bp mRNA linear EST 18-OCT-2000
LOCUS PM1-AN0094-070900-003-c08 AN0094 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF081983
ACCESSION BF081983.1 GI:10875813
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 227)
Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Brines, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunnerstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=et2=PM1-AN0094-070
900-003-c08et3=2000-09-07&et4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 227.
Location/Qualifiers
source
1. 227
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="AN0094"
/note="Organ: amnion normal; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 5.0%; Score 119; DB 7; Length 227;
Best Local Similarity 100.0%; Pred. No. 9.4e-45;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1239 GAATGAATCCCCCTTCATCATGCAACAGATGTTGGCCCTTGAGAAATTGG 1298
DB 109 GAATGAATCCCCCTTCATCATGCAACAGATGTTGGCCCTTGAGAAATTGG 168
QY 1299 CTTCCTGAAGATTAAGGAAAGTAAAGGGAAATCTCTGAAAGCCAAATGAAAA 1357
DB 169 CTTCCTGAAGATTAAGGAAAGTAAAGGGAAATCTCTGAAAGCCAAATGAAAA 227

RESULT 26
AI246037/c 415 bp mRNA linear EST 28-JAN-1999
LOCUS qk44h12.x1 NCI_CGAP Co8 Homo sapiens cDNA clone IMAGE:1871879 3'
DEFINITION similar to gb:M92424 MDW2 PROTEIN (HUMAN);, mRNA sequence.
ACCESSION AI246037
VERSION AI246037.1 GI:3841434
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 415)
Email: cgabds-r@mail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/ULNL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 1343 Std Error: 0.00
Seq primer: -40UP from Gihco
High quality sequence stop: 409.
Location/Qualifiers
source
1. 415
/organism="Homo sapiens"

ORIGIN

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1871879"
/issue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Co8"
/note="Organ: Colon; Vector: pT73D-Paci; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 4.8%; Score 115; DB 1; Length 415;
Best Local Similarity 99.4%; Pred. No. 7,4e-43;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 651 GAATCATCGAGCTCAGTACATCTGTGAGTGAAGACGCTGACCTGAGGTGGAGT 710
Db 278 GAATCATCGAGCTCAGTACATCTGTGAGTGAAGACGCTGACCTGAGGTGGAGT 219
Qy 711 GATCAAGAGCCTTGTACAGAGCTTCAAGAGAACTTCATCTTCACTTTGGTT 770
Db 218 GATCTAAGAGCCTTGTACAGAGCTTCAAGAGAACTTCATCTTCACTTTGGTT 159
Qy 771 TCTAGACCATCTTACCTCATCTTGAAGAGAGCAATTAGTACAGAG 816
Db 158 TCTAGACCATCTTACCTCATCTTGAAGAGAGCAATTAGTACAGAG 113

RESULT 27

LOCUS AA568852 366 bp mRNA linear EST 09-SEP-1997
DEFINITION nm27a12.s1 NCI CGAP Lip2 Homo sapiens cDNA clone IMAGE:1061374
similar to gb:M92424 MDM2 PROTEIN (HUMAN); contains Alu repetitive
element; mRNA sequence.

ACCESSION AA568852
VERSION AA568852.1 GI:2341906
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 366)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsabbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnlnl.gov/bhrp/image/image.html
Insert Length: 636 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 273.
Location/Qualifiers

FEATURES

source
1..366
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1061374"
/issue_type="liposarcoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lip2"

ORIGIN

/note="Vector: pAMP10; mRNA made from liposarcoma, cDNA
made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."

Query Match 4.6%; Score 108; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.6e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1947 AATCTACTAATTAATTTGACCTGAATATGATGCTCATCTTACACCACTCTAATTTT 2006
Db 37 AATCTACTAATTAATTTGACCTGAATATGATGCTCATCTTACACCACTCTAATTTT 96
Qy 2007 AATTAATTTCTACTCTGTCTTAATGAGAAGTACTGTTTTTTTTTTT 2054
Db 97 AATTAATTTCTACTCTGTCTTAATGAGAAGTACTGTTTTTTTTTTT 144

RESULT 28

LOCUS R80235 456 bp mRNA linear EST 09-JUN-1995
DEFINITION Y196d02.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:147075 3' similar to gb:M92424 MDM2 PROTEIN (HUMAN);, mRNA
sequence.

ACCESSION R80235
VERSION R80235.1 GI:856516
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 456)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, B., Waterston, R., Williamson, A., Wohlmann, P., and
Wilson, R.

TITLE The MaSHU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Insert Size: 529
High quality sequence stops: 322
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnlnl.gov) for further information.
Insert Length: 529 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 322.
Location/Qualifiers

FEATURES

source
1..456
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:558688"
/db_xref="taxon:9606"
/clone="IMAGE:147075"
/sex="Female"
/dev stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares Placenta Nb2HP"
/note="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AATCGAAGAATTCGCGCGGAGAAATTTTATTTTATTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT713 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN

Query Match 4.5%; Score 106; DB 10; Length 456;
Best Local Similarity 99.4%; Pred. No. 1.4e-38;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 234 CCCCCTGAAGAAATGCGGAGCTTTGAGGACCCCGACTCCAGCCGGAACCCCGG 293
DB 108 CCCCCTGAAGAAATGCGGAGCTTTGAGGACCCCGACTCCAGCCGGAACCCCGG 167
QY 294 ATGGTGAGAGACGAGCAATGCAATACCAATGCTGACTGACTGATGATGCTGTGA 353
DB 168 ATGGTGAGAGACGAGCAATGCAATACCAATGCTGACTGACTGATGATGCTGTGA 227
QY 354 ACCACCTCAGAGATTCCAGCTTCGGAACAGAGACC 390
DB 228 ACCACCTCAGAGATTCCAGCTTCGGAACAGAGACC 264

RESULT 29
CC000590 489 bp DNA linear GSS 31-MAR-2003
LOCUS UP 479-4N T7 RPl11 Human Male BAC library Homo sapiens genomic
DEFINITION Clone 479-4N, genomic survey sequence.

ACCESSION CC000590
VERSION CC000590.1 GI:29379150
KEYWORDS GSS.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 489)

AUTHORS Cheung, V.G., Dalrymple, H.L., Narasimhan, S., Watts, J., Schuler, G.,
Raap, A.K., Morley, M. and Bruzel, A.
A resource of mapped human bacterial artificial chromosome clones
Genome Res. 9 (10), 989-993 (1999)

TITLE JOURNAL PUBMED
10523527
COMMENT Contact: Narasimhan SL, Morley M, Burdick J, Cheung VG
Department of Pediatrics
University of Pennsylvania
3516 Civic Center Blvd, ARC 516, Philadelphia, PA 19104, USA
Tel: 215 590 2664
Fax: 215 590 3709
Email: mlennox@mail.med.upenn.edu
Plate: 479 row: N column: 4
Seq primer: T7
Classes: BAC ends.

FEATURES
source Location/Qualifiers
1..489

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="479-4N"
/sex="Male"
/cell_type="Lymphocytes"
/clone_1ib="RPl11 Human Male BAC library"
/note="Vector: pBACE3.6; RPl11 Human Male BAC library"

ORIGIN

Query Match 4.1%; Score 98; DB 12; Length 489;
Best Local Similarity 100.0%; Pred. No. 9.2e-35;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTGTAGAGACAGGCTTCAACCGTGTAGCCAGGATGCTCGATCTCGACTCGT 2319
DB 454 TTTTGTAGAGACAGGCTTCAACCGTGTAGCCAGGATGCTCGATCTCGACTCGT 395
QY 2320 GATCCGCCACCTCGGCTCCCAAGTGTGGATTAC 2357

DB 394 GATCCGCCACCTCGGCTCCCAAGTGTGGATTAC 357

RESULT 30

LOCUS N20967 385 bp mRNA linear EST 19-DEC-1995
DEFINITION yk57c04.61 Soares melanocyte 2NBM Homo sapiens cDNA clone
IMAGE:265830 3' similar to contains Alu repetitive element; contains
element 11 repetitive element ;, mRNA sequence.

ACCESSION N20967.1 GI:1126137
VERSION N20967.1
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 385)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaekie, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 313
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
Insert Length: 2267 Std Error: 0.00
Seq primer: ml3 -40 forward
High quality sequence stop: 313.

FEATURES
source Location/Qualifiers
1..385

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3875472"
/db_xref="taxon:9606"
/clone="IMAGE:265830"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_1ib="Soares melanocyte 2NBM"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer (5',
TGTTCACATCTGAAAGTGGAGCGGCGGCGGCACTTTTCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 4.0%; Score 94; DB 10; Length 385;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTGTAGCCAGGATGCTCGATCTCGACTCGTATCGCCCACTC 2333
DB 13 GGGTTTACCGTGTGTAGCCAGGATGCTCGATCTCGACTCGTATCGCCCACTC 72
QY 2334 GGGCTCCCAAGTGTGGATTACAGCATGAGC 2367
DB 73 GGGCTCCCAAGTGTGGATTACAGCATGAGC 106

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RESULT 31
BE019522      437 bp      mRNA      linear      EST 06-JUN-2000
LOCUS
DEFINITION    bb57c10.y1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3010770 5'
               similar to gb:92424 MDM2 PROTEIN (HUMAN); gb:X58876 Murine mdm2
ACCESSION     BE019522
VERSION
KEYWORDS      mRNA for mdm2 protein (MOUSE);, mRNA sequence.
SOURCE
ORGANISM      Homo sapiens (human)
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homiidae; Homo.
REFERENCE
AUTHORS       1 (bases 1 to 437)
TITLE         NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL       National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT       Unpublished (1999)
               Contact: Robert Strausberg, Ph.D.
               Email: cgaabs@mail.nih.gov
               Tissue Procurement: ATCC
               cDNA Library Preparation: Ling Hong/Rubin Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LINL at:
               image.lnl.gov/image/html/resources.shtml
               Seq primer: -40RP from Gibco
               High quality sequence step: 361.
               Location/Qualifiers
               1..437
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:3010770"
               /cissue_type="rhabdomyosarcoma"
               /lab_host="DH10B (phage-resistant)"
               /clone_1lb="NIH_MGC_17"
               /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
               Site_2: XhoI; cDNA made by oligo-dT priming.
               Directionally cloned into EcoRI/XhoI sites using the
               following 5' adaptor: GGACGAG(G). Size-selected >500bp
               for average insert size 1.8kb. Library constructed by
               Ling Hong in the laboratory of Gerald M. Rubin (University
               of California, Berkeley) using ZAP-cDNA synthesis kit
               (Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

FEATURES

source

```

Query Match      4.0%; Score 94; DB 7; Length 437;
Best Local Similarity 100.0%; Pred. No. 7.4e-33;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 AGATGACGACGAAGACCGAGCGGGGCGCGGACCCCTCGACCGAGATCTCTG 112
    |||||||
DB 1 AAGATGACGACGAAGACCGAGCGGGGCGCGGACCCCTCGACCGAGATCTCTG 60
    |||||||

QY 113 TCGTTTCGACGACGAGACCGTCTCCCTCCCGG 146
    |||||||
DB 61 TCGTTTCGACGACGAGACCGTCTCCCTCCCGG 94
    |||||||

RESULT 32
BF949018      147 bp      mRNA      linear      EST 22-JAN-2001
LOCUS
DEFINITION    MR3-NN0220-011100-009-b11 NN0220 Homo sapiens cDNA, mRNA sequence.
ACCESSION     BF949018
VERSION
KEYWORDS      EST.
SOURCE
ORGANISM      Homo sapiens (human)
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
```

REFERENCE

AUTHORS

Homiidae; Homo.
1 (bases 1 to 147)
Dias Neto,F., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FADESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&t2=MR3-NN0220-
011100-009-b11&t3=2000-11-01&t4=1)
Seq primer: puc 18 forward
High quality sequence step: 147.
Location/Qualifiers

FEATURES

source

```

1..147
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="NN0220"
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESRES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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ORIGIN

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Query Match      3.9%; Score 92; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 7e-32;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1266 TGCACAGATGTTGGCCCTTGCTGAGATTGGCTTCGAGATTAAGGAAGTAA 1325
    |||||||
DB 56 TGCACAGATGTTGGCCCTTGCTGAGATTGGCTTCGAGATTAAGGAAGTAA 115
    |||||||

QY 1326 GGGGAATCTCTGAGAAACCAAACTGAAAA 1357
    |||||||
DB 116 GGGGAATCTCTGAGAAACCAAACTGAAAA 147
    |||||||

RESULT 33
BF949413      147 bp      mRNA      linear      EST 22-JAN-2001
LOCUS
DEFINITION    MR3-NN0220-031100-009-b11 NN0220 Homo sapiens cDNA, mRNA sequence.
ACCESSION     BF949413
VERSION
KEYWORDS      EST.
SOURCE
ORGANISM      Homo sapiens (human)
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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REFERENCE
AUTHORS       1 (bases 1 to 147)
               Dias Neto,F., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
               Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
               Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
               Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
               O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
               Simpson,A.J.
```

Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&cl2=MR3-NN0220-
031100-009-b1&cl3=2000-11-03&cl4=1)
Seq primer: puc 18 forward
High quality sequence stop: 147.
Location/Qualifiers
1. 147
/organism="Homo sapiens"
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/dev_stage="Adult"
/clone_lib="NN0220"
/note="Torgan: nervous normal; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 3.9%; Score 92; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 7e-32;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1266 TGCAACAGATGTTGGCCCTTGTGAGATTGCTCTCGAAGATTAAGGAGAAATATA 1325
DB 56 TGCAACAGATGTTGGCCCTTGTGAGATTGCTCTCGAAGATTAAGGAGAAATATA 115
QY 1326 GGGGAAATCTCTGAGAAAGCCAACTGGAAAA 1357
DB 116 GGGGAAATCTCTGAGAAAGCCAACTGGAAAA 147
RESULT 34
F35659 151 bp mRNA linear EST 13-MAY-1999
LOCUS HSPD32490 HM3 Homo sapiens cDNA clone SHS-000005-0/C05, mRNA
DEFINITION HSPD32490 HM3 Homo sapiens cDNA clone SHS-000005-0/C05, mRNA
ACCESSION F35659
VERSION F35659.1 GI:4821285
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 151)
Lanfanchi,G., Muraro,T., Caldera,F., Pacchioni,B., Pallavicini,A.,
Pandoito,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
Identification of 4370 expressed sequence tags from a
3'-end-specific cDNA library of human skeletal muscle by DNA
sequencing and filter hybridization
Genome Res. 6 (1), 35-42 (1996)
8681137
JOURNAL CONTACT: Valle G.
PUBMED CRIBI Biotechnology Centre
COMMENT University of Padua
Via Trieste 75, 35121 Padua, Italy

ABI Chromatograms and other information are available on WWW at
http://grp.bio.unipd.it.
Location/Qualifiers
1. 151
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SHS-000005-0/C05"
/sex="female"
/tissue_type="Pectoral muscle (after mastectomy)"
/clone_lib="HM3"
/note="Vector: pCDNA11 (Invitrogen); Site 1: BstXI;
Site 2: NotI; The library was constructed by G.
Lanfanchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated
oligo-dT-NotI primer
(5'-biotin-AACCCGGCTCGAGCGCCGCTTTTCTTTTCTTTT-3'). The
ds cDNA was sonicated and size-selected in the range
350-550 bp. The 3' specific fragments were selected by
streptavidin coated magnetic beads, ligated to
non-palindromic BstXI adapters, NotI digested and
directionally cloned into BstXI-NotI cut pCDNA11 vector."
ORIGIN
Query Match 3.7%; Score 88; DB 10; Length 151;
Best Local Similarity 100.0%; Pred. No. 5.ee-30;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTACCGTGTAGCCAGATGCTTCATCTCTGACCTGTATCCGCCACCTC 2333
DB 18 GGGTTTACCGTGTAGCCAGATGCTTCATCTCTGACCTGTATCCGCCACCTC 77
QY 2334 GGCCTCCCAAGTGCTGGGATTACAGGC 2361
DB 78 GGCCTCCCAAGTGCTGGGATTACAGGC 105
RESULT 35
BG956827 298 bp mRNA linear EST 12-JUN-2001
LOCUS IL3-CT0674-210201-486-A08 CT0674 Homo sapiens cDNA, mRNA sequence.
DEFINITION IL3-CT0674-210201-486-A08 CT0674 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG956827
VERSION BG956827.1 GI:14374998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 298)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&cl2=IL3-CT0674-
210201-486-A08&cl3=2001-02-21&cl4=1)
Seq primer: puc 18 forward

FEATURES High quality sequence stop: 216.
Location/Qualifiers
source 1..298

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0674"
/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 3.7%; Score 88; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.5e-30;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCCAGATGTCATCTCTGACTCTGTCGATCCGCCACCTC 2333

Db 158 GGGTTTACCGTGTAGCCAGATGTCATCTCTGACTCTGTCGATCCGCCACCTC 217

QY 2334 GGCTCCCAAGGCTGGGATTACAGGC 2361

Db 218 GGCTCCCAAGGCTGGGATTACAGGC 245

RESULT 36

LOCUS DW419606 303 bp mRNA linear EST 14-JAN-2006
DEFINITION HHAGE019336 Human liver regeneration after partial hepatectomy Homo sapiens cDNA, mRNA sequence.

ACCESSION DW419606
VERSION DW419606.1 GI:84921162

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Xu,C.S.

1 (bases 1 to 303)

Liver regeneration after PH

Unpublished (2003)

Contact: Cun-Shuan Xu

Henan Bioengineering Key Lab

Henan Normal University

No. 148 Jianshe Road, Xinxiang City, P.R.China

Tel: 0086373328084

Fax: 0086373326524

Email: xucs@x263.net.

Location/Qualifiers

1..303
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="liver"
/clone_lib="Human liver regeneration after partial hepatectomy"

FEATURES

source

ORIGIN

Query Match 3.7%; Score 88; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 5.5e-30;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTTCACGAGTGTCTGATCTCTGACTCTGTCGATCCGCCACCTCGGCTCCCAA 2344

Db 116 TGTTCACGAGTGTCTGATCTCTGACTCTGTCGATCCGCCACCTCGGCTCCCAA 57

QY 2345 GTGCTGGATTACAGCATGAGCCACG 2372

Db 56 GTGCTGGATTACAGCATGAGCCACG 29

RESULT 37
LOCUS AQ094950/c 389 bp DNA linear GSS 27-AUG-1998
DEFINITION HS_3028_A2_C05_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=10 Row=B, genomic survey sequence.

ACCESSION AQ094950
VERSION AQ094950.1 GI:3466397
KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

AUTHORS

JOURNAL
PUBMED
CONTACT: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3028 row: B column: 10
Class: BAC ends
High quality sequence stop: 389.

FEATURES
source

1..389
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3028 Col=10 Row=B"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 3.7%; Score 88; DB 11; Length 389;
Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTACCGTGTAGCCAGATGTCATCTCTGACTCTGTCGATCCGCCACCTC 2333

Db 127 GGGTTACCGTGTAGCCAGATGTCATCTCTGACTCTGTCGATCCGCCACCTC 68

QY 2334 GGCTCCCAAGGCTGGGATTACAGGC 2361

Db 67 GGCTCCCAAGGCTGGGATTACAGGC 40

RESULT 38

LOCUS AO153405 454 bp DNA linear GSS 08-OCT-1998
DEFINITION HS_2234_B2_F01_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=2 Row=L, genomic survey sequence.

ACCESSION AO153405
VERSION AO153405.1 GI:3546075
KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo
1 (bases 1 to 454)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2234 row: L column: 2
Class: BAC ends
High quality sequence stop: 454.
Location/Qualifiers
1. .454
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2234 Col=2 Row=L"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelOAC11; BAC Clones in E-Coli DH10B"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2274 GGGTTTACCGCTGTAGCCAGATGCTCGATCTCCGACCTCGATCCGCCACCTC 2333
|||||
DB 135 GGGTTTACCGCTGTAGCCAGATGCTCGATCTCCGACCTCGATCCGCCACCTC 194
|||||
OY 2334 GGCTCCCAAGTCTGGGATTACAGGC 2361
|||||
DB 195 GGCTCCCAAGTCTGGGATTACAGGC 222
|||||

RESULT 39
AL048925/c
LOCUS AL048925 474 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp434K1818_r1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION DKFZp434K1818, mRNA sequence.
VERSION AL048925
KEYWORDS AL048925.2 GI:5866752
SOURCE EST.
ORGANISM Homo sapiens (human)
Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 474)
Ostenweider,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Ostenweider, et al.)
Unpublished (1999)
On Apr 30, 1999 this sequence version replaced gi:4728234.
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA

sequencing consortium of the German Genome Project. No sl sequence available.
This clone (DKFZp434K1818) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. .474
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2274 GGGTTTACCGCTGTAGCCAGATGCTCGATCTCCGACCTCGATCCGCCACCTC 2333
|||||
DB 285 GGGTTTACCGCTGTAGCCAGATGCTCGATCTCCGACCTCGATCCGCCACCTC 226
|||||
OY 2334 GGCTCCCAAGTCTGGGATTACAGGC 2361
|||||
DB 225 GGCTCCCAAGTCTGGGATTACAGGC 198
|||||

RESULT 40
B0351361/c
LOCUS B0351361 330 bp mRNA linear EST 20-MAY-2002
DEFINITION QV0-HT0367-120600-261-e09 HT0367 Homo sapiens cDNA, mRNA sequence.
ACCESSION B0351361
VERSION B0351361.1 GI:21015417
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 330)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S.C. Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV0&r2=QV0-HT0367-120600-261-e09&t3=2000-06-12&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 330.
Location/Qualifiers
1. .330
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

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/dev_stage="Adult"  
/clone.lib="HT0367"  
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;  
Site_2: SmaI; A mini-library was made by cloning products  
derived from ORESSES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."
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ORIGIN

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Query Match          3.7%; Score 87; DB 3; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.6e-29;  
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2274 GGGTTTCAACCGTGTAGCCAGAGAGTCTCGATCTCTGACCTCGTATCGGCCACCTC 2333  
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Db 296 GGGTTTCAACCGTGTAGCCAGAGAGTCTCGATCTCTGACCTCGTATCGGCCACCTC 237  
      |||||||  
  
QY 2334 GGCTTCCCAAGTGTGGGATTACAG 2360  
      |||||||  
Db 236 GGCTTCCCAAGTGTGGGATTACAG 210  
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Search completed: August 4, 2006, 16:54:12
Job time : 11336 secs

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